FEL results preliminary

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check one alignment

zeiformes nd1 FEL results

```
filepath <- read_json("~/bin/mtDNA_redo/data/FEL/zeiformes-nd1-align-dna.fas.FEL.json") #read in json

heads <- filepath$MLE$headers %>% unlist() %>% .[c(TRUE,FALSE)] #get headers and ignore header descrip

#get MLE contents and make them a data frame

temp <- filepath$MLE$content$`0` %>% unlist %>% matrix(ncol = 6, byrow = TRUE) %>% as.data.frame()

#make the headers the variable names

names(temp) <- heads
```

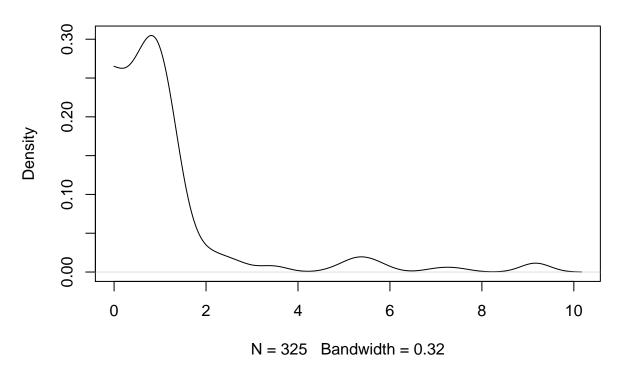
kernel density and plots?

Kernel density and plot for alpha for single FEL result

```
d_alpha <- density(log(temp$alpha), kernel = "gaussian", from = 0) #Kernel density for alpha rate estim
#start from 0 and log transform to control outliers

d_alpha %>% plot() #plot the density
```

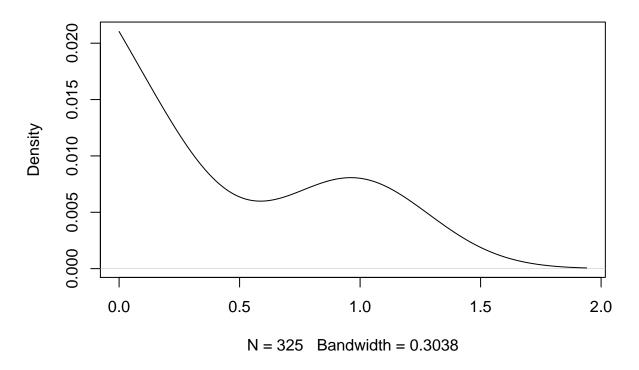
density.default(x = log(temp\$alpha), kernel = "gaussian", from = 0)



Kernel density and plot for beta for single FEL result

```
d_beta <- density(log(temp$beta), kernel = "gaussian", from = 0) #Kernel density for the beta rate est
d_beta %>% plot() #plot the density
```

density.default(x = log(temp\$beta), kernel = "gaussian", from = 0)



check a second alignment:

acipenseriformes at 8 FEL results

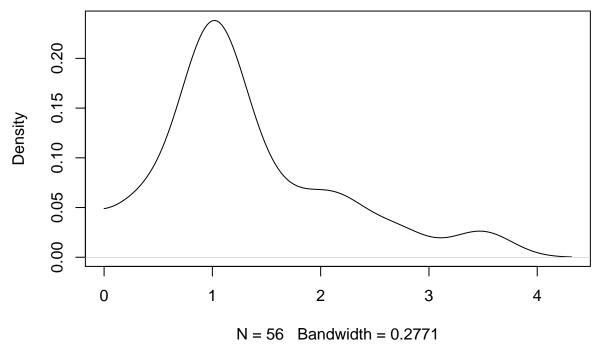
```
filepath <- read_json("~/bin/mtDNA_redo/data/FEL/acipenseriformes-atp8-align-dna.fas.FEL.json") #read i
heads <- filepath$MLE$headers %>% unlist() %>% .[c(TRUE,FALSE)] #get headers and ignore header descrip
#get MLE contents and make them a data frame
temp_2 <- filepath$MLE$content$`0` %>% unlist %>% matrix(ncol = 6, byrow = TRUE) %>% as.data.frame()
#make the headers the variable names
names(temp_2) <- heads
```

kernel density and plots?

