Plaice

2024-07-17

```
library(dplyr)
```

```
## Warning: package ’dplyr’ was built under R version 4.3.3
```

```
##
## Attaching package: ’dplyr’
```

```
## The following objects are masked from ’package:stats’:
##
##     filter, lag
```

```
## The following objects are masked from ’package:base’:
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

```
## Warning: package ’ggplot2’ was built under R version 4.3.3
```

```
library(bbmle)
```

```
## Warning: package ’bbmle’ was built under R version 4.3.3
```

```
## Loading required package: stats4
```

```
##
## Attaching package: ’bbmle’
```

```
## The following object is masked from ’package:dplyr’:
##
##     slice
```

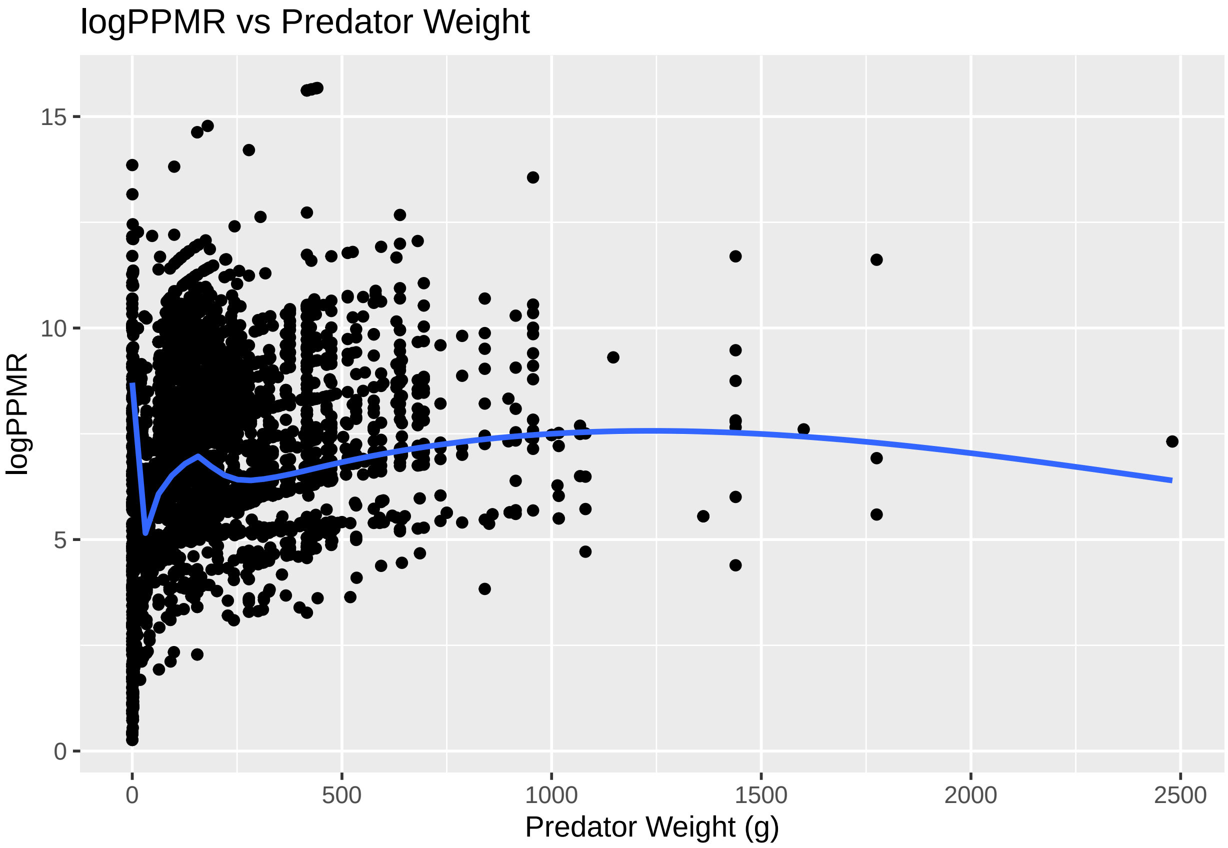
```
load("C:/Users/lucab/Downloads/stomach_dataset.Rdata")

sprat <- stom_df%>%filter(pred_taxa=="Pleuronectes platessa")
```

```
ggplot(sprat, aes(x=pred_weight_g, y=log(ppmr)))+
  geom_point()+
  geom_smooth(method="gam", se=FALSE, aes(weight = nprey_perpred))+
  labs(title="logPPMR vs Predator Weight", x="Predator Weight (g)", y="logPPMR")
```

```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```

```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (`stat_smooth()`).
```

```
## Warning: Removed 111 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

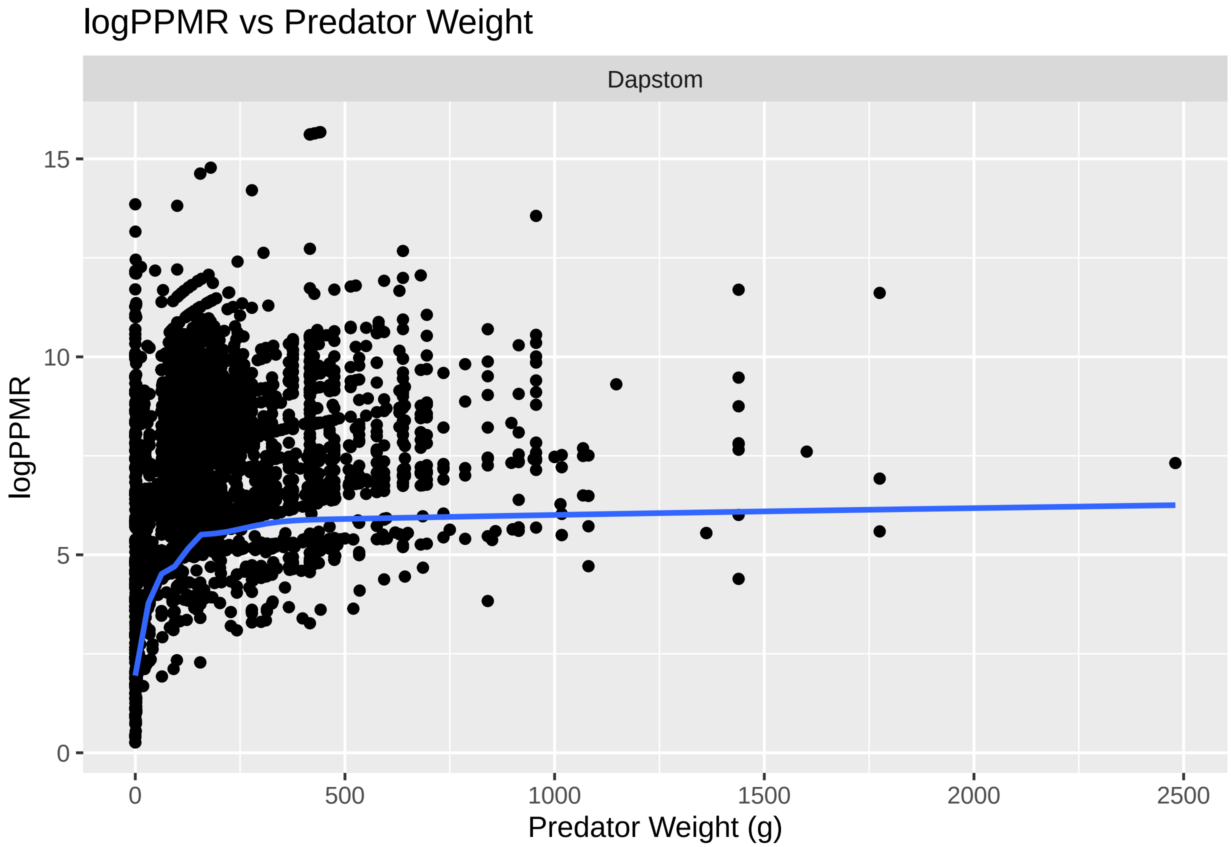


