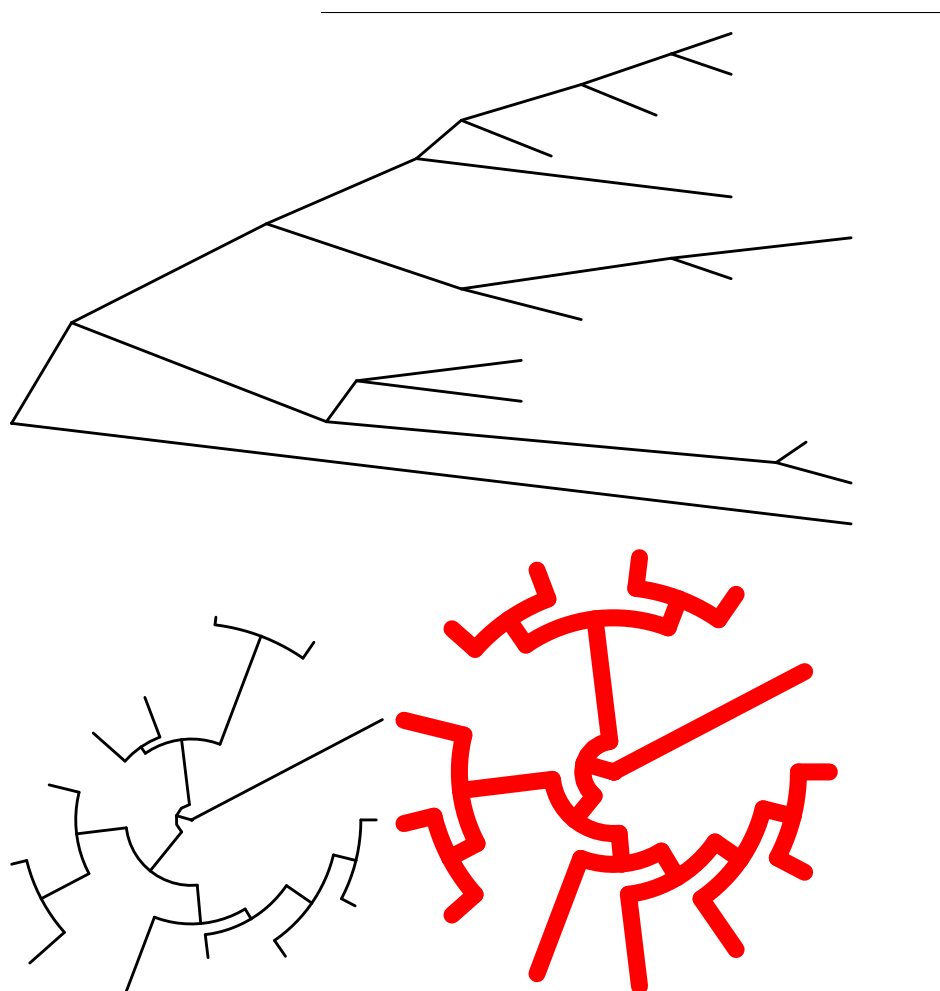


Phylogenetic trees with ggtree: Exercises

Exercise 1

Look at the help again for `?ggtree`, specifically at the `layout=` option. By default, it produces a rectangular layout.

1. Create a slanted phylogenetic tree.
2. Create a circular phylogenetic tree.
3. Create a circular unscaled cladogram with thick red lines.

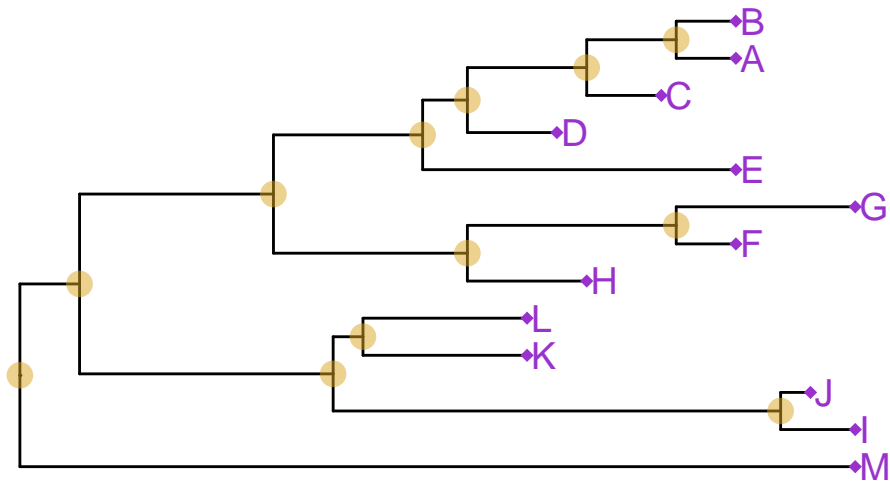


Exercise 2

Similar to how we change the aesthetics for the tree inside the `ggtree()` call, we can also change the aesthetics of the points themselves by passing graphical parameters inside the `geom_nodepoint()` or `geom_tippoint()` calls. Create a phylogeny with the following aesthetic characteristics:

- tips labeled in purple
- purple-colored diamond-shape tip points (hint: Google search “R point characters”)
- large semitransparent yellow node points (hint: `alpha=`)
- Add a title with + `ggtitle(...)`

Exercise 2 Figure: Not the prettiest phylogenetic aesthetics, b



Exercise 3

Produce the figure below.

1. First, find what the MRCA is for taxa **B+C**, and taxa **L+J**. You can do this in one of two ways:
 - a. Easiest: use `MRCA(tree, tip=c("taxon1", "taxon2"))` for B/C and L/J separately.
 - b. Alternatively: use `ggtree(tree) + geom_text(aes(label=node), hjust=-.3)` to see what the node labels are on the plot. You might also add tip labels here too.
2. Draw the tree with `ggtree(tree)`.
3. Add tip labels.
4. Highlight these clades with separate colors.
5. Add a clade label to the larger superclade (node=17) that we saw before that includes A, B, C, D, and E. You'll probably need an offset to get this looking right.
6. Link taxa C to E, and G to J with a dashed gray line (hint: get the geom working first, then try changing the aesthetics. You'll need `linetype=2` somewhere in the `geom_taxalink()`).
7. Add a scale bar to the bottom by changing the theme.
8. Add a title.
9. Optionally, go back to the original `ggtree(tree, ...)` call and change the layout to "circular".

Exercise 3 title: Not sure what we're trying to show here...