Kernel density and plot for alpha for single FEL result

```
d_alpha_2 <- density(log(temp_2$alpha), kernel = "gaussian", from = 0)
d_alpha_2 %>% plot()
```

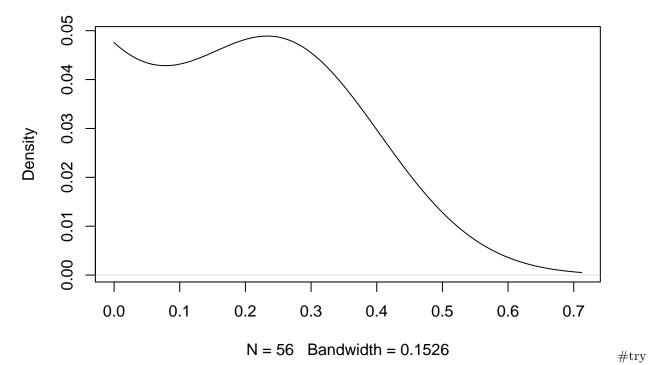
density.default(x = log(temp_2\$alpha), kernel = "gaussian", from = (



##Kernel density and plot for beta for single FEL result

```
d_beta_2 <- density(log(temp_2$beta), from = 0)
d_beta_2 %>% plot()
```

density.default(x = log(temp_2\$beta), from = 0)



different ways of calculating the KL or JSD ##using the entropy library:

```
#uses entropy library to calculate Kullback-Leibler divergence (KL) as it is needed to do the JSD
library("entropy")

KL <- KL.plugin(freqs1 = d_alpha$x, freqs2 = d_beta$x)

## Warning in KL.plugin(freqs1 = d_alpha$x, freqs2 = d_beta$x): Vanishing value(s)

## in argument freqs2!

KL_2 <- KL.plugin(freqs1 = d_alpha_2$x, freqs2 = d_beta_2$x)

## Warning in KL.plugin(freqs1 = d_alpha_2$x, freqs2 = d_beta_2$x): Vanishing

## value(s) in argument freqs2!

#both of these return an error: Vanishing value(s) in argument freqs2!</pre>
```

Using a calculation from stackoverflow:

```
#from stackoverflow https://stackoverflow.com/questions/11226627/jensen-shannon-divergence-in-r p <- d_beta_2$x q <- d_alpha_2$x n <- 0.5 * (p + q)  
JS <- 0.5 * (sum(p * log(p / n)) + sum(q * log(q / n))) #returns an NaN
```

