Look for shared taxa throughout the tree

F = Family
G = Genus
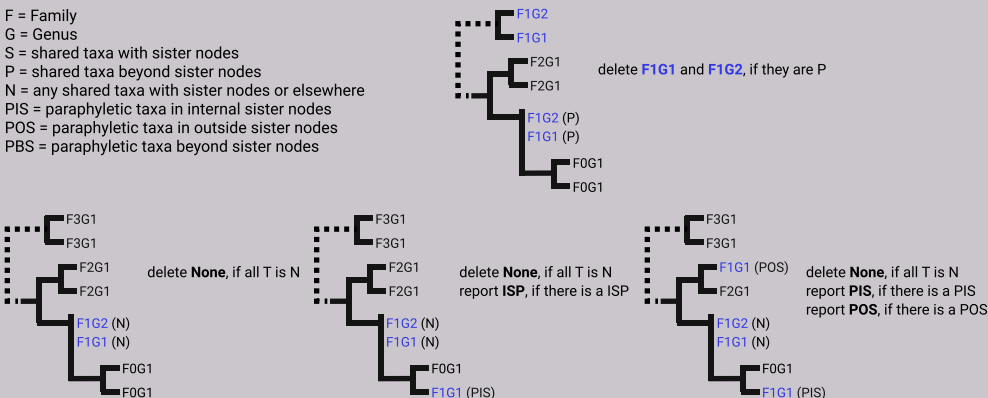S = shared taxa with sister nodes
P = shared taxa beyond sister nodes
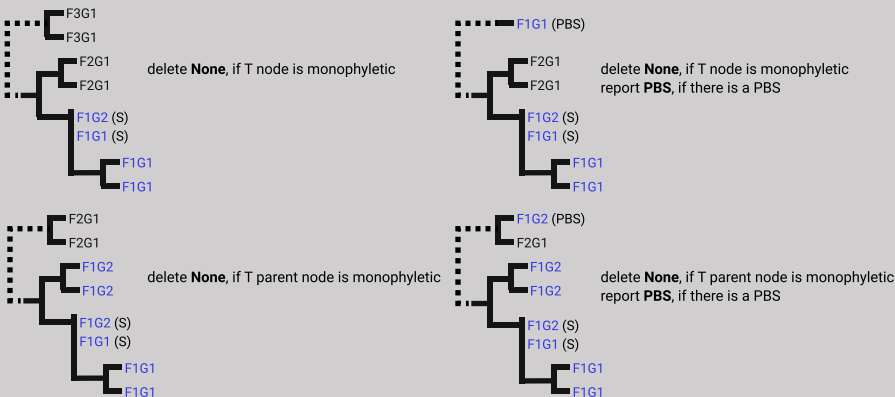N = any shared taxa with sister nodes or elsewhere
PIS = paraphyletic taxa in internal sister nodes
POS = paraphyletic taxa in outside sister nodes
PBS = paraphyletic taxa beyond sister nodes

F1G2
F1G1
F2G1
F2G1
F1G2 (P)
F1G1 (P)
F0G1
F0G1

delete **F1G1** and **F1G2**, if they are P

F3G1
F3G1
F2G1
F2G1
F1G2 (N)
F1G1 (N)
F0G1
F0G1

delete **None**, if all T is N

F3G1
F3G1
F2G1
F2G1
F1G2 (N)
F1G1 (N)
F0G1
F1G1 (PIS)

delete **None**, if all T is N
report **ISP**, if there is a ISP

F3G1
F3G1
F1G1 (POS)
F2G1
F1G2 (N)
F1G1 (N)
F0G1
F1G1 (PIS)

delete **None**, if all T is N
report **PIS**, if there is a PIS
report **POS**, if there is a POS

Look for monophyletic groups around the T node

F3G1
F3G1
F2G1
F2G1
F1G2 (S)
F1G1 (S)
F1G1
F1G1

delete **None**, if T node is monophyletic

F1G1 (PBS)
F2G1
F2G1
F1G2 (S)
F1G1 (S)
F1G1
F1G1

delete **None**, if T node is monophyletic
report **PBS**, if there is a PBS

F2G1
F2G1
F1G2
F1G2
F1G2 (S)
F1G1 (S)
F1G1
F1G1

delete **None**, if T parent node is monophyletic

F1G2 (PBS)
F2G1
F1G2
F1G2
F1G2 (S)
F1G1 (S)
F1G1
F1G1

delete **None**, if T parent node is monophyletic
report **PBS**, if there is a PBS

Look for shared taxa in sister nodes

F2G1
F2G1
F1G2
F1G1
F1G2 (S)
F1G1 (S)
F0G1
F0G1

delete **F1G1** and **F1G2**, if they are S

F3G1
F3G1
F2G1
F2G1
F1G2 (S)
F1G1 (S)
F0G1
F1G1
F2G1

delete **F1G1** and **F1G2**, if they are S