```r
dig <- 1

ggplot(sprat, aes(x=pred_weight_g, y=log(ppmr)))+
  geom_point()+
  facet_wrap(~data)+
  geom_smooth(method="gam", se=FALSE, aes(weight = nprey_perpred*sprat$prey_ind_weight_g^dig))+
  labs(title="logPPMR vs Predator Weight", x="Predator Weight (g)", y="logPPMR")
```

```
## Warning: Use of `sprat$prey_ind_weight_g` is discouraged.
## i Use `prey_ind_weight_g` instead.
```

```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```

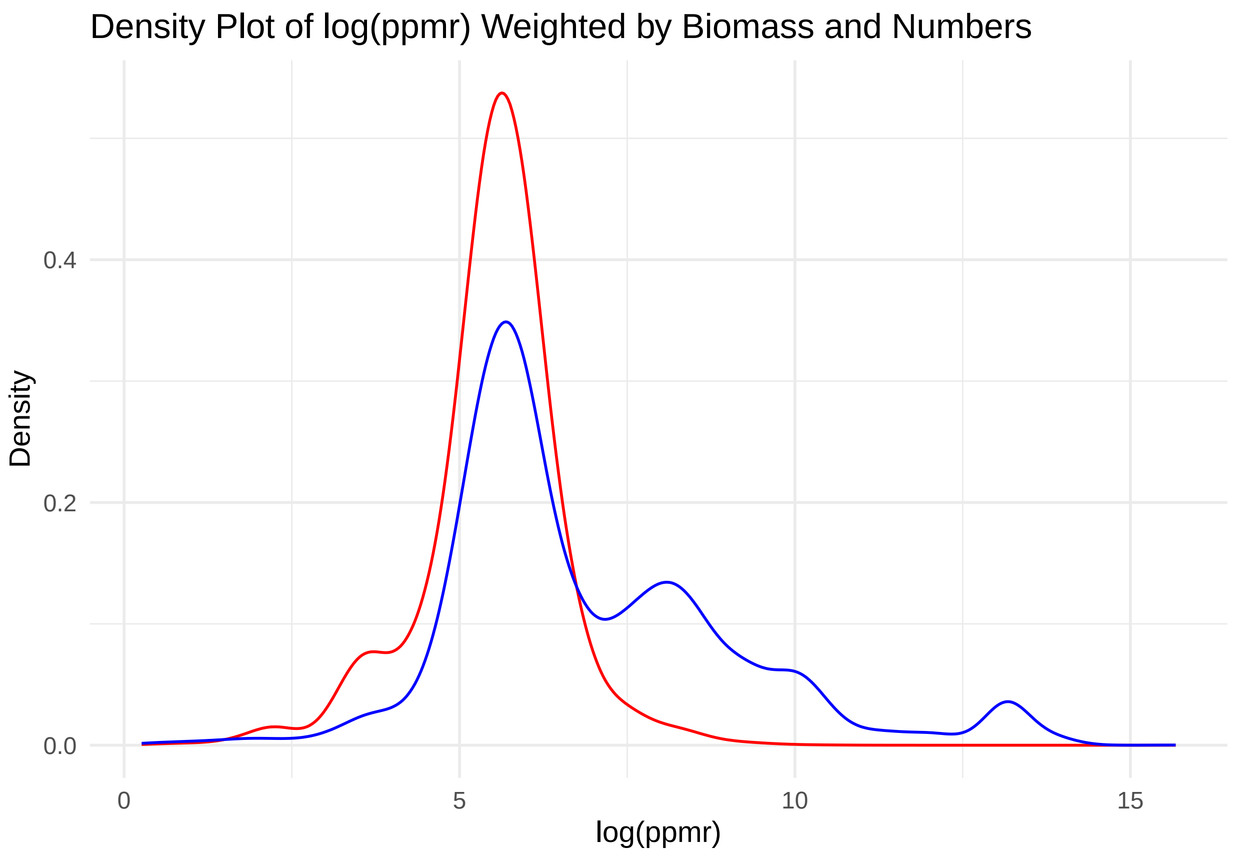
```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (`stat_smooth()`).
## Warning: Removed 111 rows containing missing values or values outside the scale range
## (‘geom_point()‘).
```



The PPMR does seem to increase at the largest sizes, should I remove or just ignore?

```
sprat$weight_numbers <- sprat$nprey_perpred
sprat$weight_biomass <- sprat$nprey_perpred*sprat$prey_ind_weight_g^dig

ggplot() +
  geom_density(data = sprat, aes(x = log(ppmr), weight = weight_biomass), color = "red") +
  geom_density(data = sprat, aes(x = log(ppmr), weight = weight_numbers), color = "blue") +
  labs(title = "Density Plot of log(ppmr) Weighted by Biomass and Numbers",
       x = "log(ppmr)",
       y = "Density") +
  theme_minimal()
```

```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
## Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
```



