

Dragon Phylogeny Assignment

Jayde MacMillan 20068250

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Github - jaydealexandra (<https://github.com/jaydealexandra/DragonPhylogeny.git>)

Setup

Loads the required libraries.

```
library(ape)
library(reshape2)
library(ggplot2)
library(ggtree)
```

```
## ggtree v3.2.1 For help: https://yulab-smu.top/treedata-book/
##
## If you use ggtree in published research, please cite the most appropriate paper(s):
##
## 1. Guangchuang Yu. Using ggtree to visualize data on tree-like structures. Current Protocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
## 2. 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
## 3. 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
```

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

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

```
library(ggimage)
```

Imports 'DragonMatrix.nex' into an object called 'DragonNexus'.

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

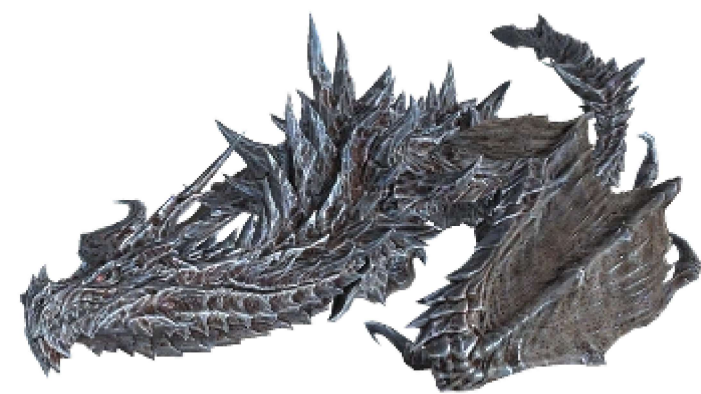
Dragons

The following dragons were added into the 'DragonMatrix.nex' dataset.

Ord from Dragon Tales. This image is from Dragon Tales Wikia (<https://dragontales.fandom.com/wiki/Ord>)



Alduin from Elder Scrolls. This image is from Skyrim Wiki (<https://skyrim.fandom.com/wiki/Alduin>)



Spyro from Spyro the Dragon. This image is from Wikipedia ([https://en.wikipedia.org/wiki/Spyro_\(character\)\)](https://en.wikipedia.org/wiki/Spyro_(character))))



Weights

Imports 'Weight.csv' into a single vector and splits it into substrings.

```
WeightsDat<-read.csv("input/Weights.csv") #imports 'Weights.csv'  
Weights<-paste0(WeightsDat$Weight,collapse="") #links vectors together after converting to character  
Weights<-strsplit(Weights,split="")[[1]] #splits the character vector into substrings
```

Converts each letter to a value using a custom function.

```
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)
```

Multiplies the weight value by the trait vector for each dragon.

```
WtDragonNexus<-DragonNexus # Make a new weighted data frame object  
for (i in 1:length(DragonNexus)){  
  RepWeight<-DragonNexus[[i]]==1  
  WtDragonNexus[[i]][RepWeight]<-WeightsNum[RepWeight]  
  RepWeight<-NA  
}
```

Distance Matrix

Uses the `unlist` function to turn the object into a vector, then converting it to a matrix.

```
WtDragonNexusDF<-data.frame(matrix(unlist(WtDragonNexus),ncol=78,byrow=T)) #unlists and creates a dataframe  
row.names(WtDragonNexusDF)<-names(WtDragonNexus) #sets the row names  
  
WtDragonDist<-dist(WtDragonNexusDF,method='euclidean') #computes the distance between the rows of the data matrix using the euclidean method
```

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

```
WtDragonDistMat<-as.matrix(WtDragonDist) #creates a matrix using the weighted data
```

Tree Formatting

Builds a phylogeny.

```
WtDragonTree<-fastme.bal(WtDragonDist)
```

Colour by OTU.

```
base <- gsub("[0-9\\.]+(?:^[^X]+)X*", "\\1", WtDragonTree$tip.label) # Remove Leading numbers

baseGroups<-split(WtDragonTree$tip.label, base=="Fiction") # Splits 'WtDragonTree$tip.Label' by Fiction

WtDTcol<-groupOTU(WtDragonTree, baseGroups) # Groups OTUs

imagesDF <- data.frame(node = c(78,79,80), #specifies nodes
                        images = c("images/A7_MACMILLAN_JAYDE_Ord.png", #specifies images
                                   "images/A7_MACMILLAN_JAYDE_Alduin.png",
                                   "images/A7_MACMILLAN_JAYDE_Spyro.png"))

ggtree(WtDTcol, branch.length='none') %<+% imagesDF +
  geom_tree(aes(colour=group)) +
  geom_tiplab(aes(image=images), geom = "image", offset=2, size = 0.05) +
  geom_tiplab(size=2) +
  theme(legend.position = "none") +
  xlim(0,50)
```

```
## Warning: Removed 77 rows containing missing values (geom_image).
```

