a

Run the below code in your R console

Require R >= 3.6

1). Install devtools package
install.packages("devtools", dep=T)

2). Install ggtree and treeio
if (!requireNamespace("BiocManager")
install.packages("BiocManager")
BiocManager::install("ggtree")
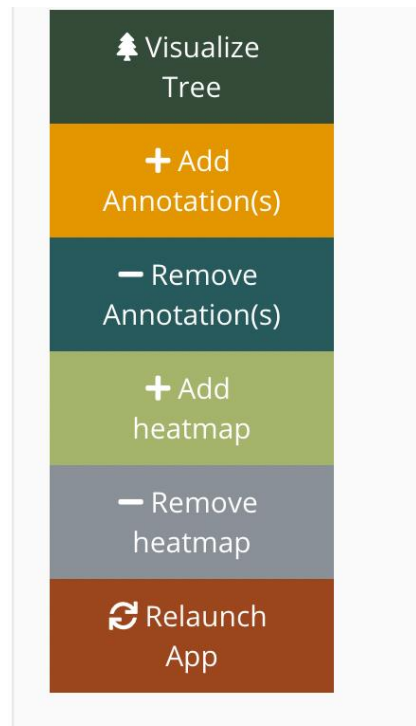
Note – this will install both ggtree and treeio

3). Install & launch the tinselR app
devtools::install_github("jennahamlin/tinselR")
library(tinselR)
run_app()

b