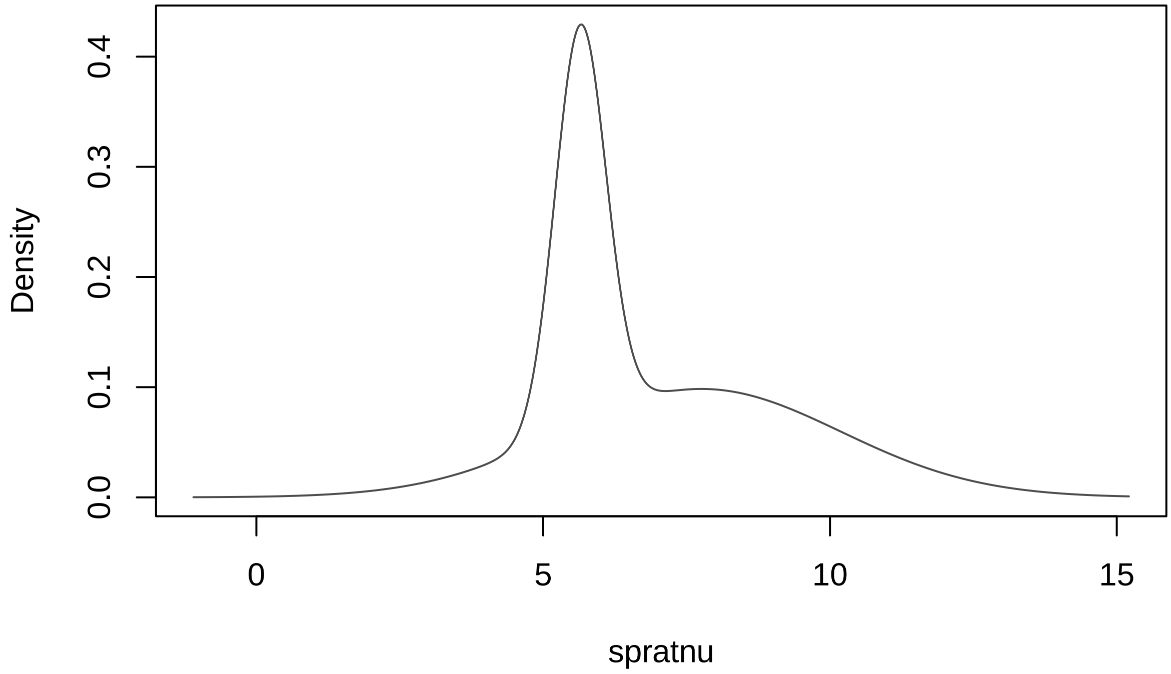
This looks like 2 mixture gaussains.

```
library(mclust)
```

```
## Warning: package 'mclust' was built under R version 4.3.3
```

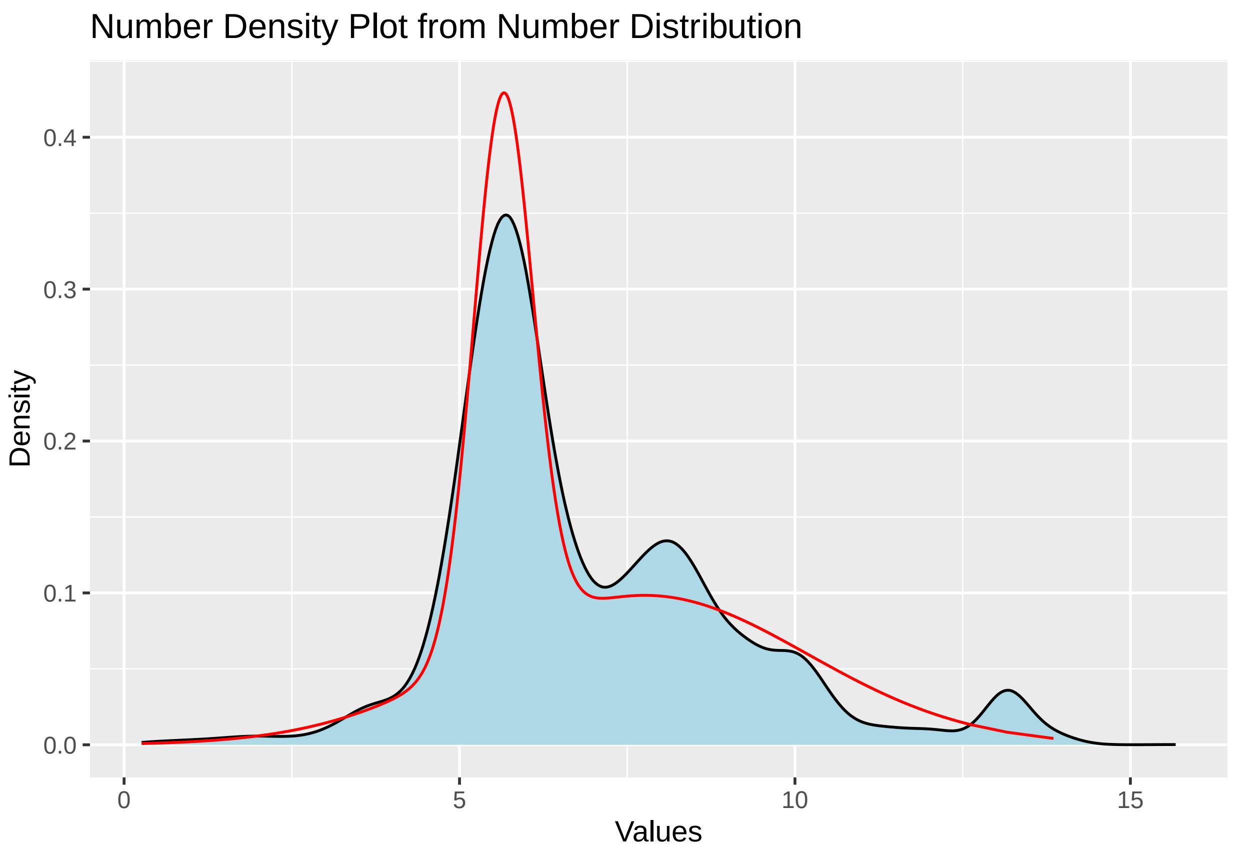
```
## Package 'mclust' version 6.1.1
## Type 'citation("mclust")' for citing this R package in publications.
```

```
repeat_elements <- function(data, weights) {

    valid_indices <- !is.na(data) & !is.na(weights)
  data <- data[valid_indices]
  weights <- weights[valid_indices]

  final_vector <- c()

  for (i in seq_along(data)) {

    rounded_weight <- round(weights[i])

    repeated_values <- rep(data[i], times = rounded_weight)

    final_vector <- c(final_vector, repeated_values)
  }
  return(final_vector)
}

spratnu <- repeat_elements(log(sprat$ppmr), sprat$nprey_perpred)

gmm <- densityMclust(spratnu, G=2)
```



```
dplot <- data.frame(x=gmm[["data"]], density=gmm[["density"]])


(numbfit <- ggplot() +
    geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers), fill="lightblue")+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  labs(x = "Values", y = "Density") +
  ggtitle("Number Density Plot from Number Distribution"))
```