Using a formula from a website:

```
#actually, lets try the way this site does it: https://enterotype.embl.de/enterotypes.html
JSD \leftarrow function(x,y) \ sqrt(0.5 * KLD(x, (x+y)/2) + 0.5 * KLD(y, (x+y)/2))
KLD <- function(x,y) sum(x * log(x/y))
KLD(d_beta_2$x, d_alpha_2$x)
## [1] NaN
JSD(d_beta_2$x, d_alpha_2$x)
## [1] NaN
dist.JSD <- function(inMatrix, pseudocount=0.000001, ...) {</pre>
    KLD <- function(x,y) sum(x *log(x/y))
    JSD<- function(x,y) sqrt(0.5 * KLD(x, (x+y)/2) + 0.5 * KLD(y, (x+y)/2))
    matrixColSize <- length(colnames(inMatrix))</pre>
    matrixRowSize <- length(rownames(inMatrix))</pre>
    colnames <- colnames(inMatrix)</pre>
    resultsMatrix <- matrix(0, matrixColSize, matrixColSize)</pre>
  inMatrix = apply(inMatrix,1:2,function(x) ifelse (x==0,pseudocount,x))
    for(i in 1:matrixColSize) {
        for(j in 1:matrixColSize) {
            resultsMatrix[i,j]=JSD(as.vector(inMatrix[,i]),
            as.vector(inMatrix[,j]))
        }
```

```
colnames -> colnames(resultsMatrix) -> rownames(resultsMatrix)
   as.dist(resultsMatrix)->resultsMatrix
   attr(resultsMatrix, "method") <- "dist"</pre>
   return(resultsMatrix)
}
```

```
calculate the JSD between alpha and beta
d.temp <- dist.JSD(temp %>% select(alpha, beta))
d.temp
           alpha
## beta 108.0882
this last method works and gives me the JSD between the nonsynonymous (beta) and synonymous (alpha)
rate distributions.
so now what if we want the distance for every FEL result?
first, get list of all FEL results:
dir <- "~/bin/mtDNA_redo/data/FEL"</pre>
FEL_jsons <- list.files(path = dir,</pre>
                       pattern = '*FEL.json', recursive = TRUE, full.names = TRUE)
write function for JSD calculation:
JSD.calc <- function(filename){</pre>
  results <- read_json(filename) #read in json
  heads <- results$MLE$headers %% unlist() %% .[c(TRUE,FALSE)] #get headers and ignore header descri
  #get MLE contents and make them a data frame
  temp <- results$MLE$content$`0` %% unlist %% matrix(ncol = 6, byrow = TRUE) %>% as.data.frame()
#make the headers the variable names
  names(temp) <- heads</pre>
#Kernel density for alpha rate estimation
#start from 0 and log transform to control outliers
# d_alpha <- density(log(temp$alpha), kernel = "gaussian", from = 0)</pre>
 # d_beta <- density(log(temp$beta), kernel = "gaussian", from = 0)</pre>
  d.temp <- dist.JSD(temp %>% select(alpha, beta))
  return(d.temp)
check that it works:
#JSD.calc(paste0(dir,FEL_jsons[1]))
this returns a named number of JSD calculations
```

```
t <- sapply(FEL_jsons, JSD.calc)
```

/Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-atp6-align-dna.fas.FEL.json

```
##
                                                                                  60.1693124
         /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-atp8-align-dna.fas.FEL.json
##
##
                                                                                   6.0910806
         /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-cox1-align-dna.fas.FEL.json
##
##
                                                                                  19.6441866
         /Users/Sadie/bin/mtDNA redo/data/FEL/acipenseriformes-cox2-align-dna.fas.FEL.json
##
##
                                                                                  58.1551711
         /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-cox3-align-dna.fas.FEL.json
##
##
                                                                                  28.2511289
##
          /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-nd1-align-dna.fas.FEL.json
##
                                                                                  84.3809173
          /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-nd2-align-dna.fas.FEL.json
##
##
                                                                                  97.8256070
          /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-nd3-align-dna.fas.FEL.json
##
##
                                                                                   8.5137675
##
          /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-nd5-align-dna.fas.FEL.json
##
                                                                                  35.0844530
##
          /Users/Sadie/bin/mtDNA_redo/data/FEL/acipenseriformes-nd6-align-dna.fas.FEL.json
##
                                                                                  22.2316634
##
         /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ATP6-Aligned-DNA.fas.FEL.json
##
                                                                                 135.5566605
         /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ATP8-Aligned-DNA.fas.FEL.json
##
##
                                                                                  59.6080050
         /Users/Sadie/bin/mtDNA redo/data/FEL/Anguilliformes-COX1-Aligned-DNA.fas.FEL.json
##
##
                                                                                 151.8205989
##
         /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-COX3-Aligned-DNA.fas.FEL.json
##
                                                                                  67.7325563
         /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-CYTB-Aligned-DNA.fas.FEL.json
##
##
                                                                                 162.0590693
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND1-Aligned-DNA.fas.FEL.json
##
##
                                                                                 173.3868351
##
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND2-Aligned-DNA.fas.FEL.json
##
                                                                                 275.1854043
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND3-Aligned-DNA.fas.FEL.json
##
##
                                                                                  76.2457216
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND4-Aligned-DNA.fas.FEL.json
##
##
                                                                                 200.5529607
##
         /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND4L-Aligned-DNA.fas.FEL.json
##
                                                                                 109.8130988
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND5-Aligned-DNA.fas.FEL.json
##
##
                                                                                 290.6448624
          /Users/Sadie/bin/mtDNA_redo/data/FEL/Anguilliformes-ND6-Aligned-DNA.fas.FEL.json
##
##
                                                                                 102.4477043
           /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ATP6-Aligned-DNA.fas.FEL.json
##
                                                                                  11.5023719
##
           /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ATP8-Aligned-DNA.fas.FEL.json
##
##
                                                                                   5.5814536
           /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-COX1-Aligned-DNA.fas.FEL.json
##
##
                                                                                 112.6862892
##
           /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-COX2-Aligned-DNA.fas.FEL.json
##
                                                                                  56.6955794
           /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-COX3-Aligned-DNA.fas.FEL.json
##
##
                                                                                 111.0054078
##
           /Users/Sadie/bin/mtDNA redo/data/FEL/Anseriformes-CYTB-Aligned-DNA.fas.FEL.json
```

