Interpreting large quartet distances

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Contents

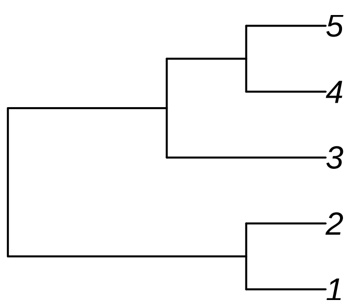
Properties of the quartet distance are explored fully in Steel (1993).
As quartet distances of 1 can only be accomplished for small trees (five or fewer leaves), it is perhaps more appropriate to consider whether or not trees are more dissimilar than a pair of random trees, whose distance will be, on average, $\frac{2}{3}$.

0.1 Minimum quartet distance

When there are six or more tips in a bifurcating tree, some quartets are necessarily shared between trees.

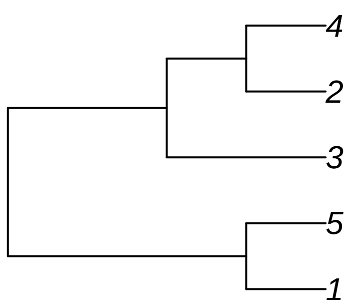
Consider the tree:

```
tree_a <- ape::read.tree(text="((1, 2), (3, (4, 5)));")
```



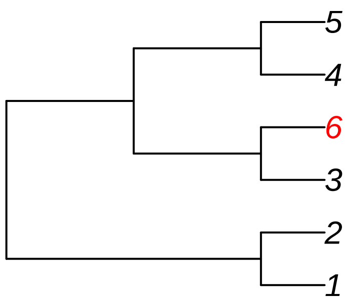
The only trees with no quartets in common with Tree A are symmetric with

```
tree_b <- ape::read.tree(text="((1, 5), (3, (2, 4)));")
```

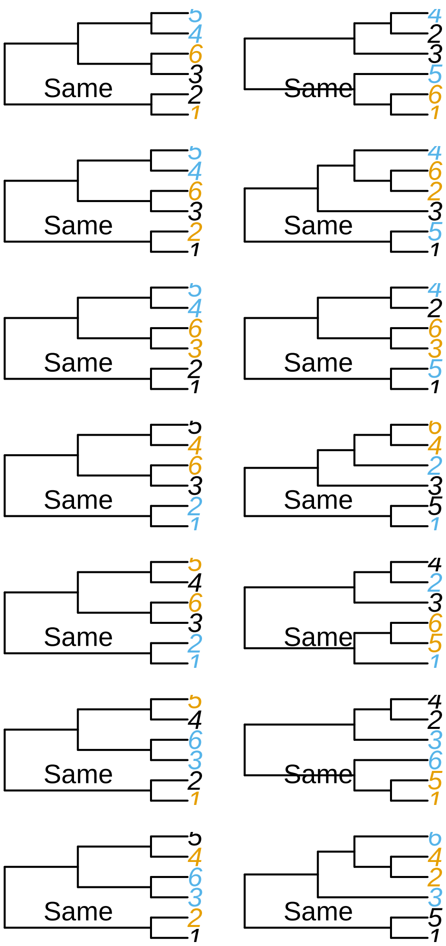


Now create Tree C by adding a 6th tip as a sister to tip `3` on Tree A.

```
tree_c <- ape::read.tree(text="((1, 2), ((3, 6), (4, 5)));")
```



There's nowhere to add tip `6` to Tree B without creating a quartet that exists in Tree C.



0.2 Quartet distance in a pair of random trees

On average, $\frac{1}{3}$ of the quartets resolved in a pair of random trees will match. This is because there are three quartets involving any set of four tips, each of which is equally likely to occur on a truly random tree.

The below code calculates the mean proportion of matching quartets for random trees with 4 to 20 tips, and the corresponding standard deviation.

```
round(vapply(4:20, function (n_tip) {
 trees <- lapply(logical(56), function (X)
   ape::rtree(n_tip, tip.label=seq_len(n_tip), br=NULL))
```

```r
 results <- QuartetStatus(trees)[1, ] / choose(n_tip, 4)
 c(mean(results[-1]), sd(results[-1]))
}, double(2)), 3)
```

```
##       [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8]  [,9] [,10] [,11]
## [1,] 0.333 0.333 0.333 0.333 0.333 0.333 0.333 0.333 0.333 0.333 0.333
## [2,] 0.516 0.516 0.516 0.516 0.516 0.516 0.516 0.516 0.516 0.516 0.516
##      [,12] [,13] [,14] [,15] [,16] [,17]
## [1,] 0.333 0.333 0.333 0.333 0.333 0.333
## [2,] 0.516 0.516 0.516 0.516 0.516 0.516
```

References

Steel, M. A., & Penny, D. (1993). Distributions of tree comparison metrics—some new results. *Systematic Biology*, *42*(2), 126–141. doi: 10.1093/sysbio/42.2.126