

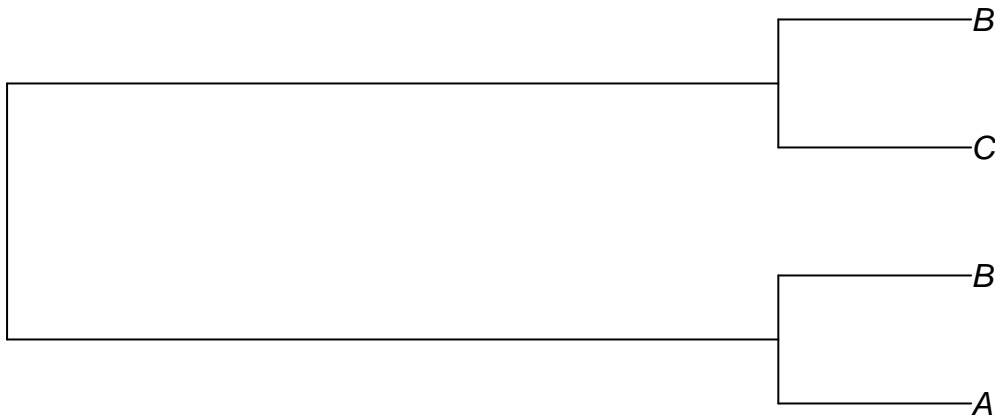
# Demonstration of the gamma statistic

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```
newick_upper <- "((A:2,B:2):8,(C:2,B:2):8);"  
phylogeny_upper <- ape::read.tree(text = newick_upper)  
gamma_upper <- ape::gammaStat(phylogeny_upper)  
plot(phylogeny_upper, main = gamma_upper)
```

**0.816496580927726**



```
newick_lower <- "((A:8,B:8):2,(C:8,B:8):2);"  
phylogeny_lower <- ape::read.tree(text = newick_lower)  
gamma_lower <- ape::gammaStat(phylogeny_lower)  
plot(phylogeny_lower, main = gamma_lower)
```

**-1.90515868883136**