##	74.6076430
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND1-Aligned-DNA.fas.FEL.json
##	44.5790006
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND2-Aligned-DNA.fas.FEL.json
##	36.7039634
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND3-Aligned-DNA.fas.FEL.json
##	8.6128959
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND4L-Aligned-DNA.fas.FEL.json
## ##	59.3546685 /Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND5-Aligned-DNA.fas.FEL.json
##	/ osers/saure/ bin/ mcbwx_redo/data/FEL/ knserironmes=wb3=krighed=bwx.ras.FEL.json 109.5224266
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anseriformes-ND6-Aligned-DNA.fas.FEL.json
##	11.4155994
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ATP6-Aligned-DNA.fas.FEL.json
##	315.7656893
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-COX1-Aligned-DNA.fas.FEL.json
##	332.1441192
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-COX2-Aligned-DNA.fas.FEL.json
## ##	272.3949743 /Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-COX3-Aligned-DNA.fas.FEL.json
##	267.2814818
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-CYTB-Aligned-DNA.fas.FEL.json
##	330.1180978
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND1-Aligned-DNA.fas.FEL.json
##	352.3513714
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND2-Aligned-DNA.fas.FEL.json
##	404.3609935
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND3-Aligned-DNA.fas.FEL.json 218.4365688
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND4-Aligned-DNA.fas.FEL.json
##	522.1790318
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND4L-Aligned-DNA.fas.FEL.json
##	231.4169433
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Anura-ND6-Aligned-DNA.fas.FEL.json
##	367.6941205
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-atp6-align-dna.fas.FEL.json 423.9026471
##	423.9020471 /Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-atp8-align-dna.fas.FEL.json
##	102.0017266
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-cox1-align-dna.fas.FEL.json
##	577.6827304
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-cox2-align-dna.fas.FEL.json
##	451.8164325
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-cox3-align-dna.fas.FEL.json
## ##	391.5672423 /Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-cytb-align-dna.fas.FEL.json
##	467.3369903
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd1-align-dna.fas.FEL.json
##	444.3244802
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd2-align-dna.fas.FEL.json
##	444.5465296
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd3-align-dna.fas.FEL.json
##	348.9899404
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd4-align-dna.fas.FEL.json

