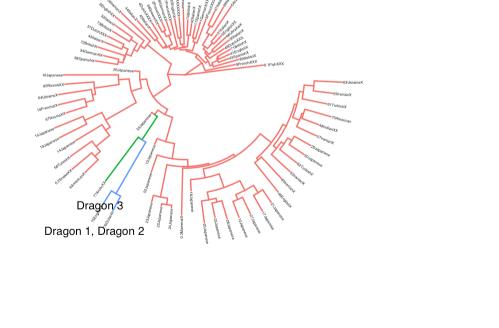
```
Assignment #8 - Dragon Phylogenies
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GitHub Link: https://github.com/jademgoodman/Dragons
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Loading Packages
 library(BiocManager)
 library(Biostrings)
 ## Loading required package: BiocGenerics
 ## Attaching package: 'BiocGenerics'
 ## The following objects are masked from 'package:stats':
      IQR, mad, sd, var, xtabs
 ## The following objects are masked from 'package:base':
 ##
 ##
      anyDuplicated, aperm, append, as.data.frame, basename, cbind,
      colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
      get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
      match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
      Position, rank, rbind, Reduce, rownames, sapply, saveRDS, setdiff,
      table, tapply, union, unique, unsplit, which.max, which.min
 ## Loading required package: S4Vectors
 ## Loading required package: stats4
 ## Attaching package: 'S4Vectors'
 ## The following object is masked from 'package:utils':
      findMatches
 ## The following objects are masked from 'package:base':
      expand.grid, I, unname
 ## Loading required package: IRanges
 ## Loading required package: XVector
 ## Loading required package: GenomeInfoDb
 ## Attaching package: 'Biostrings'
 ## The following object is masked from 'package:base':
      strsplit
 library(reshape2)
 library(rentrez)
 library(annotate)
 ## Loading required package: AnnotationDbi
 ## Loading required package: Biobase
 ## Welcome to Bioconductor
 ##
      Vignettes contain introductory material; view with
      'browseVignettes()'. To cite Bioconductor, see
      'citation("Biobase")', and for packages 'citation("pkgname")'.
 ## Loading required package: XML
 library(ape)
 ## Attaching package: 'ape'
 ## The following object is masked from 'package:Biostrings':
      complement
 library(ggtree)
 ## ggtree v3.14.0 Learn more at https://yulab-smu.top/contribution-tree-data/
 ## Please cite:
 ## 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
 ## The following object is masked from 'package:Biostrings':
      collapse
 ## The following object is masked from 'package:IRanges':
      collapse
 ## The following object is masked from 'package:S4Vectors':
     expand
 library(ggplot2)
Reading the Nexus Data
 library(ape)
 data<-read.nexus.data("DragonMatrixAppended.nex") #reading updated nexus file</pre>
 head(data)
 ## $`0.1FishXXX`
 ## [77] "0" "0"
 ## $`0.2SnakeXX`
 ## [77] "0" "0"
 ## $`0.3MammalX`
 ## [77] "0" "0"
 ## $`1GermanXXX`
 ## [58] "0" "0" "0" "1" "0" "0" "1" "0" "0" "1" "0" "?" "?" "?" "?" "?" "0" "1"
 ## [77] "1" "1"
 ## $`2FrenchXXX`
 ## $`3FrenchXXX`
 ## [77] "1" "1"
Adding Weights
 #"Weights.csv" was downloaded from https://github.com/ColauttiLab/DragonPhylogeny
 WeightsDat<-read.csv("Weights.csv")</pre>
 head(WeightsDat)
 ## Code
              Origin Weight
           Appendages ZZZZ
 ## 1
     1
               Mass 1111
            Body Type CC
            ClawType 5555
     5 Dorsal Ridges 111111
      6 Ear Morphology 111
 ##
                                                                                     Ra
 tionale
 ## 1 Highly Highly conserved (all tertrapods came from the same fish; loss of limbs more common (e.g. lizards to
 snakes)
 ## 2
                                                                    Weak: e.g. squirrel vs. K
 angaroo
 ## 3
                                                   Body type somewhat conserved (e.g. snakes vs. l
 izards)
 ## 4
                                                              Somewhat Strong: e.g. mammals v
 s. eagle
 ## 5
                                                                             Weak: e.g. di
 nosaurs
 ## 6
                                                                     Weak: e.g. deer mouse v
 s. vole
 Weights<-paste0(WeightsDat$Weight, collapse="")</pre>
 Weights<-strsplit(Weights,split="")[[1]]</pre>
 WeightsNum<-rep(NA,length(Weights))</pre>
 for(i in 1:length(WeightsNum)){
  if(Weights[i] %in% LETTERS){
    WeightsNum[i]<-which(LETTERS==Weights[i])+9</pre>
    WeightsNum[i]<-Weights[i]</pre>
  } #fixing weights
 WeightsNum<-as.numeric(WeightsNum) #sets it to numeric</pre>
 WtDragonNexus<-data
 for(i in 1:length(data)){
  RepWeight<-data[[i]]==1</pre>
  WtDragonNexus[[i]][RepWeight]<-WeightsNum[RepWeight]</pre>
  RepWeight<-NA
 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
Dragon Images
 knitr::include_graphics("dragon1.png")
                               https://www.twinkl.ch/teaching-wiki/dragon
 knitr::include_graphics("dragon2.jpg")
Victoria Yurkovets (https://www.artstation.com/artwork/L3mE2v)
 knitr::include_graphics("dragon3.png")
                                            https://www.deviantart.com/fafnirx/art/wyvern-348460727
Phylogeny
 #estimating evolutionary tree
```



```
CountryGroups<-split(WtDragonTree$tip.label, Country)</pre>
WtDTcol<-groupOTU(WtDragonTree,CountryGroups)</pre>
#relevant nodes are Nodes 97 and 98 (represents Dragons 1, 2, and 3)
WtDTclade <- groupClade(WtDragonTree, .node = c(97, 98))</pre>
ggtree(WtDTclade, layout = "circular", aes(colour = group)) +
 geom_cladelabel(node = 97, label = "Dragon 3",
                hjust = 0.5, vjust = 0, offset.text = 0,
                fontsize = 3, angle = 0, barcolor = NA, barsize = 0) +
 geom_cladelabel(node = 98, label = "Dragon 1, Dragon 2",
                hjust = 0.5, vjust = 0.5, offset.text = 7,
                fontsize = 3, angle = 0, barcolor = NA, barsize = 0) +
 xlim(NA, 60) +
 geom_tiplab(color = "black", size = 1) +
 guides(colour = "none")
```



