Assignment08

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Github link:

https://github.com/amyrewells/biol432_As08.git

Load libraries

```r
library(ape)
library(ggplot2)
library(viridis)
```

```
## Loading required package: viridisLite
```

```r
library(reshape2)
library(BiocManager)
```

```
## Bioconductor version '3.16' is out-of-date; the current release version '3.20'
##   is available with R version '4.4'; see https://bioconductor.org/install
```

```r
library(ggtree)
```

```
## Registered S3 methods overwritten by 'treeio':
##   method              from
##   MRCA.phylo          tidytree
##   MRCA.treedata       tidytree
##   Nnode.treedata      tidytree
##   Ntip.treedata       tidytree
##   ancestor.phylo      tidytree
##   ancestor.treedata   tidytree
##   child.phylo         tidytree
##   child.treedata      tidytree
##   full_join.phylo     tidytree
##   full_join.treedata  tidytree
##   groupClade.phylo    tidytree
##   groupClade.treedata tidytree
##   groupOTU.phylo      tidytree
##   groupOTU.treedata   tidytree
##   is.rooted.treedata  tidytree
##   nodeid.phylo        tidytree
##   nodeid.treedata     tidytree
##   nodelab.phylo       tidytree
##   nodelab.treedata    tidytree
##   offspring.phylo     tidytree
##   offspring.treedata  tidytree
##   parent.phylo        tidytree
```

```
##    parent.treedata      tidytree
##    root.treedata        tidytree
##    rootnode.phylo       tidytree
##    sibling.phylo        tidytree

## ggtree v3.15.0 Learn more at https://yulab-smu.top/contribution-tree-data/
##
## Please cite:
##
## Guangchuang Yu.  Data Integration, Manipulation and Visualization of
## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022,
## doi:10.1201/9781003279242, ISBN: 9781032233574

##
## Attaching package: 'ggtree'

## The following object is masked from 'package:ape':
##
##     rotate
```

New dragon traits

Trait	Dragon 1	Dragon 2	Dragon 3
Appendages	Four, 1001	Two, 1101	Four, 1001
Mass	1-2x human,0011	>4x human,1111	1/4 human,0000
Body	Rotund,00	Snakelike,11	Elongate,01
Claw	Absent,0000	Long Catlike,1100	Absent,0000
Dorsal ridges	Absent,000000	Absent,000000	Absent,000000
Ear morphology	Spearlike,010	Other,001	Round or Small,100
Eye morphology	Large,001	Avg,000	Avg,000
Eye position	Forward,1	Lateral,0	Lateral,0
Horn type	Absent,000	Med/Long,110	Jagged/Antlers,111
Nose Position	NA,?	NA,?	NA,?
Nasal morphology	other,0	Upturned,1	other,0
Skin-dorsal	Hairy,000110	Smooth Skin,110000	Fish Scales,000000
Skin-head	Smooth Skin,110000	Smooth Skin,110000	Smooth Skin,110000
Skin-ventral	Hairy,000110	Plates,000001	Fish Scales,000000
Snout type	Absent,0000	Moderate,1100	Moderate,1100
Tail type	Sepear,01	Blunt/Point,10	Blunt/Point,10
Teeth	NA,????	Blunt Only,1100	Pointy Only,0000
Toes-opposing	No,1	No,1	Yes,0
Toe Number	Four,1100002	Three,111000	Four,110000
Tongue length	Short,0	NA,?	NA,?
Tongue morphology	Forked,01	NA,??	NA,??
Ventral plates	No,0	Yes,1	No,0
Whiskers	Long,11	Absent,00	Absent,00
Wing structure	Full,11	Full,11	Full,11
Wing type	Hybrid,001	NA,???	Bat,100

Notes: I do not understand the difference between a lateral ad forward nose, so this row is left as NAs. The wing type of Dragon 2 does not fit with the classification, so NA is assigned.