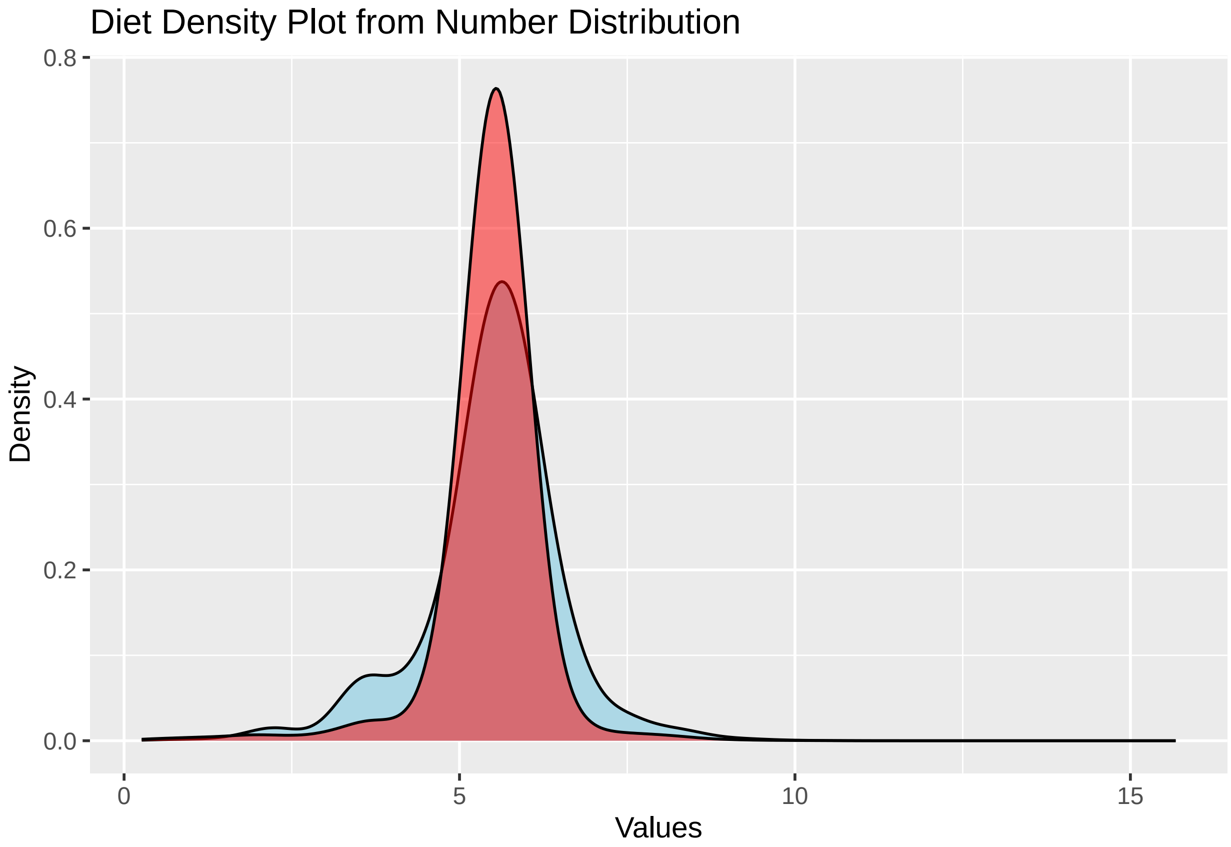
```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
```



Now lets shift over.

```
newspratdens <- gmm[["density"]]*exp(-dig*gmm[["data"]])
shifted_pdf_normalized <- newspratdens / sum(newspratdens)

#making new dataframe
dplot <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfitbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass), fill="lightblue")+
  geom_density(data=dplot, aes(x, weight=shifted_pdf_normalized), fill="red", alpha=0.5)+
 #geom_line(data=dplot, aes(x = x, y = density), color="red") +
 labs(x = "Values", y = "Density") +
 ggtitle("Diet Density Plot from Number Distribution"))
```

```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
```

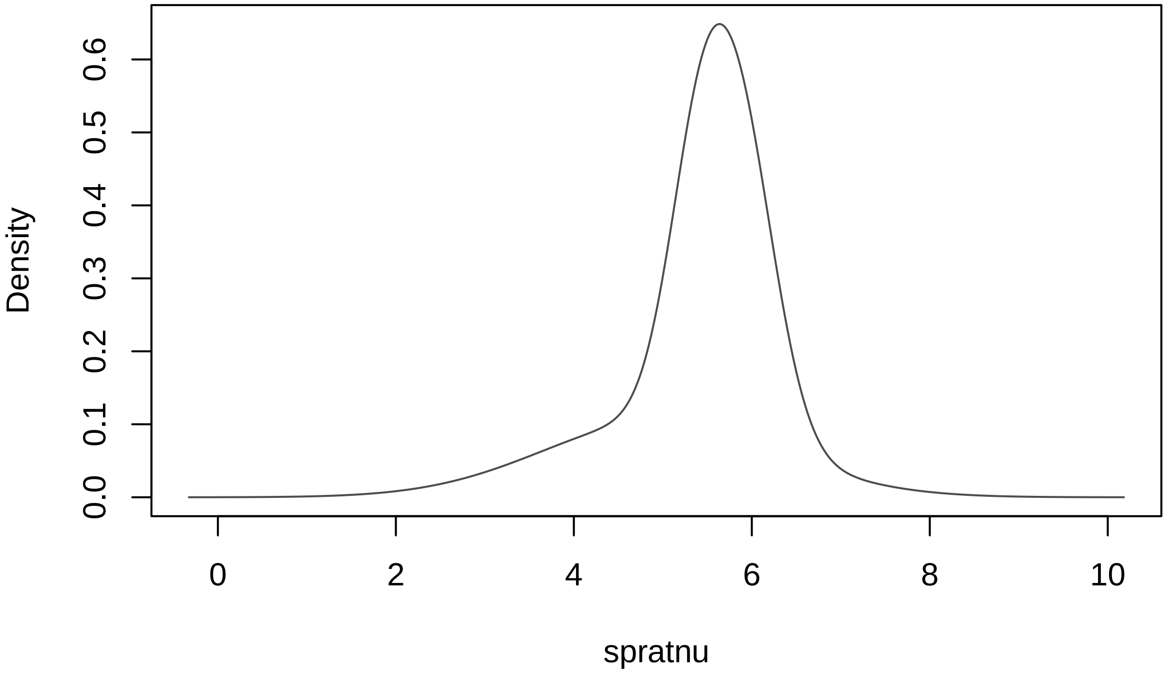


This isnt a terrible shift. (It is the best shift we have, here is the parameters)

```
print(gmm$parameters)
```

