

Assignment 7 - Caroline Tang 20115082

Project Info

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Dragon Phylogeny

New dragons

I added Gible, Goomy, and Appletun from the Pokemon series to the phylogeny. All photos and information were obtained from Bulbapedia.

Gible



Original Gible Art (Source)

Goomy



Original Goomy Art (Source)

Appletun



Original Art (Source)

Creating the phylogeny

Load in all the 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
## 2. Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods for mapping and visualizing genomic data on phylogenetic trees
## 3. Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam. ggtree: an R package for visualizing phylogenetic trees

##
## Attaching package: 'ggtree'

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

```
library(ggimage)
```

Load in dragon data and trait weights

```
dragonNexus <- read.nexus.data("A7_Tang_Caroline.nex")
weightDat <- read.csv("https://colauttilab.github.io/Data/Weights.csv")
```

Convert dragon data to weighted traits

```
#separate weights and convert them to a numeric scale (1-35 where A = 10 and Z = 35)
weights <- paste(weightDat$Weight, collapse = "")
weights <- unlist(strsplit(weights, split = ""))

numericWeight <- vector(length = length(weights))
for (i in 1:length(weights)) {
  if (weights[i] %in% LETTERS) {
    numericWeight[i] <- which(LETTERS == weights[i]) + 9
  } else {
    numericWeight[i] <- as.numeric(weights[i])
  }
}

#multiply each trait by the weight
wtDragonNexus <- dragonNexus
for (i in 1:length(dragonNexus)) {
  Repweight <- dragonNexus[[i]]==1
  wtDragonNexus[[i]] <- numericWeight * Repweight
}

#convert to dataframe
wtDragonDF <- data.frame(matrix(unlist(wtDragonNexus), ncol = length(wtDragonNexus[[1]]), byrow = T))
row.names(wtDragonDF) <- names(wtDragonNexus)
```

Calculate Euclidean distances and convert to a matrix

```
wtDragonDist <- dist(wtDragonDF, method = "euclidean")
wtDragonDM <- as.matrix(wtDragonDist)
```

Create the tree using neighbour joining methods

```
wtDragonNJ <- nj(wtDragonDist)

#separate dragons into pokemon and non-pokemon
origin <- gsub(".*\\d+([X]*).*", "\\1", row.names(wtDragonDF))
pokemon <- split(row.names(wtDragonDF), origin=="Pokemon")
wtDragoncol <- groupOTU(wtDragonNJ, pokemon)

#Create better labels for tips and add images
dragonLabel <- data.frame(dragon = row.names(wtDragonDF),
                          lab = gsub(".*\\d+([X]*).*", "\\1-\\2", row.names(wtDragonDF)),
                          image = c(rep(NA, nrow(wtDragonDF) - 3), "A7_Tang_Caroline_Gible_Pixel.png",
```

Create phylogenetic tree, added dragons are highlighted in red

```
ggtree(wtDragoncol, layout = "rectangular") %<+% dragonLabel +
  geom_tree(aes(colour = group)) +
  geom_tiplab(aes(label = lab), size = 1.5) +
  geom_tiplab(aes(image = image), geom = "image", offset = 2, size = 0.1) +
  xlim(0, 70) +
  scale_colour_manual(values = c("black", "red")) +
  theme(legend.position = "none")
```

