

Dragon_Phy_Assignment

Joel Sagman (<https://github.com/JoelSagman/Dragon-Phylogeny-A7>)

Load necessary packages

```
library(ape)
library(ggplot2)
library(reshape2)
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
   d 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'
```

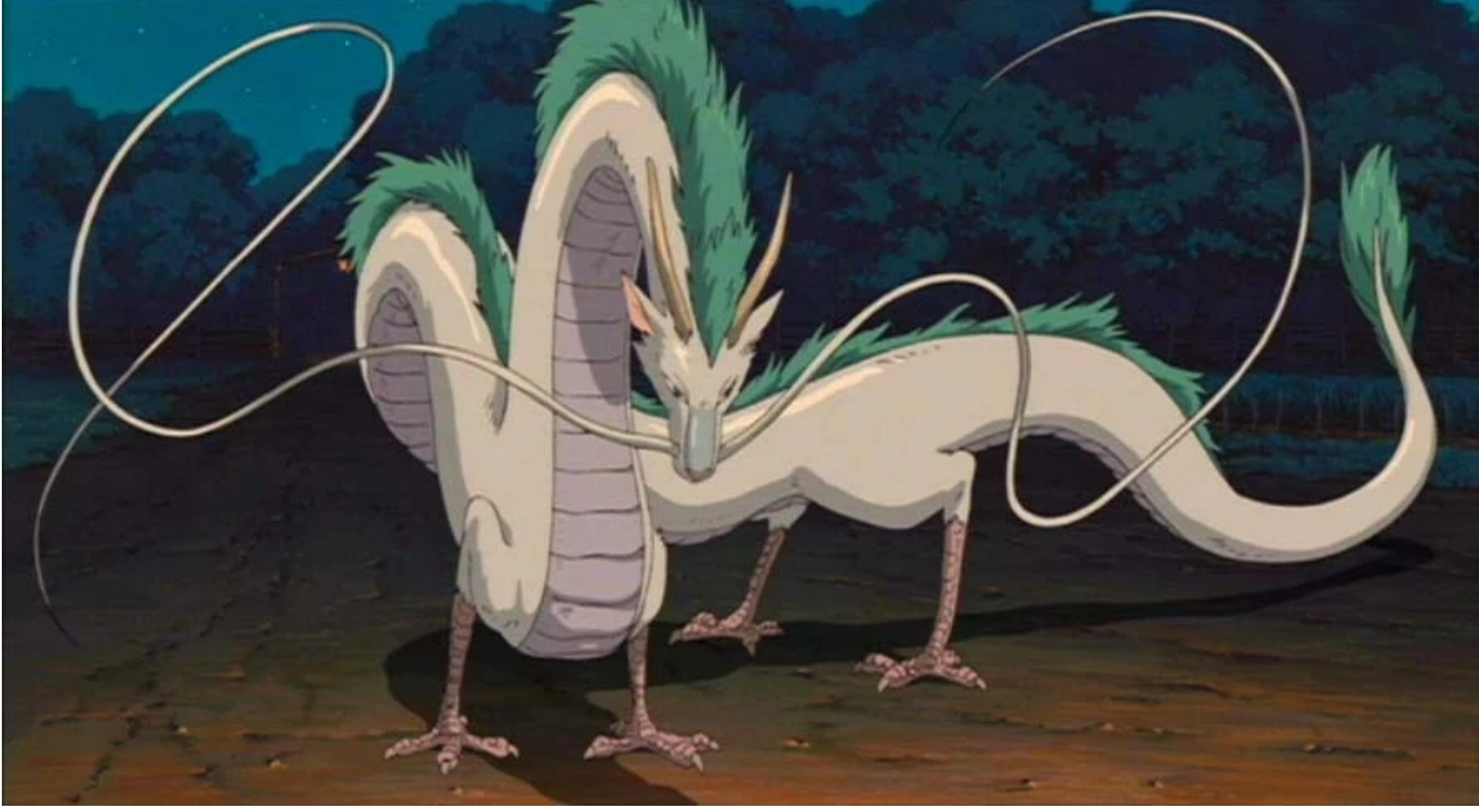
```
## The following object is masked from 'package:ape':
##
##      rotate
```

Images of added dragons



Villentretenmerth (Golden Dragon)

