a b

## Run the below code in your R console

# 1). Install devtools package

install.packages("devtools", dep=T)

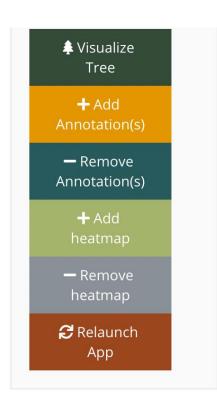
### 2). Install ggtree and treeio

if (!requireNamespace("BiocManager")
install.packages("BiocManager")
BiocManager::install("ggtree")

Note – this will install both ggtree and treeio

# 3). Install & launch the tinselR app

devtools::install\_github("jennahamlin/tinselR")
library(tinselR)
run app()



#### **Tree Display**