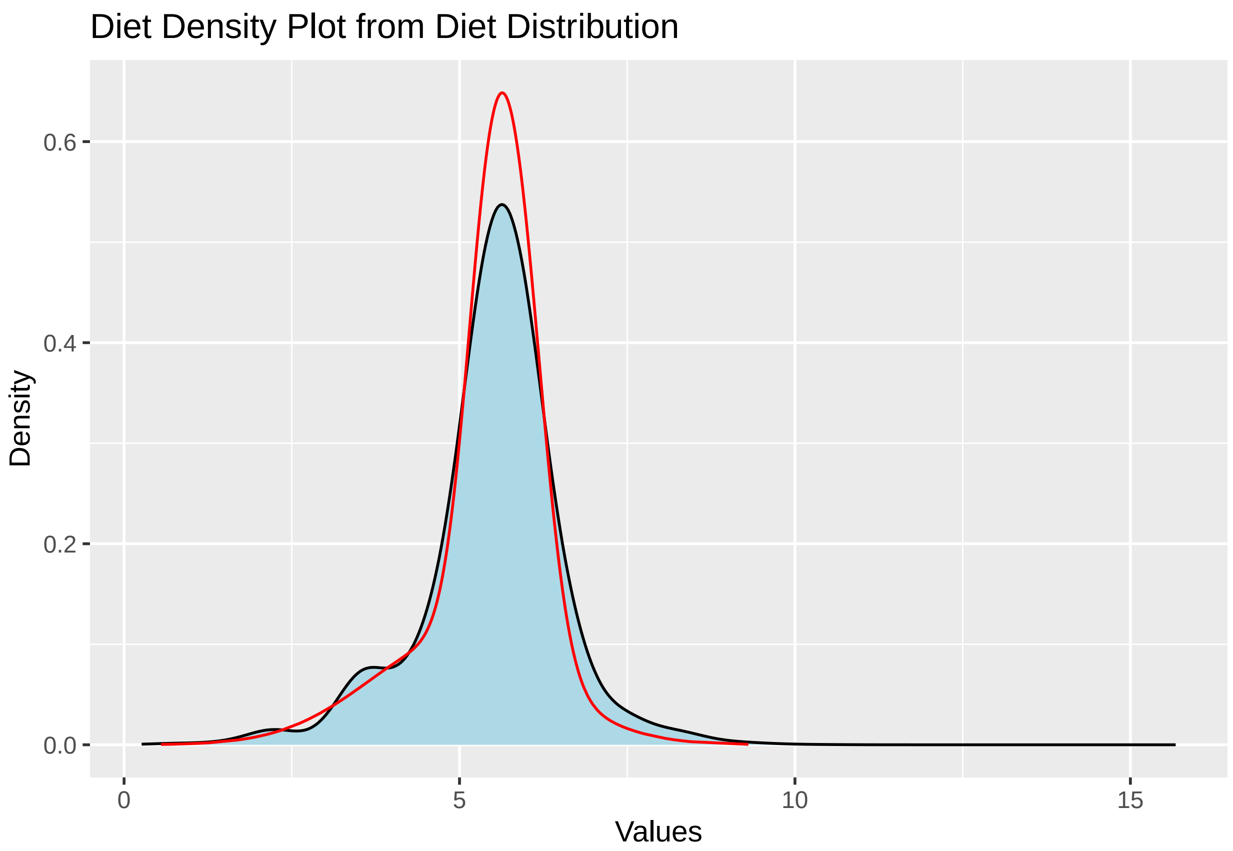
```
## $pro
## [1] 0.4013671 0.5986329
##
## $mean
##        1        2
## 5.650236 7.762250
##
## $variance
## $variance$modelName
## [1] "V"
##
## $variance$d
## [1] 1
##
## $variance$G
## [1] 2
##
## $variance$sigmasq
## [1] 0.1959833 5.8912814
##
## $variance$scale
## [1] 0.1959833 5.8912814
```

```
spratnu <- repeat_elements(log(sprat$ppmr), sprat$nprey_perpred*sprat$prey_ind_weight_g^dig)
gmm <- densityMclust(spratnu, G=3)
```



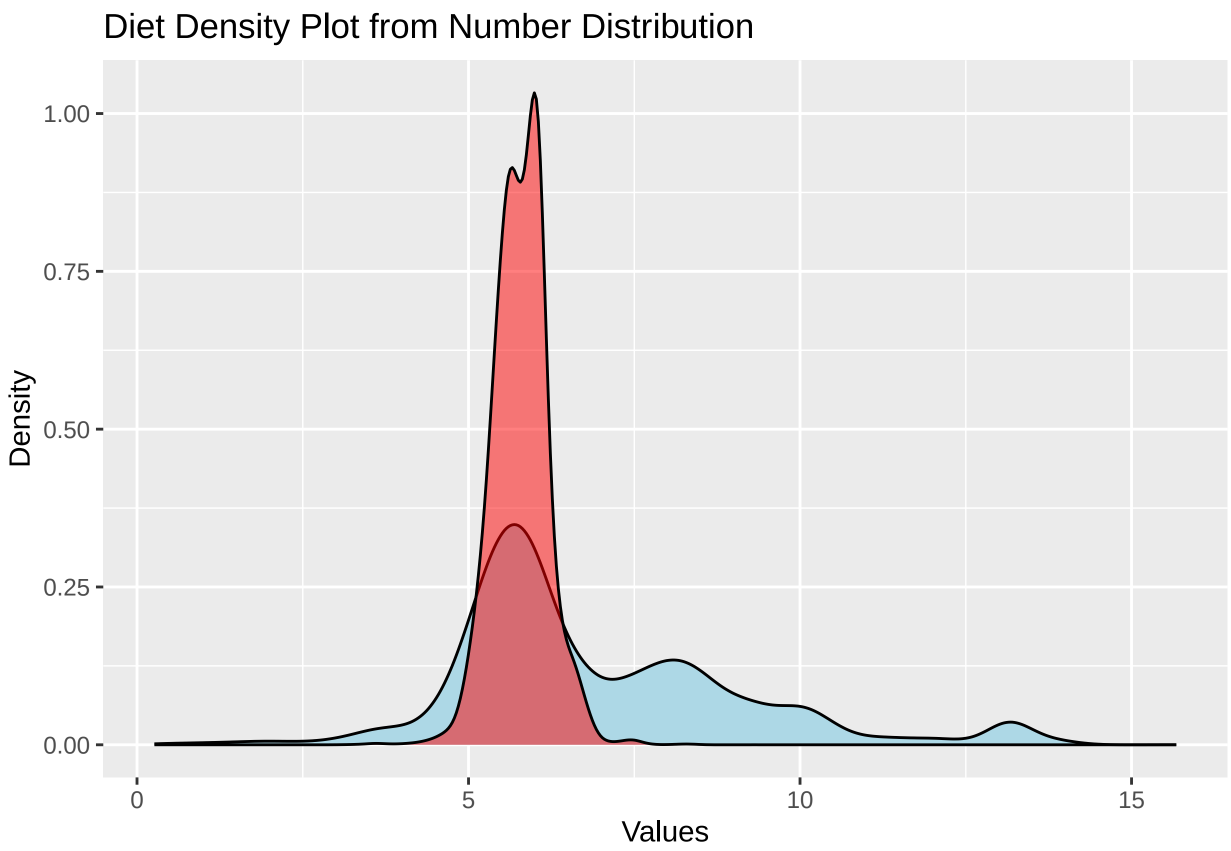
```
dplot <- data.frame(x=gmm[["data"]], density=gmm[["density"]])

(biofit <- ggplot() +
    geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass), fill="lightblue")+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  labs(x = "Values", y = "Density") +
  ggtitle("Diet Density Plot from Diet Distribution"))
```

```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
```



