

# Interpreting large quartet distances

Martin R. Smith

2019-01-09

## Contents

<b>1 Properties of the quartet distance</b>	<b>1</b>
1.1 Minimum quartet distance . . . . .	1
1.2 Quartet distance in a pair of random trees . . . . .	2
References . . . . .	3

## 1 Properties of the quartet distance

Properties of the quartet distance are explored fully in Steel (1993).

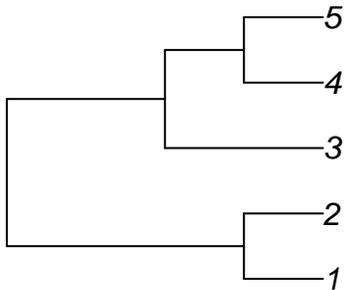
As quartet distances of 1 can only be accomplished for small trees (five or fewer tips), it is perhaps more appropriate to consider whether or not trees are more dissimilar than a pair of random trees, whose distance will be, on average,  $2/3$ .

### 1.1 Minimum quartet distance

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

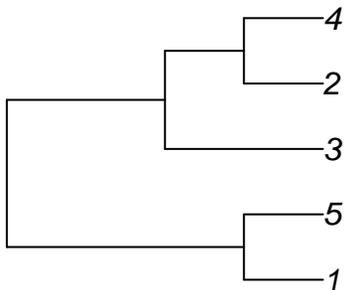
Consider the tree:

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



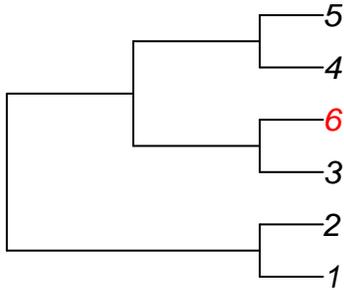
The only trees with no quartets in common with Tree A are symmetric with

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

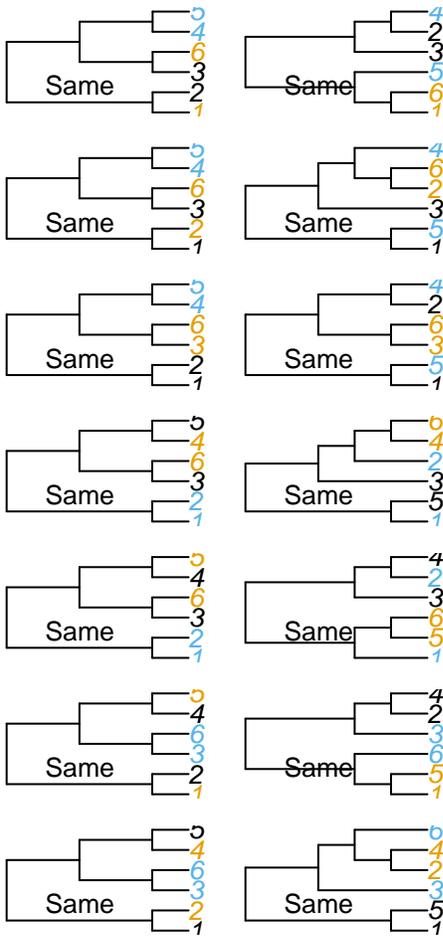


Now create Tree C by adding a 6th tip as a sister to tip 3 on Tree A.

```
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.



## 1.2 Quartet distance in a pair of random trees

On average,  $1/3$  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))
  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