Append dragons to Nexus

```r
Dragon1<-c("0010011000000000000100011000?00001101100000001100000001????1110000200101111001")
Dragon1_list <- strsplit(Dragon1, split = "")[[1]]

Dragon2<-c("110111111111100000000001000011O?1110000110000000001110010110011111000???10011???")
Dragon2_list <- strsplit(Dragon2, split = "")[[1]]

Dragon3<-c("100100000100000000001000000111?0000000110000000000110010000001100000???00011100")
Dragon3_list <- strsplit(Dragon3, split = "")[[1]]
```

create list to store info on each dragon

```r
DragonNexus<-read.nexus.data("./data/DragonMatrix.nex")

DragonNexus$"75American" <- c(DragonNexus$"75American", Dragon1_list)
DragonNexus$"76American" <- c(DragonNexus$"76American", Dragon2_list)
DragonNexus$"77American" <- c(DragonNexus$"77American", Dragon3_list)
```

append

```r
write.nexus.data(DragonNexus, file = "./input/NewDragonNexus.nex")
```

save as new .nex file

add weights

```r
WeightsDat<-read.csv("./data/Weights.csv")
Weights<-paste0(WeightsDat$Weight,collapse="")
Weights<-strsplit(Weights,split="")[[1]]
```

create single vector of weights

```r
WeightsNum<-rep(NA,length(Weights))

for(i in 1:length(WeightsNum)){
  if(Weights[i] %in% LETTERS){
    WeightsNum[i]<-which(LETTERS==Weights[i])+9
    }
  else {
    WeightsNum[i]<-Weights[i]}}

WeightsNum<-as.numeric(WeightsNum)
```

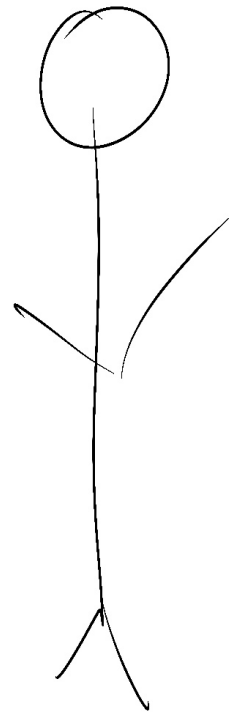convert letter to weight value

```r
WtDragonNexus<-DragonNexus

for (i in 1:length(DragonNexus)){
  RepWeight<-DragonNexus[[i]]==1
```
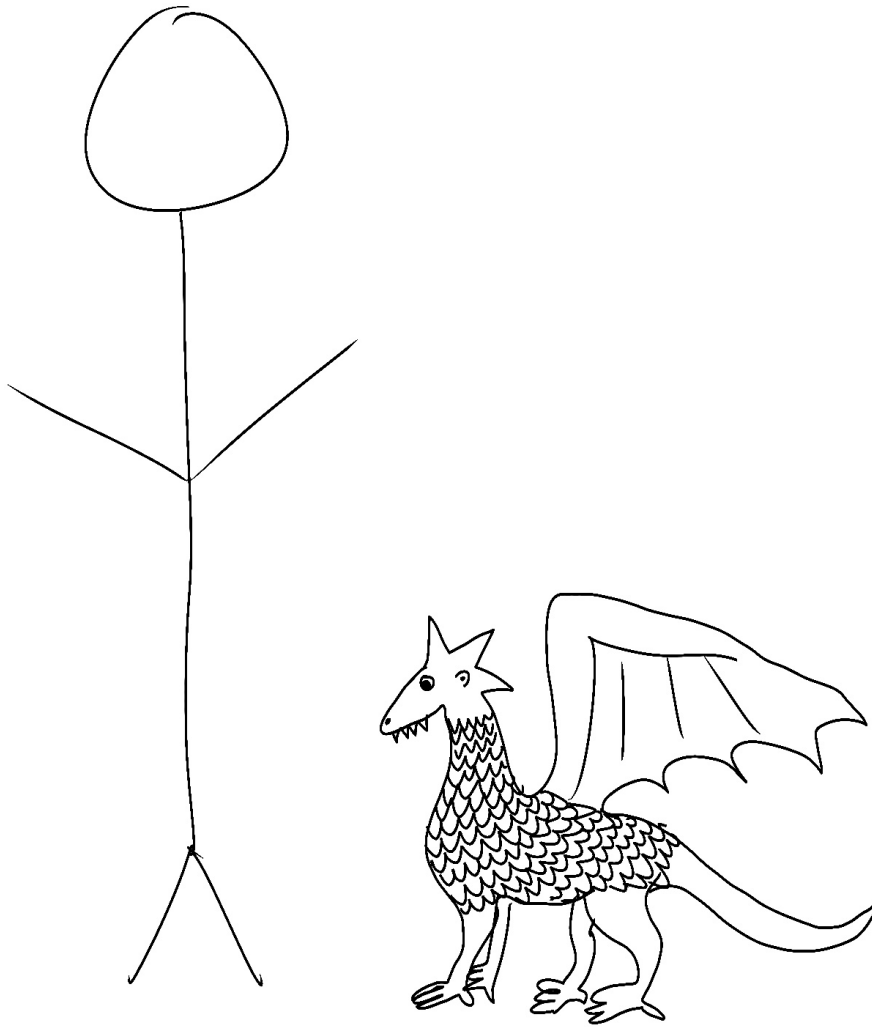
```
WtDragonNexus[[i]][RepWeight]<-WeightsNum[RepWeight]
RepWeight<-NA}
```