##	454.3912343
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd41-align-dna.fas.FEL.json
##	332.7686243
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd5-align-dna.fas.FEL.json
##	824.1333826
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/araneae-nd6-align-dna.fas.FEL.json
##	0.5327481
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ATP6-Aligned-DNA.fas.FEL.json
## ##	242.3264018 /Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-COX1-Aligned-DNA.fas.FEL.json
##	216.4810689
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-COX2-Aligned-DNA.fas.FEL.json
##	145.7238735
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-COX3-Aligned-DNA.fas.FEL.json
##	212.8345325
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-CYTB-Aligned-DNA.fas.FEL.json
##	311.9664928
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND1-Aligned-DNA.fas.FEL.json 223.0581802
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND2-Aligned-DNA.fas.FEL.json
##	188.6557516
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND3-Aligned-DNA.fas.FEL.json
##	140.9965845
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND4-Aligned-DNA.fas.FEL.json
##	318.8329257
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND4L-Aligned-DNA.fas.FEL.json 134.9826306
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ascaridida-ND6-Aligned-DNA.fas.FEL.json
##	150.9286226
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ATP6-Aligned-DNA.fas.FEL.json
##	121.7398670
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ATP8-Aligned-DNA.fas.FEL.json
## ##	84.5709280 /Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-COX1-Aligned-DNA.fas.FEL.json
##	173.9216636
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-COX2-Aligned-DNA.fas.FEL.json
##	45.7607005
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND1-Aligned-DNA.fas.FEL.json
##	170.8287453
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND2-Aligned-DNA.fas.FEL.json 259.4490344
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND4-Aligned-DNA.fas.FEL.json
##	201.8559475
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND4L-Aligned-DNA.fas.FEL.json
##	60.9612422
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND5-Aligned-DNA.fas.FEL.json
##	313.3826122
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Beloniformes-ND6-Aligned-DNA.fas.FEL.json 196.4236867
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-atp6-align-dna.fas.FEL.json
##	73.1834936
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-atp8-align-dna.fas.FEL.json
##	16.3331454
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-cox1-align-dna.fas.FEL.json

##	126.5434473
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-cox2-align-dna.fas.FEL.json
##	52.7378224
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-cox3-align-dna.fas.FEL.json
##	56.2206163
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-cytb-align-dna.fas.FEL.json
##	119.7103372
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd1-align-dna.fas.FEL.json
##	79.5026968
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd2-align-dna.fas.FEL.json
##	163.3121881
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd3-align-dna.fas.FEL.json
##	21.0526619
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd4-align-dna.fas.FEL.json
##	158.9917973
	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd4l-align-dna.fas.FEL.json
##	70sers/Sadre/Bin/mcDNA_redo/data/FEL/Berychlormes-nd4r-arigh-dna.ras.FEL.Json 52.2098358
##	
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd5-align-dna.fas.FEL.json
##	143.5212417
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/beryciformes-nd6-align-dna.fas.FEL.json
##	132.0137309
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-atp6-align-dna.fas.FEL.json
##	72.4539756
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-atp8-align-dna.fas.FEL.json
##	59.2112074
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-cox1-align-dna.fas.FEL.json
##	86.8802889
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-cox2-align-dna.fas.FEL.json
##	77.2932813
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-cytb-align-dna.fas.FEL.json
##	80.1989644
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-nd1-align-dna.fas.FEL.json
##	82.2676047
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-nd2-align-dna.fas.FEL.json
##	84.7607138
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-nd4l-align-dna.fas.FEL.json
##	62.0364782
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-nd5-align-dna.fas.FEL.json
##	86.4024146
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/carnivores-nd6-align-dna.fas.FEL.json
##	41.6872273
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Cetacea-ATP6-Aligned-DNA.fas.FEL.json
	-
##	29.8523636
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Cetacea-ATP8-Aligned-DNA.fas.FEL.json
##	5.2777819
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Cetacea-COX1-Aligned-DNA.fas.FEL.json
##	85.3163772
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Cetacea-COX2-Aligned-DNA.fas.FEL.json
##	16.8450989
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Cetacea-COX3-Aligned-DNA.fas.FEL.json
##	91.8966391
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##	y users/Sadre/Bin/mtDNA_redo/data/FEL/Farconfromes-Cffb-Afrighed-DNA.fas.FEL.json 94.6809752
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##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Mermithida-CYTB-Aligned-DNA.fas.FEL.json
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##	346.3910011 /Users/Sadie/bin/mtDNA_redo/data/FEL/Mermithida-ND4-Aligned-DNA.fas.FEL.json
##	629.9765421
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Mermithida-ND4L-Aligned-DNA.fas.FEL.json
##	306.0492371
##	$/{\tt Users/Sadie/bin/mtDNA_redo/data/FEL/Mermithida-ND5-Aligned-DNA.fas.FEL.json}$
##	654.6458154
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Mermithida-ND6-Aligned-DNA.fas.FEL.json
##	376.8323623 /Users/Sadie/bin/mtDNA_redo/data/FEL/neuroptera-atp6-align-dna.fas.FEL.json
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##	/Users/Sadie/bin/mtDNA_redo/data/FEL/neuroptera-cox3-align-dna.fas.FEL.json
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##	$/ Users/Sadie/bin/mtDNA_redo/data/FEL/Ophidii formes-ATP6-Aligned-DNA.fas.FEL.json$
##	230.2346303
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Ophidiiformes-ATP8-Aligned-DNA.fas.FEL.json

