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| **Smaller Tree (Arafat Sir)** | **Larger tree (Me+Chatgpt)** |
| **sal.tree = read.tree('test\_salmonella\_with\_ERRiiiiiiiiiiiii\_outgroup3.nex.treefile')**  **sal.meta = read.table('metadata.csv', sep=',', header=T)**  **sal.tree = midpoint(sal.tree)**  **sal.tree = read.iqtree ('test\_salmonella\_with\_ERRiiiiiiiiiiiii\_outgroup3.nex.treefile')**  **sal.tree@phylo = midpoint(sal.tree@phylo)**  **plot(sal.tree@phylo)**  **# 3.Ornamenting phylogenetic tree with metadata**  **t1 = ggtree(sal.tree) %<+% sal.meta +**  **geom\_tippoint(aes(color = Source), size = 2)**  **t1**  **# 4.Circular phylogenetic tree**  **t1 = ggtree(sal.tree, layout="circular") %<+% sal.meta +**  **geom\_tippoint(aes(color = Source), size = 2)**  **t1**  **# 5.Add bootstrap support**  **t1$data$bootstrap <- '0'**  **t1$data[which(t1$data$SH\_aLRT >= 70 & t1$data$UFboot >= 70),]$bootstrap <- '1'**  **t1 <- t1 + new\_scale\_color() +**    **geom\_tree(aes(color=bootstrap == '1')) +**    **scale\_color\_manual(name='Bootstrap', values=setNames( c('black', 'grey'), c(T,F)), guide = "none")**  **t1**  **# 6.Showing metadata in heatmap**  **# dataframe generation**  **meta.Susceptiblity <- as.data.frame(sal.meta[,'Susceptiblity'])**  **colnames(meta.Susceptiblity) <- 'Susceptiblity'**  **rownames(meta.Susceptiblity) <- sal.meta$Strain**  **meta.year <- as.data.frame(sal.meta[,'Year'])**  **colnames(meta.year) <- 'Year'**  **rownames(meta.year) <- sal.meta$Strain**  **# 7.Heatmap generation**  **# Categorical variable**  **t2 <- gheatmap(t1, meta.Susceptiblity, width = 9, offset = 0.51) +**  **scale\_fill\_viridis\_d(option="A", name="Susceptiblity") +**  **new\_scale\_fill()**  **# Continuous variable**  **t2 <- gheatmap(t2, meta.year, width= 7, offset=0.81) +**  **scale\_fill\_viridis(option="D", name="Year")**  **# 8.Plot tiplab2**  **t2 + geom\_tiplab2(aes(label=Country), color="gray40", offset=0.06, size=3)** | **# 4.Circular phylogenetic tree**  **p <- ggtree(tree, layout = "circular", size = 0.8)**  **%<+% meta +**  **geom\_tippoint(aes(color = Source), size = 2.5) +**  **theme(legend.position = "right")**  **p**  **[here size makes bold the branch and sub branch line of the tree]**  **# 5.Add bootstrap support**  **p$data$bootstrap <- '0'**  **p$data[which(p$data$SH\_aLRT >= 70 & p$data$UFboot >= 70),]$bootstrap <- '1'**  **p <- p + new\_scale\_color() +**  **geom\_tree(aes(color = bootstrap == "1"), size = 0.9) +**  **scale\_color\_manual(name = "Bootstrap", values = c("TRUE" = "black", "FALSE" = "gray70"), guide = "none")**  **p**  **[here-**  **geom\_tree(aes(color = bootstrap == "1"), size = 0.9) = increased the boldness of treeline]**  **# 6.Showing metadata in heatmap**  **meta.sus <- data.frame(Susceptibility = meta$Susceptiblity)**  **rownames(meta.sus) <- meta$Strain**  **meta.year <- data.frame(Year = meta$Year)**  **rownames(meta.year) <- meta$Strain**  **p1 <- gheatmap(p, meta.sus, offset = 1.9, width = 0.32, colnames = FALSE) +**  **scale\_fill\_viridis\_d(option = "A", name = "Susceptibility") +**  **new\_scale\_fill()**  **p2 <- gheatmap(p1, meta.year, offset = 2.6, width = 0.24, colnames = FALSE) +**  **scale\_fill\_viridis(option = "D", name = "Year")**  **final\_plot <- p2 +**  **geom\_tiplab2(aes(label = Country), offset = 0.60, size = 2.5, color = "gray40")**  **final\_plot** |