multiply by weight

images of Dragons

Create a visually attractive phylogeny. Use coloured lines to highlight the lineages where your dragons appear on the Dragon Phylogeny.

phylogeny

```
WtDragonNexusDF<-data.frame(matrix(unlist(WtDragonNexus),ncol=78,byrow=T))
row.names(WtDragonNexusDF)<-names(WtDragonNexus)

WtDragonDist<-dist(WtDragonNexusDF,method='euclidean')
```

create distance matrix

```
## Warning in dist(WtDragonNexusDF, method = "euclidean"): NAs introduced by
## coercion
```

```
WtDragonDistMat<-as.matrix(WtDragonDist)

WtPDat<-melt(WtDragonDistMat)
names(WtPDat)<-c("Query","Subject","Distance")

ggplot(data = WtPDat, aes(x=Query, y=Subject, fill=Distance)) +
  geom_tile() +
  scale_fill_viridis(option="magma") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5))
```
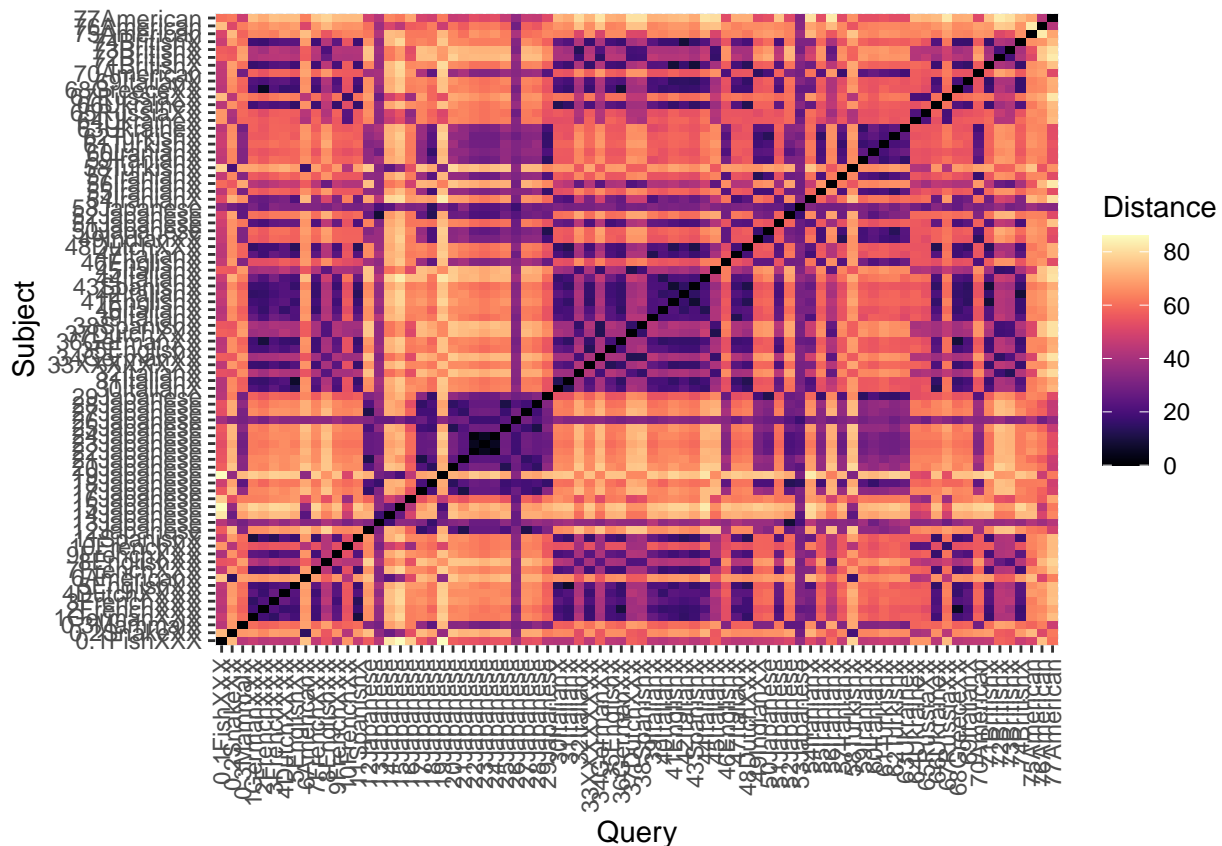