Source



Haku

Source



Kaidou

Source

Import Data

```
DragonNexus<-read.nexus.data("Input/DragonMatrix.nex") # Imports dragon nexus file that has been edited to contain the new dragons
tail(DragonNexus) # Shows that tail end of the file for confirmation purposes
```

```
## $'72BritishX`
## [1] "0" "1" "1" "0" "1" "1" "1" "0" "0" "1" "1" "0" "1" "1" "0" "0"
## [20] "1" "0" "0" "0" "1" "0" "0" "1" "0" "0" "1" "0" "0" "1" "0" "1"
## [39] "1" "1" "0" "1" "1" "0" "1" "1" "1" "0" "1" "0" "0" "1" "0" "1"
## [58] "0" "0" "1" "0" "0" "1" "0" "1" "0" "0" "0" "1" "2" "2" "2" "0" "0"
## [77] "0" "1"
##
##
## $'73BritishX`
## [1] "0" "1" "1" "0" "1" "1" "1" "0" "0" "1" "1" "0" "0" "1" "1" "0" "0"
## [20] "1" "0" "0" "0" "1" "1" "0" "0" "1" "1" "1" "1" "0" "0" "1" "1" "0" "0"
## [39] "1" "1" "0" "0" "1" "1" "0" "1" "1" "1" "0" "1" "0" "0" "1" "1" "0" "0"
## [58] "0" "0" "0" "0" "0" "1" "0" "1" "0" "0" "1" "2" "2" "2" "0" "1"
## [77] "0" "0"
##
##
## $'74BritishX`
## [1] "0" "1" "1" "0" "0" "1" "1" "1" "0" "0" "1" "1" "0" "0" "1" "1" "0" "0"
## [20] "1" "0" "0" "0" "0" "1" "0" "0" "1" "1" "1" "1" "0" "0" "0" "1" "1" "1" "0"
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## [58] "0" "0" "0" "0" "0" "1" "0" "1" "0" "0" "0" "1" "2" "2" "2" "0" "1"
## [77] "1" "1"
##
##
## $'75HakuXXXX`
## [1] "1" "0" "0" "1" "0" "1" "0" "1" "1" "1" "1" "0" "0" "1" "0" "0" "1"
## [20] "1" "0" "0" "0" "0" "1" "0" "0" "1" "1" "1" "1" "0" "1" "0" "1" "0" "0" "0"
## [39] "1" "1" "0" "0" "0" "0" "0" "0" "0" "0" "0" "1" "1" "1" "1" "0" "0" "0"
## [58] "0" "0" "0" "0" "1" "1" "0" "0" "0" "0" "0" "0" "0" "1" "1" "1" "0" "2"
## [77] "2" "2"
##
##
## $'76RaidouXX`
## [1] "1" "1" "0" "1" "1" "1" "1" "1" "1" "1" "1" "1" "0" "0" "0" "1" "0" "1"
## [20] "0" "0" "1" "0" "0" "0" "0" "1" "1" "1" "1" "1" "0" "0" "0" "0" "0" "1"
## [39] "0" "0" "1" "0" "0" "0" "0" "0" "0" "0" "0" "1" "1" "1" "1" "0" "2" "1"
## [58] "0" "0" "0" "0" "1" "1" "0" "0" "0" "0" "0" "0" "1" "1" "1" "0" "0" "0"
## [77] "2" "2"
##
##
## $'77GoldenXX`
## [1] "1" "0" "0" "1" "0" "1" "0" "1" "1" "0" "0" "1" "0" "0" "0" "1" "0" "0"
## [20] "0" "0" "0" "0" "0" "0" "0" "1" "1" "0" "0" "1" "0" "0" "0" "0" "0" "0"
## [39] "1" "0" "1" "0" "0" "0" "0" "2" "2" "2" "2" "2" "1" "1" "0" "0" "1" "0" "0"
## [58] "0" "0" "0" "1" "1" "1" "1" "0" "0" "0" "1" "2" "2" "2" "0" "0" "1" "1" "1"
## [77] "0" "0"
```

Importing Weight data and converting them into a single vector

```
WeightsDat<-read.csv("Data/Weights.csv") # Imports Weights so be applied to dragon data
Weights<-paste0(WeightsDat$Weight,collapse="") # Isolates just the weights from the data
Weights<-strsplit(Weights,split="")[[1]] # Splits up the the weights into individual characters
```

Converting each Weights into numerical values

```
WeightsNum<-rep(NA,length(Weights)) # create empty vector for weights numbers
for(i in 1:length(WeightsNum)){ # A loop that converts that weights from letters and number to just number that r
represents their weight
  if(Weights[i] %in% LETTERS){
    WeightsNum[i]<-which(LETTERS==Weights[i])+9
  } else {
    WeightsNum[i]<-Weights[i]
  }
}
WeightsNum<-as.numeric(WeightsNum) # Converts to numerical values for weight
```

Creates a new data frame that includes the weights

```
WtDragonNexus<-DragonNexus # Make a new weighted data frame object
for (i in 1:length(DragonNexus)){ # a for loop that applies the weights to the new weighted data frame
  RepWeight<-DragonNexus[[i]]*w1
  WtDragonNexus[[i]][RepWeight]<-WeightsNum[RepWeight]
  RepWeight<-NA
}
```

