```
library(ape)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

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

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(reshape2)
library(ggplot2)
library(BiocManager)
install("ggtree")
```

```
## Bioconductor version 3.16 (BiocManager 1.30.19), R 4.2.2 (2022-10-31 ucrt)
```

```
## Warning: package(s) not installed when version(s) same as or greater than current; use
##   `force = TRUE` to re-install: 'ggtree'
```

```
## Installation paths not writeable, unable to update packages
##   path: C:/Program Files/R/R-4.2.2/library
##   packages:
##     boot, class, codetools, foreign, MASS, Matrix, nlme, spatial, survival
```

```
## Old packages: 'BiocManager', 'classInt', 'fastmap', 'haven', 'utf8', 'xfun'
```

```
library(ggtree)
```

```
## ggtree v3.6.2 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
##
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.
## ggtree: an R package for visualization and annotation of phylogenetic
## trees with their covariates and other associated data. Methods in
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628
##
## Shuangbin Xu, Lin Li, Xiao Luo, Meijun Chen, Wenli Tang, Li Zhan, Zehan
## Dai, Tommy T. Lam, Yi Guan, Guangchuang Yu. Ggtree: A serialized data
## object for visualization of a phylogenetic tree and annotation data.
## iMeta 2022, 4(1):e56. doi:10.1002/imt2.56
##
## Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods
## for mapping and visualizing associated data on phylogeny using ggtree.
## Molecular Biology and Evolution. 2018, 35(12):3041-3043.
## doi:10.1093/molbev/msy194
```

```
##
## Attaching package: 'ggtree'
```

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

Append new dragons to the nexus dataset

```
DragonNexus <- read.nexus.data("C:/Users/kerri/OneDrive - Queen's University/5th year/Winter/BIOL432/Extra/data/DragonMatri
x.nex")

DragonNexusDF <- data.frame(matrix(unlist(DragonNexus), ncol = 78, byrow = T))
row.names(DragonNexusDF) <- names(DragonNexus)

d1 <- strsplit("100100010000100110000100011110111000001010000000011000101000011110000??10000000", split = "")[[1]]
d2 <- strsplit("100111110111000100100000101110101010000001001000001000100001011100001??00011010", split = "")[[1]]
d3 <- strsplit("100111110110000110000101001101111000000010000000111000100110110000???10011100", split = "")[[1]]

DragonsNew <- list(d1,d2,d3)
DragonNexusNew <- c(DragonNexus, DragonsNew)
names(DragonNexusNew)[78:80] <- c("75Dragon1X", "76Dragon2X", "77Dragon3X")

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

Trait weightings

```
WeightsDat <- read.csv("C:/Users/kerri/OneDrive - Queen's University/5th year/Winter/BIOL432/Extra/data/Weights.csv")
weights <- paste0(WeightsDat$Weight, collapse = "")
weights <- strsplit(weights, split = "")[[1]]

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)
length(weightsnum)
```

```
## [1] 78
```

```
#multiply weight value by trait vector
WtDragonNexus <- DragonNexusNew

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

Dragon 1 https://cdn.pixabay.com/photo/2023/01/07/09/20/ai-generated-7702855__340.jpg (https://cdn.pixabay.com/photo/2023/01/07/09/20/ai-generated-7702855__340.jpg) Dragon 2 https://images-wixmp-ed30a86b8c4ca887773594c2.wixmp.com/f/4a7e0b9d-26a5-4d59-b0e9-4ca9f3724ff2/drpuu9-c8ae732f-0ed6-45e5-b738-5b1d01966b08.png?token=eyJ0eXAiOiJKV1QiLCJhbGciOiJIUzI1NiJ9.eyJzdWIiOiJ1cm46YXBwOjdlMGQxODg5ODIyNjQzNzNhNWYwZDQxNWVhMGQyNmUwIiwiaXNzIjoidXJuOmFwFv iD796tmBex_Trmt-4R3KIvWXQmodi9EE6-w (https://images-wixmp-ed30a86b8c4ca887773594c2.wixmp.com/f/4a7e0b9d-26a5-4d59-b0e9-4ca9f3724ff2/drpuu9-c8ae732f-0ed6-45e5-b738-5b1d01966b08.png?token=eyJ0eXAiOiJKV1QiLCJhbGciOiJIUzI1NiJ9.eyJzdWIiOiJ1cm46YXBwOjdlMGQxODg5ODIyNjQzNzNhNWYwZDQxNWVhMGQyNmUwIiwiaXNzIjoidXJuOmFwFv iD796tmBex_Trmt-4R3KIvWXQmodi9EE6-w) Dragon 3 https://static.wikia.nocookie.net/seraphina/images/b/b2/Dragonseraphina.jpg/revision/latest/scale-to-width-down/1200?cb=20160103194957 (https://static.wikia.nocookie.net/seraphina/images/b/b2/Dragonseraphina.jpg/revision/latest/scale-to-width-down/1200?cb=20160103194957)

