## A7\_Pollock\_Caleb

### 2023-02-28

https://github.com/caleb-pollock/BIOL432\_Assignment7 (https://github.com/caleb-pollock/BIOL432\_Assignment7)

This code chunk is responsible for adding the new dragon taxa into the .nex file.

```
library(ape)
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
##
## LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR
## Jones, T Bradley, H Zhu, Y Guan, Y Jiang, G Yu. treeio: an R package
## for phylogenetic tree input and output with richly annotated and
## associated data. Molecular Biology and Evolution. 2020, 37(2):599-603.
## doi: 10.1093/molbev/msz240
##
## 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
```

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

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

```
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
##
# import the data using ape
dat <- readLines("C:/Users/omgwh/OneDrive/Desktop/BIOL432_Assignment7/input/DragonMatrix.nex")</pre>
# new dragon taxa
newDragons <- c(
 )
# appends the new dragons above the 0.1FishXXX and below the matrix
matrixFind <- grep("0.1FishXXX", dat)</pre>
# updates the taxa number
dat <- gsub("ntax=77", "ntax=80",dat)</pre>
# splits until matrixFind, then adds new data, then adds everything back
dat <- c(dat[1:matrixFind-1], newDragons, dat[matrixFind:length(dat)])</pre>
# write to .nex
```

This next code chunk will import the nexus data and observe the structure.

```
DragonNexus <- read.nexus.data("C:/Users/omgwh/OneDrive/Desktop/BIOL432_Assignment7/input/Dragon
Matrix.nex")
head(DragonNexus)</pre>
```

writeLines(dat, "C:/Users/omgwh/OneDrive/Desktop/BIOL432 Assignment7/input/DragonMatrix.nex")

```
## $EldenRing1
## [77] "0" "1"
## $MalvgosWoW
## [77] "0" "1"
##
## $Sartharion
## [77] "0" "0"
##
## $`0.1FishXXX`
## [77] "0" "0"
##
## $`0.2SnakeXX`
## [77] "0" "0"
##
## $`0.3MammalX`
## [77] "0" "0"
```

```
names(DragonNexus)
```

```
[1] "EldenRing1" "MalygosWoW" "Sartharion" "0.1FishXXX" "0.2SnakeXX"
   [6] "0.3MammalX" "1GermanXXX" "2FrenchXXX" "3FrenchXXX" "4DutchXXXX"
## [11] "5EnglishXX" "6AmericanX" "7FrenchXXX" "8EnglishXX" "9FrenchXXX"
## [16] "10FrenchXX" "11SpanishX" "12Japanese" "13Japanese" "14Japanese"
## [21] "15Japanese" "16Japanese" "17Japanese" "18Japanese" "19Japanese"
## [26] "20Japanese" "21Japanese" "22Japanese" "23Japanese" "24Japanese"
## [31] "25Japanese" "26Japanese" "27Japanese" "28Japanese" "29Japanese"
## [36] "30ItalianX" "31ItalianX" "32ItalianX" "33XXXXXXXXX" "34GermanXX"
## [41] "35EnglishX" "36GermanXX" "37DutchXXX" "38SpanishX" "39ItalianX"
## [46] "40ItalianX" "41EnglishX" "42ItalianX" "43SpanishX" "44ItalianX"
## [51] "45ItalianX" "46EnglishX" "47ItalianX" "48DutchXXX" "49IndianXX"
## [56] "50Japanese" "51Japanese" "52Japanese" "53Japanese" "54IranianX"
## [61] "55IranianX" "56IranianX" "57IranianX" "58TurkishX" "59IranianX"
## [66] "60IranianX" "61TurkishX" "62TurkishX" "63UkraineX" "64UkraineX"
## [71] "65RussiaXX" "66UkraineX" "67RussiaXX" "68GreeceXX" "69ItalianX"
## [76] "70American" "71BritishX" "72BritishX" "73BritishX" "74BritishX"
```

We will import the weights.csv data and apply it to the DragonNexus data

```
# import weights
WeightsDat <- read.csv("C:/Users/omgwh/OneDrive/Desktop/BIOL432_Assignment7/data/Weights.csv")
# from tutorial, applying the weights to each of the traits
Weights <- paste@(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)</pre>
```

