Getting started with Quartet

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Contents

This document should contain all you need to get started measuring tree distances with 'Quartet'. If you get stuck, please let me know so I can improve this documentation.

Loading trees

Instructions for loading phylogenetic trees into R can be found in a separate vignette. For these examples, we'll enter two simple trees by hand:

```
tree1 <- ape::read.tree(text = '(A, ((B, (C, (D, E))), ((F, G), (H, I))));')
tree2 <- ape::read.tree(text = '(A, ((B, (C, (D, (H, I)))), ((F, G), E)));')
```

Calculating distances

We can calculate distances between pairs of trees using the 'Quartet' package.

First we'll install the package. We can either install the stable version from the CRAN repository:

```
install.packages('Quartet')
```

or the development version, from GitHub – which will contain the latest features but may not be as extensively tested:

```
devtools::install_github('ms609/Quartet')
```

Then we'll load the package into R's working environment:

```
library('Quartet')
```

Now the package's functions are available within R. Let's proceed to calculate some tree distances.

Pairs of trees

Calculating the distance between two trees is a two stage process. For a quartet distance, we first have to calculate the status of each quartet:

```
statuses <- QuartetStatus(tree1, tree2)
```

Then we convert these counts into a distance metric (or similarity measure) that suits our needs – perhaps the Quartet Divergence:

```
QuartetDivergence(statuses, similarity = FALSE)
```

```
## [1] 0.6031746
```

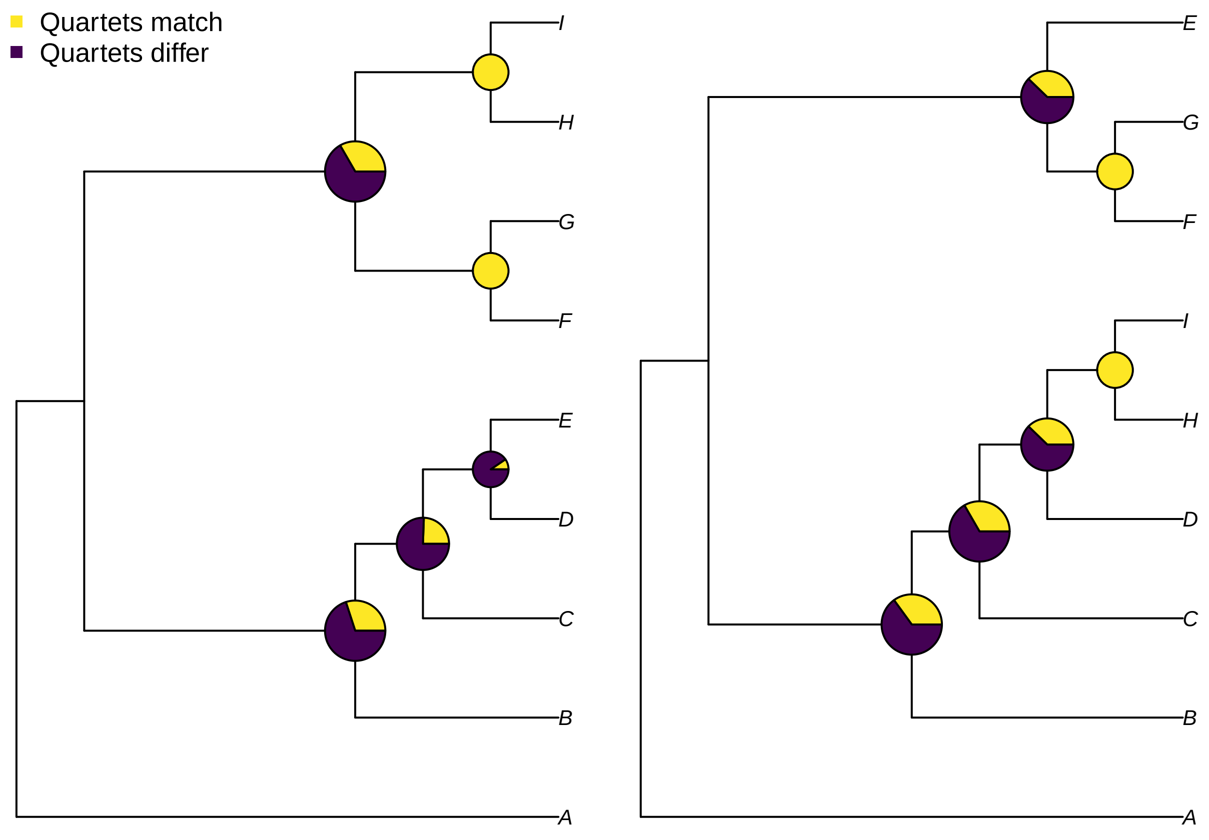
We can calculate all similarity metrics at once using:

```
SimilarityMetrics(statuses, similarity = TRUE)
```

```
##      DoNotConflict ExplicitlyAgree StrictJointAssertions
## [1,]     0.3968254       0.3968254             0.3968254
##      SemiStrictJointAssertions SymmetricDifference MarczewskiSteinhaus
## [1,]                 0.3968254           0.3968254           0.2475248
##      SteelPenny QuartetDivergence SimilarityToReference
## [1,]  0.3968254         0.3968254             0.3968254
```