Phylogeny

```
WtDragonNexusDF <- data.frame(matrix(unlist(WtDragonNexus), ncol = 78, byrow = T))
row.names(WtDragonNexusDF) <- names(WtDragonNexus)
WtDragonDist <- dist(WtDragonNexusDF, method = 'euclidean')
```

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

```
WtDragonTreeNJ <- nj(WtDragonDist)

ggtree(WtDragonTreeNJ, layout = "rectangular") +
  geom_tiplab(size = 3) +
  geom_hilight(node = 78, fill = "red")+
  geom_hilight(node = 79, fill = "green") +
  geom_hilight(node = 80, fill = "blue") +
  geom_hilight(node = 145, fill = "grey")
```

```
## ! The tree contained negative edge length. If you want to ignore the edge, you
## can set `options(ignore.negative.edge=TRUE)`, then re-run ggtree.
```
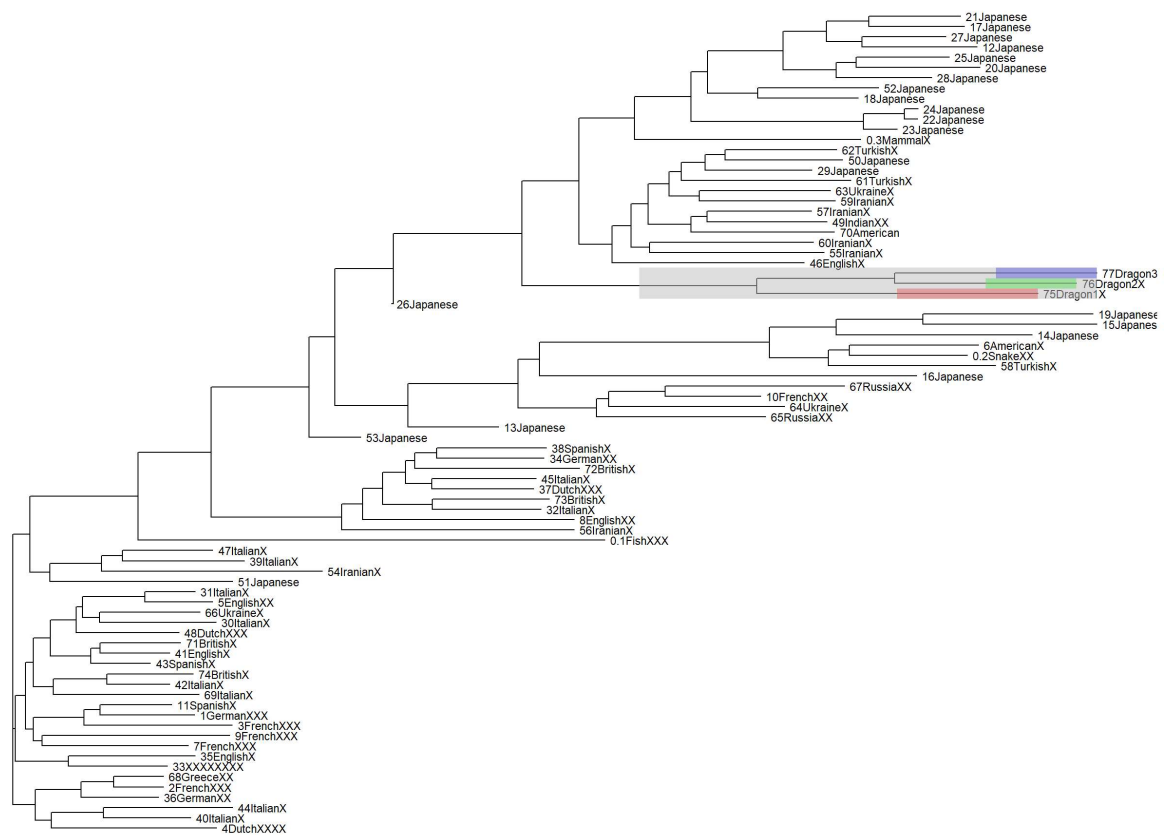

Figure 1. Phylogeny showing the relatedness of dragons and three other species from different countries (n = 78). The coloured boxes represents the position of each added dragon, as well as the overall clade they belong to.

Data interpretation

The added dragons have fairly similar traits with only a few differences between them. All three added dragons form their own clade and have diverged from dragobs from other countries. Dragon 2 and dragon 3 are the closest of the three suggesting that they originate from the same country. Dragon 1 isn't very different from the other two dragons so it's possible that it also originates from the same country, but perhaps a distant region.