Figure 1. Weighed Distance Matrix of Dragon phylogenies. Weighs were assigned to morphological traits based on the how conserved they are across evolution, with more highly conserved traits having a higher

weight.

```
WtDragonTree<-nj(WtDragonDist)

tree<- ggtree(WtDragonTree, layout="rectangular") +
  geom_nodelab(aes(x=branch,label=node), vjust=0, size=2)+
  geom_tiplab(size = 3, color = "lightblue")

print(tree)
```


create simple tree
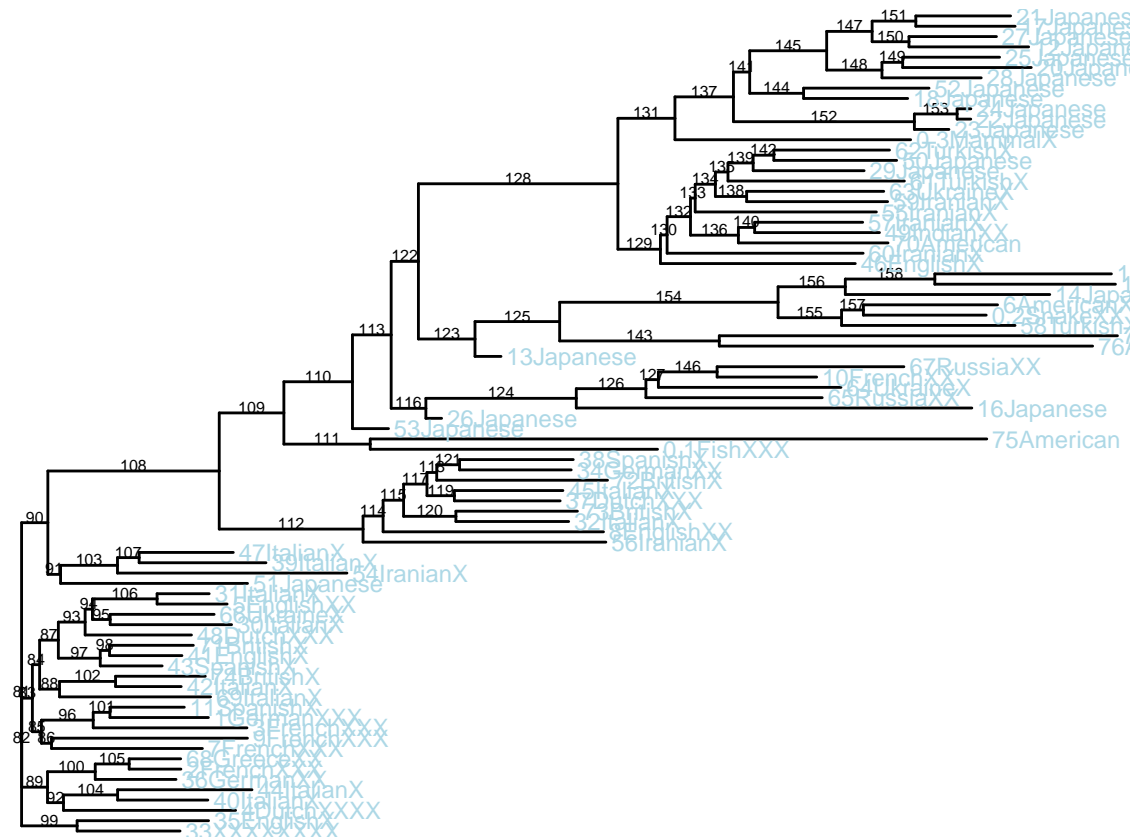
```
dragon_tips<- c("75American", "76American", "77American")
tip_labels <- tree$data$label
group <- ifelse(tip_labels %in% dragon_tips, "New", "Original")
tree$data$group <- group
```