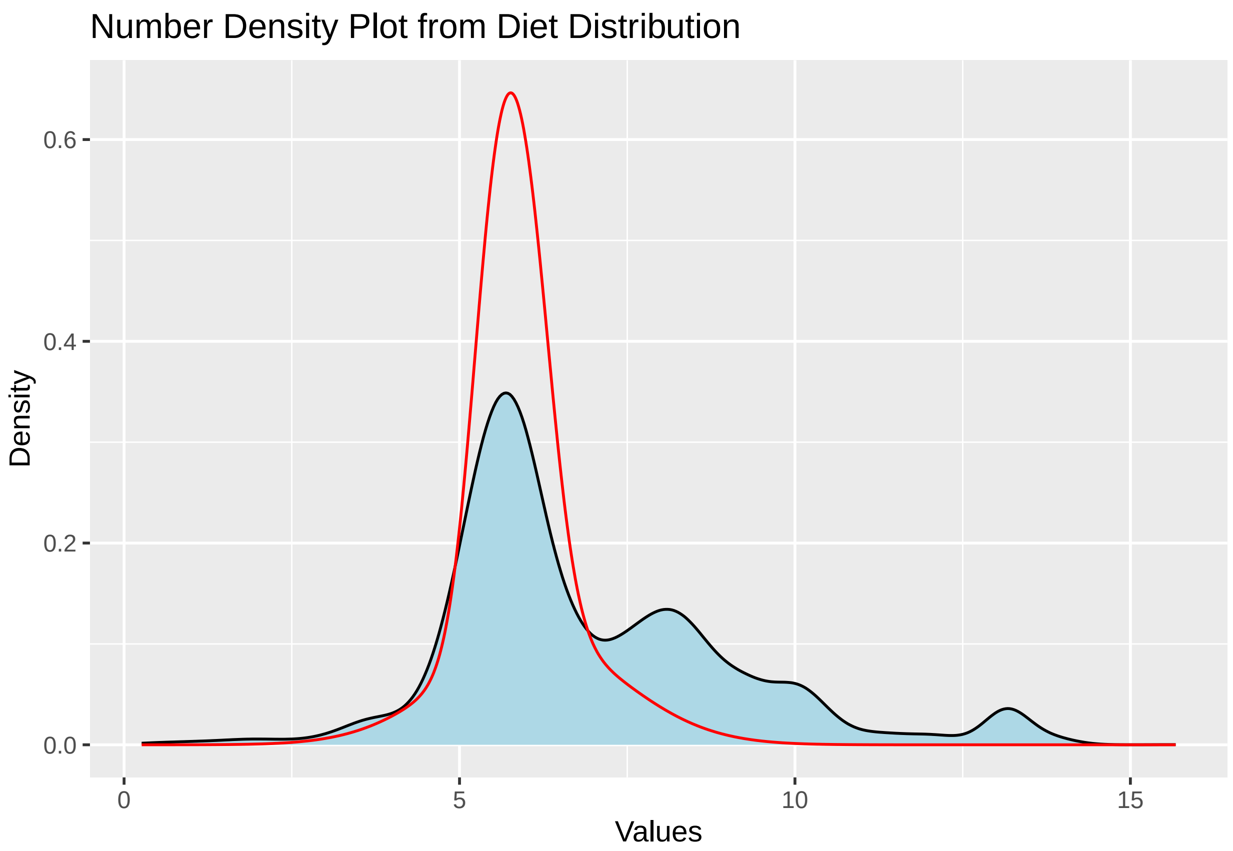
```
newspratdens <- gmm[["density"]]*exp(dig*gmm[["data"]])

shifted_pdf_normalized <- newspratdens / sum(newspratdens)

dplot <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfitbio <- ggplot() +
    geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers), fill="lightblue")+
    geom_density(data=dplot, aes(x, weight=shifted_pdf_normalized), fill="red", alpha=0.5)+
  #geom_line(data=dplot, aes(x = x, y = density), color="red") +
  labs(x = "Values", y = "Density") +
  ggtitle("Diet Density Plot from Number Distribution"))
```

```
## Warning: Removed 111 rows containing non-finite outside the scale range
## (‘stat_density()‘).
```



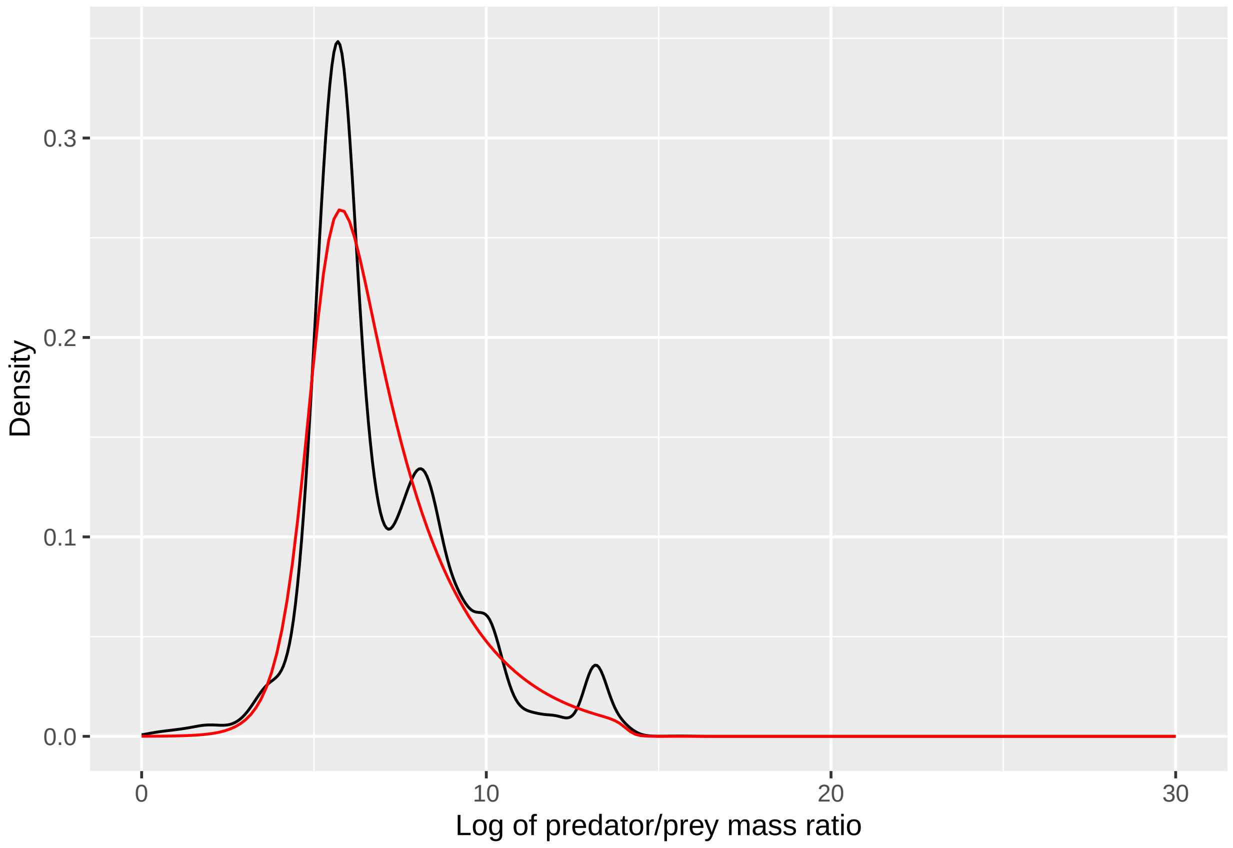
```
#I dont think I have done it right here, so I will do it in another way

shifted_fit <- gmm
shifted_fit[["parameters"]][["mean"]] <- shifted_fit[["parameters"]][["mean"]]+
  (2/3)*shifted_fit[["parameters"]][["variance"]][["sigmasq"]]

sprat$l <- log(sprat$ppmr)
sprat <- sprat[!is.na(sprat$l),]
x_vals <- seq(min(sprat$l), max(sprat$l), length.out = 1000)

#generating the density values
shifted_pdf <- sapply(x_vals, function(x) {
  sum(shifted_fit$parameters$pro * dnorm(x, mean = shifted_fit$parameters$mean, sd = sqrt(shifted_fit$pa
})

plot_data <- data.frame(x = x_vals, shifted_pdf = shifted_pdf)

(biofitnum <- ggplot() +
    geom_density(data=sprat, aes(log(sprat$ppmr), weight=weight_numbers), fill="lightblue")+
  geom_line(data=plot_data, aes(x = x_vals, y = shifted_pdf), color="red") +
  labs(x = "Values", y = "Density") +
  ggtitle("Number Density Plot from Diet Distribution"))
```

```
## Warning: Use of ‘sprat$ppmr‘ is discouraged.
## i Use ‘ppmr‘ instead.
```