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##
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##
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```

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                                                                                 368.8145365
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##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-CYTB-Aligned-DNA.fas.FEL.json
##	263.9130950
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND1-Aligned-DNA.fas.FEL.json
##	152.0801005
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND2-Aligned-DNA.fas.FEL.json
##	205.0136334
## ##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND3-Aligned-DNA.fas.FEL.json 198.3977185
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND4-Aligned-DNA.fas.FEL.json
##	225.5084729
##	/Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND4L-Aligned-DNA.fas.FEL.json

```
##
                                                                                   14.7791568
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND5-Aligned-DNA.fas.FEL.json
##
##
                                                                                  333.5461916
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Unionoida-ND6-Aligned-DNA.fas.FEL.json
##
##
                                                                                  204.6207937
##
              /Users/Sadie/bin/mtDNA redo/data/FEL/Veneroida-ATP6-Aligned-DNA.fas.FEL.json
##
                                                                                   29.3940929
##
              /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-COX1-Aligned-DNA.fas.FEL.json
##
                                                                                  120.8186476
##
              /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-COX2-Aligned-DNA.fas.FEL.json
##
                                                                                  145.5236314
              /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-COX3-Aligned-DNA.fas.FEL.json
##
##
                                                                                   84.8585775
##
              /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-CYTB-Aligned-DNA.fas.FEL.json
##
                                                                                   83.8770733
##
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-ND1-Aligned-DNA.fas.FEL.json
##
                                                                                  118.6079550
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-ND2-Aligned-DNA.fas.FEL.json
##
                                                                                   88.1262381
##
##
               /Users/Sadie/bin/mtDNA redo/data/FEL/Veneroida-ND3-Aligned-DNA.fas.FEL.json
##
                                                                                  106.2712731
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-ND4-Aligned-DNA.fas.FEL.json
##
##
                                                                                  134.5214304
##
              /Users/Sadie/bin/mtDNA redo/data/FEL/Veneroida-ND4L-Aligned-DNA.fas.FEL.json
##
                                                                                   11.2818741
##
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-ND5-Aligned-DNA.fas.FEL.json
                                                                                  157.1095235
##
##
               /Users/Sadie/bin/mtDNA_redo/data/FEL/Veneroida-ND6-Aligned-DNA.fas.FEL.json
##
                                                                                  119.2177476
                /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-atp6-align-dna.fas.FEL.json
##
##
                                                                                   75.2843074
##
                /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-atp8-align-dna.fas.FEL.json
##
                                                                                   86.8787157
##
                /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-cox1-align-dna.fas.FEL.json
##
                                                                                  111.8207667
                 /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-nd1-align-dna.fas.FEL.json
##
##
                                                                                  108.0882303
##
                /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-nd41-align-dna.fas.FEL.json
##
                                                                                   77.8975053
##
                 /Users/Sadie/bin/mtDNA_redo/data/FEL/zeiformes-nd5-align-dna.fas.FEL.json
##
                                                                                  181.3668198
##
                 /Users/Sadie/bin/mtDNA redo/data/FEL/zeiformes-nd6-align-dna.fas.FEL.json
                                                                                   95.6693558
take that clean it up so you have gene, order, alpha/beta JSD.
cleanup <- str extract all(names(t), "\\w+(?=-)", simplify = T)</pre>
f <- tibble(order = cleanup[,1], gene = cleanup[,2], JSD_alpha_beta = t)</pre>
stopped here
```

#hclust(f\$JSD_alpha_beta) %>% plot()