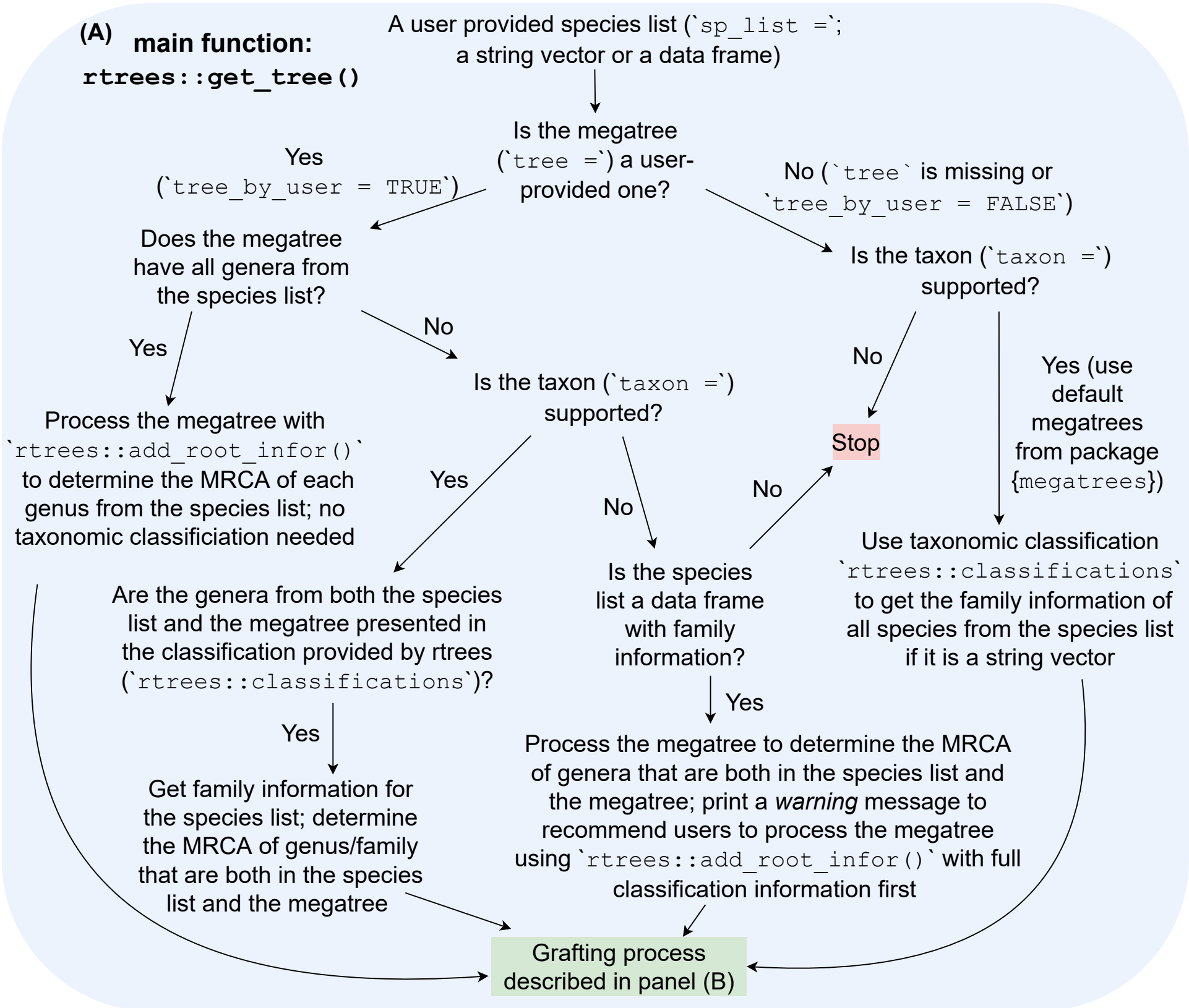


(A) main function:
`rtrees::get_tree()`



(B) Comparing species list to determine missing species that are needed to be grafted to the megatree