Ok, so the number density to biomass is not too bad. WIll try exponential for fun.

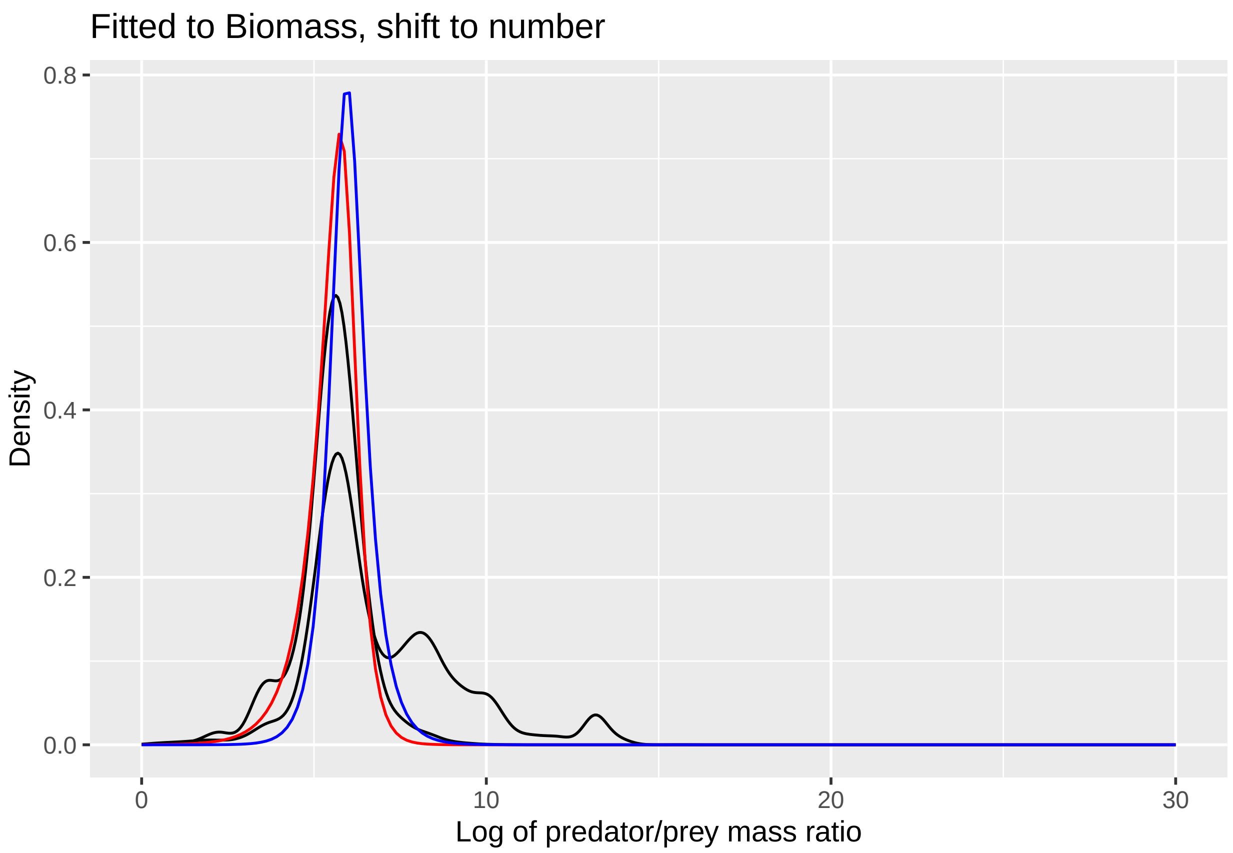
```
sprat <- sprat %>%
  filter(!is.na(l))
stomach <- sprat
stomach$l <- log(stomach$ppmr)
stomach <- stomach[!is.na(stomach$l),]
stomach <- stomach %>% mutate(weight_numbers = nprey_perpred)

fl <- function(l, alpha, ll, ul, lr, ur) {
  dl <- ll - l
  dr <- l - lr
  fl_values <- exp(alpha * l) / (1 + exp(ul * dl)) / (1 + exp(ur * dr))

  # Debugging output
  if (any(!is.finite(fl_values))) {
    print("Non-finite fl values found")
    print(fl_values)
  }

  return(fl_values)
}

## Define the truncated exponential PDF with debugging
dtexp <- function(l, alpha, ll, ul, lr, ur) {
  fl_values <- fl(l, alpha, ll, ul, lr, ur)
  integral_result <- tryCatch(
    integrate(fl, 0, 30, alpha = alpha, ll = ll, ul = ul, lr = lr, ur = ur),
    error = function(e) {
      print("Integration failed")
     print(e)
      return(NULL)
    }
   )

   if (is.null(integral_result)) {
     return(rep(NA, length(l)))
   }

   d <- fl_values / integral_result$value

  # Debugging output
  if (any(!is.finite(d))) {
    print("Non-finite d values found")
    print(d)
  }

  return(d)
}

 #Define the MLE function with debugging
mle_texp <- function(df) {
  loglik <- function(alpha, ll, ul, lr, ur) {
    L <- dtexp(df$l, alpha, ll, ul, lr, ur)

    # Debugging output
    if (any(!is.finite(L) | L <= 0)) {
     print("Non-finite or non-positive L values found")
      print(which(!is.finite(L) | L <= 0))
      return(Inf)
    }

    -sum(log(L) * df$weight_numbers)
  }

  result <- tryCatch(
    mle2(loglik, start = list(
      alpha = 0.5,
      ll = min(df$l),
      lr = max(df$l),
      ul = 5,
      ur = 5
    ), method = "L-BFGS-B", control = list(maxit = 10000)),
    error = function(e) {
      print("MLE fitting failed")
      print(e)
      return(NULL)
    }
  )
  return(result)
}

est <- mle_texp(stomach)

biomassco <- est@coef

grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassco[1]), ll = biomassco[2], ul = biomassco[3],
              lr = biomassco[4], ur = biomassco[5])

dist <- data.frame(l=grid, Density=dist)

  ggplot(stomach) +
  geom_density(aes(l, weight=weight_numbers))+
 xlab("Log of predator/prey mass ratio") +
  geom_line(aes(l, Density), data = dist, color = "red")
```