It can be instructive to visualize how each split in the tree is contributing to the quartet similarity:

```
VisualizeQuartets(tree1, tree2)
```



Rather than using quartets, we might want to use partitions as the basis of our comparison:

```
SimilarityMetrics(SplitStatus(tree1, tree2))
```

```
##      DoNotConflict ExplicitlyAgree StrictJointAssertions
## [1,]     0.3333333       0.3333333             0.3333333
##      SemiStrictJointAssertions SymmetricDifference MarczewskiSteinhaus
## [1,]                 0.3333333           0.3333333                 0.2
##      SteelPenny QuartetDivergence SimilarityToReference
## [1,]  0.3333333         0.3333333             0.3333333
```

Multiple comparisons

If you have more than two trees to compare, you can send a list of trees (class: `list` or `multiPhylo`) to the distance comparison function.

You can calculate the similarity between one tree and a forest of other trees:

```
library('TreeTools', quietly = TRUE, warn.conflicts = FALSE)
oneTree <- CollapseNode(as.phylo(0, 11), 14)
twoTrees <- structure(list(bal = BalancedTree(11), pec = PectinateTree(11)),
                      class = 'multiPhylo')

status <- SharedQuartetStatus(twoTrees, cf = oneTree)
QuartetDivergence(status)
```

```
##       bal       pec
## 0.4939394 0.6272727
```

Or between one tree and (itself and) all other trees in the forest:

```
forest <- as.phylo(0:5, 11)
names(forest) <- letters[1:6]
status <- SharedQuartetStatus(forest)
QuartetDivergence(status)
```

```
##         a         b         c         d         e         f
## 1.0000000 0.9757576 0.9757576 0.9333333 0.9121212 0.9333333
```

Or between each pair of trees in a forest:

```
status <- ManyToManyQuartetAgreement(forest)
QuartetDivergence(status, similarity = FALSE)
```

```
##            a          b          c          d          e          f
## a 0.00000000 0.02424242 0.02424242 0.06666667 0.08787879 0.06666667
## b 0.02424242 0.00000000 0.02424242 0.08787879 0.06666667 0.06666667
## c 0.02424242 0.02424242 0.00000000 0.08484848 0.08484848 0.04242424
## d 0.06666667 0.08787879 0.08484848 0.00000000 0.04242424 0.04242424
## e 0.08787879 0.06666667 0.08484848 0.04242424 0.00000000 0.04242424
## f 0.06666667 0.06666667 0.04242424 0.04242424 0.04242424 0.00000000
```

Or between one list of trees and a second:

```
status <- TwoListQuartetAgreement(forest[1:4], forest[5:6])
QuartetDivergence(status, similarity = FALSE)
```

```
##            e          f
## a 0.08787879 0.06666667
## b 0.06666667 0.06666667
## c 0.08484848 0.04242424
## d 0.04242424 0.04242424
```

Other calculations

To calculate how many quartets are unique to a certain tree (akin to the partitionwise equivalent `ape::prop.clades`), use:

```
interestingTree <- as.phylo(42, 7)
referenceTrees <- list(BalancedTree(7), PectinateTree(7))
status <- CompareQuartetsMulti(interestingTree, referenceTrees)
```

`status['x_only']` = 23 quartets are resolved in a certain way in `interestingTree`, but not resolved that way in any `referenceTrees`.

What next?

You may wish to:

- Read more about Quartet distances
- Review alternative distance measures and corresponding functions
- Interpret or contextualize tree distance metrics