Calculating the distance matrix with weighted data

```
WtDragonNexusDF<-data.frame(matrix(unlist(WtDragonNexus),ncol= length(DragonNexus[[1]]),byrow=T)) # converts
row.names(WtDragonNexusDF)<-names(WtDragonNexus) #Adds the same row names as the previous data set
WtDragonDist<-dist(WtDragonNexusDF,method='euclidean') # Euclidean algorithm used to calculate distance with weig
```

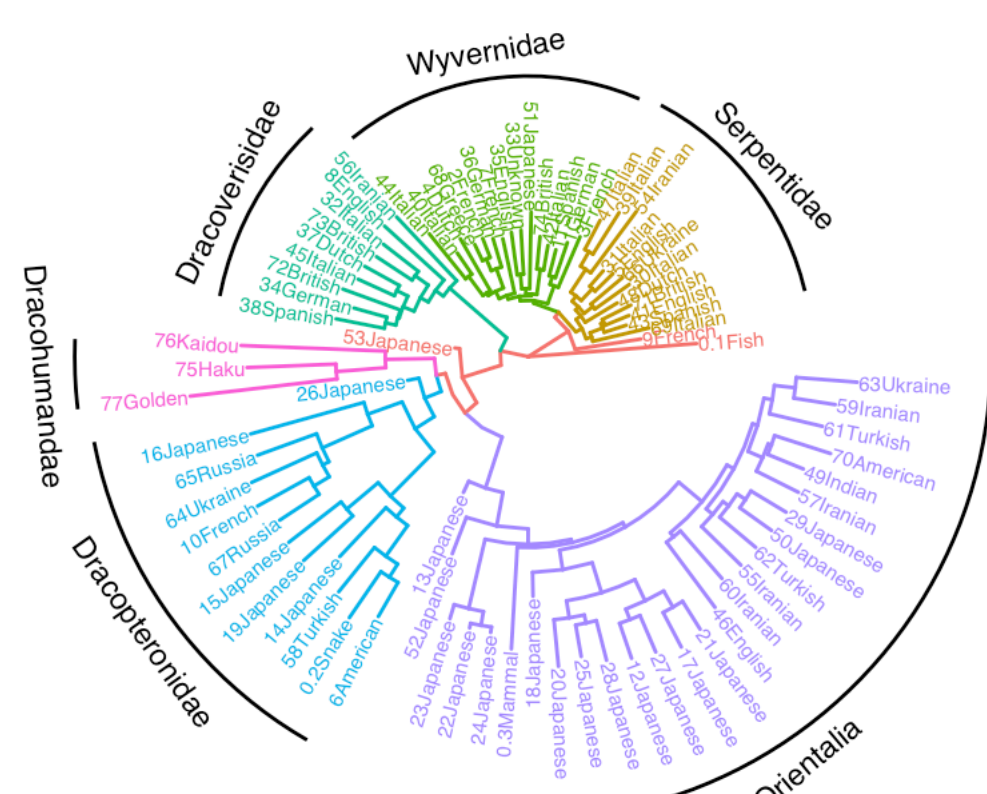
```
## Warning in dist(WtDragonNexusDF, method = "euclidean"): NAs introduced by coercion
```

Preping data for building tree

```
WtDragonTree<-fastme.bal(WtDragonDist) #
WtDragonTree$tip.label <- gsub("([1-9\\.\\.]*)([\\^X])X*", "\\1\\2", WtDragonTree$tip.label) # Removes just the follow
ing X(s) from the tip label
```

```
gtDtree=groupClade(WDrtnTree, node=c(148,134,124, 11, 85, 122)) # Species clade groups
wtDtree(WtDtree, layout="fan", aes(colour=group)) + # Makes plot a plot where each clade is labeled and coloured
  geom_tiplab(size=2, aes(angle=angle)) +
  geom_cladelabel(node=148, label="Serpentidae", hjust=0.5, offset=15, offset.text=4, fontsize=3, angle=-47) +
  geom_cladelabel(node=134, label="Wyvernidae", hjust=0.5, offset=18, offset.text=4, fontsize=3, angle=10) +
  geom_cladelabel(node=87, label="Orientalia", hjust=0.5, offset=19, offset.text=4, fontsize=3, angle=40) +
  geom_cladelabel(node=111, label="Dracopterisidae", hjust=0.5, offset=18, offset.text=4, fontsize=3, angle=55) +
  geom_cladelabel(node=124, label="Dracoverisidae", hjust=0.5, offset=17, offset.text=4, fontsize=3, angle=64) +
  geom_cladelabel(node=122, label="Dracohumandae", hjust=0.5, offset=16, offset.text=4, fontsize=3, angle=85) +
  theme(legend.position="none")
```

```
## Scale for 'y' is already present. Adding another scale for 'y', which will
## replace the existing scale.
```



Phylogenetic tree of dragons with dragons sapared into clades. Dragons sapared into clades based on calculated