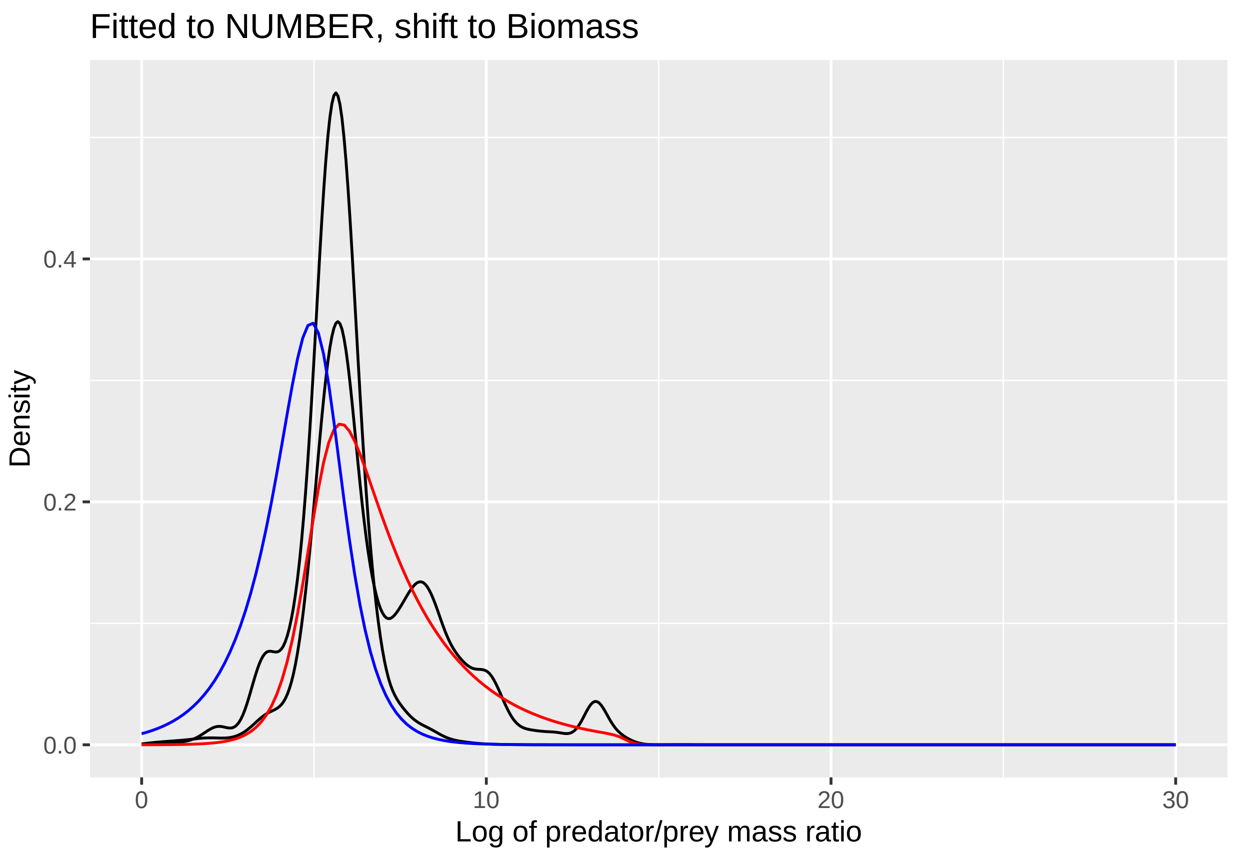
Lets try to plot both.

```
stomach <- stomach %>% mutate(weight_numbers = nprey_perpred * prey_ind_weight_g)
est <- mle_texp(stomach)
biomassestco <- est@coef
```

```r
stomach <- stomach %>% mutate(weight_numbers = nprey_perpred)
est <- mle_texp(stomach)
numberestco <- est@coef

grid = seq(0, 30, length.out = 200)
dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomasse
biomassdist <- data.frame(l=grid, Density=dist)
shiftdist <- dtexp(grid, alpha = (biomassestco[1]+1), ll = biomassestco[2], ul = biomassestco[3], lr = b
shiftbiomassdist <- data.frame(l=grid, Density=shiftdist)


dist <- dtexp(grid, alpha = (numberestco[1]), ll = numberestco[2], ul = numberestco[3], lr = numberestco
numberdist <- data.frame(l=grid, Density=dist)
shiftdist <- dtexp(grid, alpha = (numberestco[1]-1), ll = numberestco[2], ul = numberestco[3], lr = numb
shiftnumberdist <- data.frame(l=grid, Density=shiftdist)
#now plot these two together

stomach <- stomach %>% mutate( biomass = nprey_perpred * prey_ind_weight_g)

ggplot(stomach) +
  geom_density(aes(l, weight=weight_numbers))+
  geom_density(aes(l, weight=biomass))+
 xlab("Log of predator/prey mass ratio") +
  geom_line(aes(l, Density), data = biomassdist, color = "red")+
  geom_line(aes(l, Density), data = shiftbiomassdist, color = "blue")+
  ggtitle("Fitted to Biomass, shift to number")
```



```
ggplot(stomach) +
  geom_density(aes(l, weight=weight_numbers))+
  geom_density(aes(l, weight=biomass))+
 xlab("Log of predator/prey mass ratio") +
  geom_line(aes(l, Density), data = numberdist, color = "red")+
  geom_line(aes(l, Density), data = shiftnumberdist, color = "blue")+
  ggtitle("Fitted to NUMBER, shift to Biomass")
```



The exponential fit is not good. SO we will use the mixture gaussian.