(Dragon 1) and 76Oolacile (Dragon 2) being highlighted in blue as these are most closely related, and dragon 77ArcticXX (Dragon 3) being highlighted in green. **Backstory and Data Interpetation**

Fig. 1. Phylogenetic tree displaying the evolutionary relationships between different dragon species. Labels at the tips of the tree display the ID codes for each species. The lineages for the three dragon species added to this analysis are highlighted in different colours, with 75EnglishX

Our three dragons are all closely related, with dragon 75EnglishX (Dragon 1) and 76Oolacile (Dragon 2) being most closely related, and 77ArcticXX (Dragon 3) being the next closely related species. This lineage of dragons diverged very early on in the ancestry of the dragons, being most closely related to dragons of the Orientalia clade. However, the lineage with our three dragons diverged from the rest of the Orientalia clade at the common recent ancestor to all other Orientalia dragons, meaning that this offshoot group is not closely related to most of the other dragons

the dark green skin colour of Dragons 1 and 2 reflects the forest habitat they live in.

in this clade, instead it is most closely related to dragon 53Japanese. Dragons numbered 1-14 in the Dragons_Pics.pdf are photographed to be of much smaller size and mass than our three dragons, especially in comparison to humans. They are shown to be in closer contact with human populations, indicating their habitats are more densely populated. In

contrast, our dragons have been found to live in more isolated forests or Arctic environments, allowing for bigger growth. These populations share common ancestors with the other European and East Asian dragons, though an early population with our three dragons migrated to northern Europe. From here, Divergence of our three dragons can be further explained through habitat differences. 77DragonXX (our

Dragon 3) lived north of the tree line, in icy Arctic habitats, thus adopting a light blue skin colour to blend in with the winter environment. In contrast,