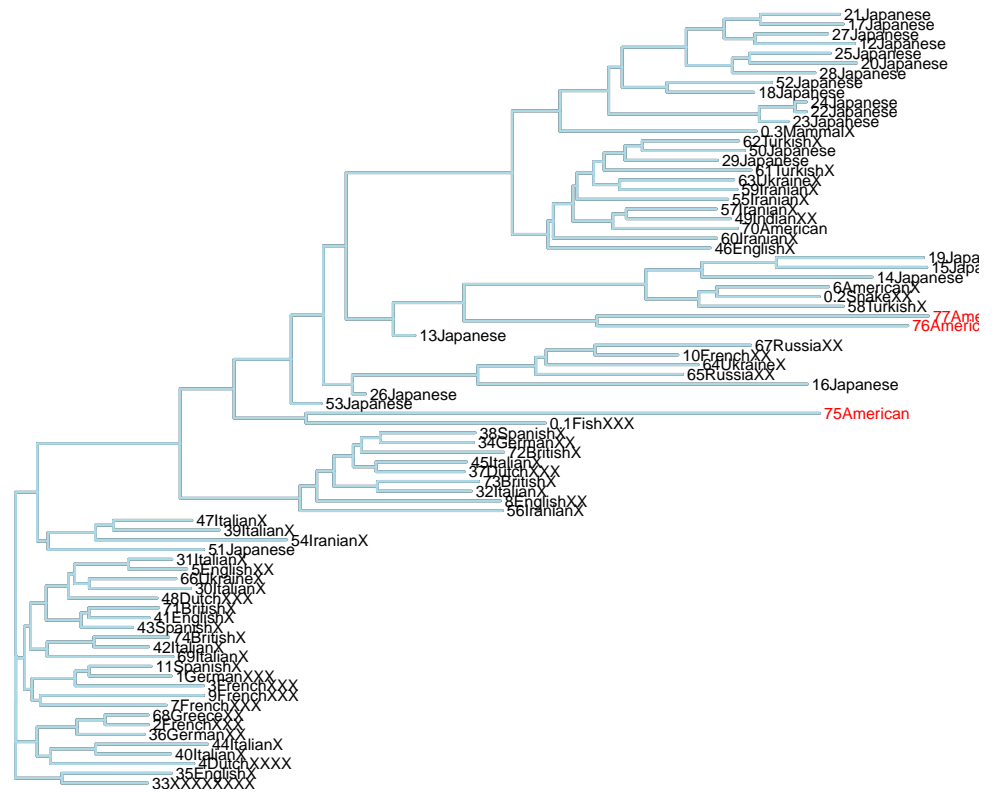**add group to distinguish recently added dragons**

```
better_tree <- ggtree(WtDragonTree, layout = "rectangular") +
  geom_tiplab(aes(color = group), size = 2) +
  geom_tree(color = "lightblue") +
  theme_tree() +
  scale_color_manual(values = c("New" = "red", "Original" = "black"))+
  labs(title = "Dragon Phylogeny")
```

```
print(better_tree)
```

Dragon Phylogeny

create better phylogeny

Figure 2. Dragon Phylogeny based on morphological traits. Newly classified dragons are highlighed in red. Phylogeny contains 80 Dragons total.

Interpretation

Dragon 2 and Dragon 3 are more closely related to eachother than either are to Dragon 1. This is based on morphological traits, however, so classification may improve once genetic evidence becomes available.