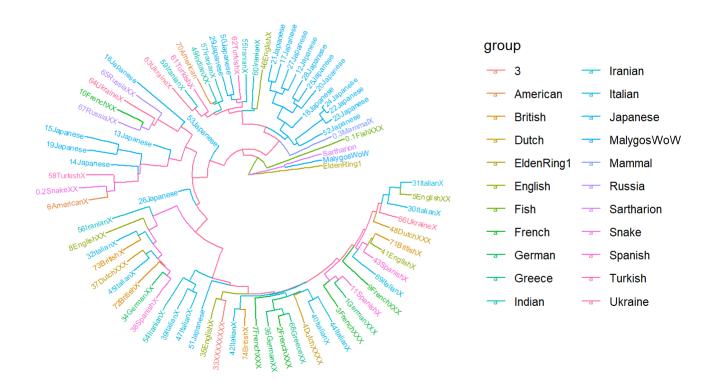
```
## [1] 78
```

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

Converting into a dataframe

```
WtDragonNexusDF <- data.frame(matrix(unlist(WtDragonNexus),ncol=78, byrow=T))</pre>
row.names(WtDragonNexusDF) <- names(WtDragonNexus)</pre>
WtDragonDist<-dist(WtDragonNexusDF, method='euclidean')</pre>
## Warning in dist(WtDragonNexusDF, method = "euclidean"): NAs introduced by
## coercion
WtDragonDistMat <- as.matrix(WtDragonDist)</pre>
              <- fastme.bal(WtDragonDist)</pre>
WtDragonTree
WtDragonTreeNJ <- nj(WtDragonDist)</pre>
Country <-gsub("[0-9\\.]+([^X]+)X*","\label)
CountryGroups <- split(WtDragonTree$tip.label, Country)</pre>
WtDTcol <- groupOTU(WtDragonTree, CountryGroups)</pre>
str(WtDTcol)
## List of 4
## $ edge
                 : int [1:157, 1:2] 81 81 82 83 84 84 85 86 87 87 ...
## $ edge.length: num [1:157] 22.63 6.03 1.91 5.97 13.87 ...
```

```
ggtree(WtDTcol, layout="circular",aes(colour=group)) +
  geom_tiplab(size=2, aes(angle=angle))
```



# **Dragon Choices**

Here are the dragons I choose for the phylogeny



### Elden Ring

Source: Elden Ring https://cdn1.dotesports.com/wp-content/uploads/2022/03/03190345/Elden-Ring-Screenshot.jpg (https://cdn1.dotesports.com/wp-content/uploads/2022/03/03190345/Elden-Ring-Screenshot.jpg)")



Malygos

Source: World of Warcraft Classic https://www.warcrafttavern.com/wp-content/uploads/2022/09/WotLK-Classic-Malygos-Strategy-Guide-Featured-Image-scaled.jpg (https://www.warcrafttavern.com/wp-content/uploads/2022/09/WotLK-Classic-Malygos-Strategy-Guide-Featured-Image-scaled.jpg)



### Sartharion

Source: World of Warcaft Classic https://www.warcrafttavern.com/wp-content/uploads/2022/09/WotLK-Classic-Sartharion-Strategy-Guide-Featured-Image-scaled.jpg (https://www.warcrafttavern.com/wp-content/uploads/2022/09/WotLK-Classic-Sartharion-Strategy-Guide-Featured-Image-scaled.jpg)

### Backstory and Intepretation

### Introduction

This research seeks to characterize the existence of a dragon from the popular game Elden Ring, and two dragons from the popular game World of Warcraft. Through creating a phylogeny of popular dragon artwork and assigning codes to certain traits, we hope to create a phylogeny of dragon taxa.

### Methods

To preform this, visual inspection of dragon images was preformed to create a code corresponding to a dragons given trait. Traits were qualitatively observed and characterize the morphology of the dragon, such as number of appendages, talon size, presence or absence of scales or other Armour etc. Using ape and ggtree a phylogeny will be constructed once the new dragon data has entered into the .nex file.

#### Results

Analysis was able to plot the new dragons on the phylogeny of dragon taxa, with the Elden Ring dragon as well as the two World of Warcraft dragons found on the phylogeny above.

### Discussion

The two World of Warcraft dragons were determined to be closely related according to the phylogeny. This makes sense, as they are both from the same series, and have very similar morphologies as noted in the photos above. The Elden Ring dragon is classified close to the World of Warcraft Dragons, which is interesting considering they are from different series. However, the basic morphology of these dragons are similar enough for them to be related based on the phylogeny I produced.