

# Final Predation kernels

2024-07-22

##Cod

```
dig <- 1
sprat <- stom_df %>% filter(pred_taxa=="Gadus morhua")
sprat <- sprat %>% filter(nprey_perpred>0)
sprat$weight_numbers <- sprat$nprey_perpred
sprat$weight_biomass <- sprat$nprey_perpred*sprat$prey_ind_weight_g^dig
stomach <- sprat
stomach <- stomach %>% mutate(l=log(ppmr)) %>% filter(!is.na(l))

est <- mle_texp(stomach)

biomassco <- est@coef

numberestco <- biomassco

grid = seq(min(stomach$l), max(stomach$l), length.out = 200)
dist <- dtexp(grid, alpha = (numberestco[1]), ll = numberestco[2], ul = numberestco[3], lr = numberestco[4])
numberdist <- data.frame(l=grid, Density=dist)
dist <- dtexp(grid, alpha = (numberestco[1]-1), ll = numberestco[2], ul = numberestco[3], lr = numberestco[4])
biomassdist <- data.frame(l=grid, Density=dist)
#now plot these two together

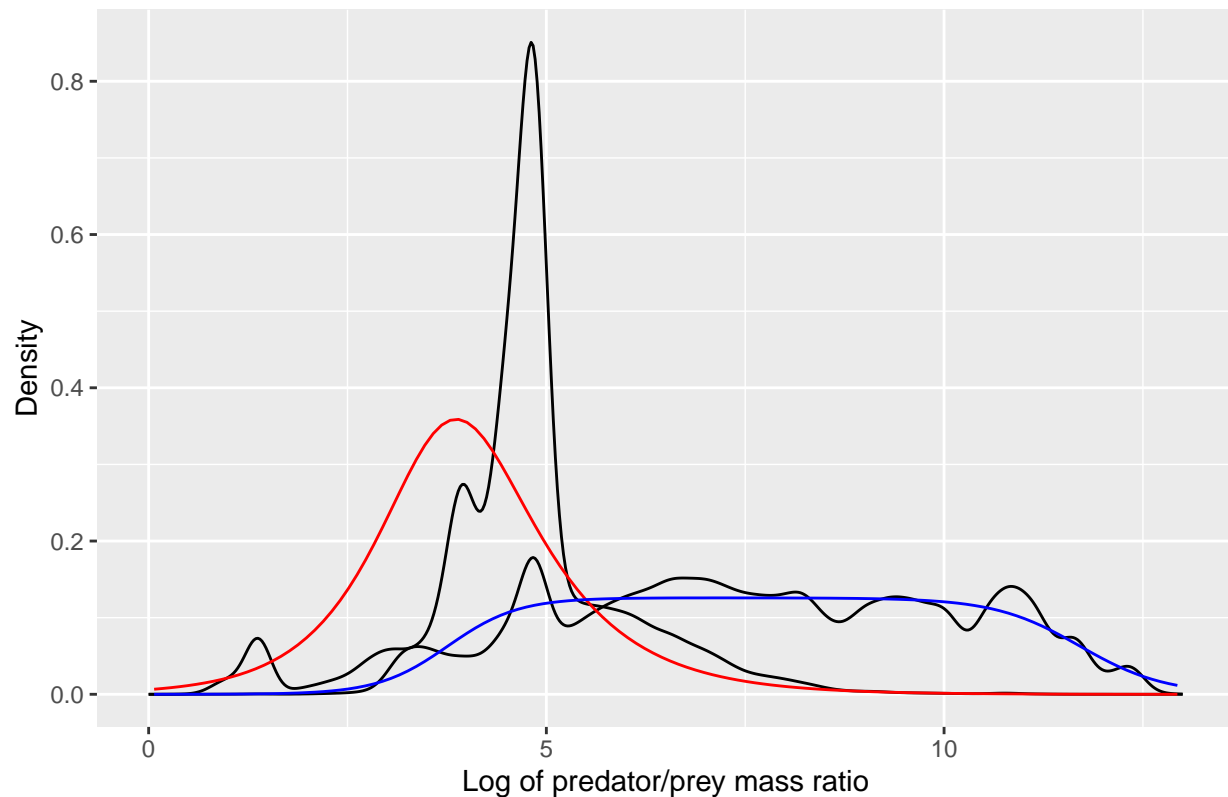
stomach <- stomach %>% mutate(biomass = nprey_perpred * prey_ind_weight_g)

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 = numberdist, color = "blue")+
  xlim(0,13)+
  ggtitle("Cod - Fit to number, shift to diet")

## Warning: Removed 80 rows containing non-finite outside the scale range
## ('stat_density()').
## Removed 80 rows containing non-finite outside the scale range
## ('stat_density()').

## Warning: Removed 78 rows containing missing values or values outside the scale range
## ('geom_line()').
## Removed 78 rows containing missing values or values outside the scale range
## ('geom_line()').
```

## Cod – Fit to number, shift to diet



## Blue Whiting

```
sprat <- stom_df %>% filter(pred_taxa == "Micromesistius poutassou")
sprat <- sprat %>% filter(npred_perpred > 0)
stomach <- sprat
stomach <- stomach %>% mutate(l = log(ppmr)) %>% filter(!is.na(l))
stomach <- stomach %>% mutate(weight_numbers = npred_perpred * prey_ind_weight_g)
stomach$biomass <- stomach$npred_perpred * stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

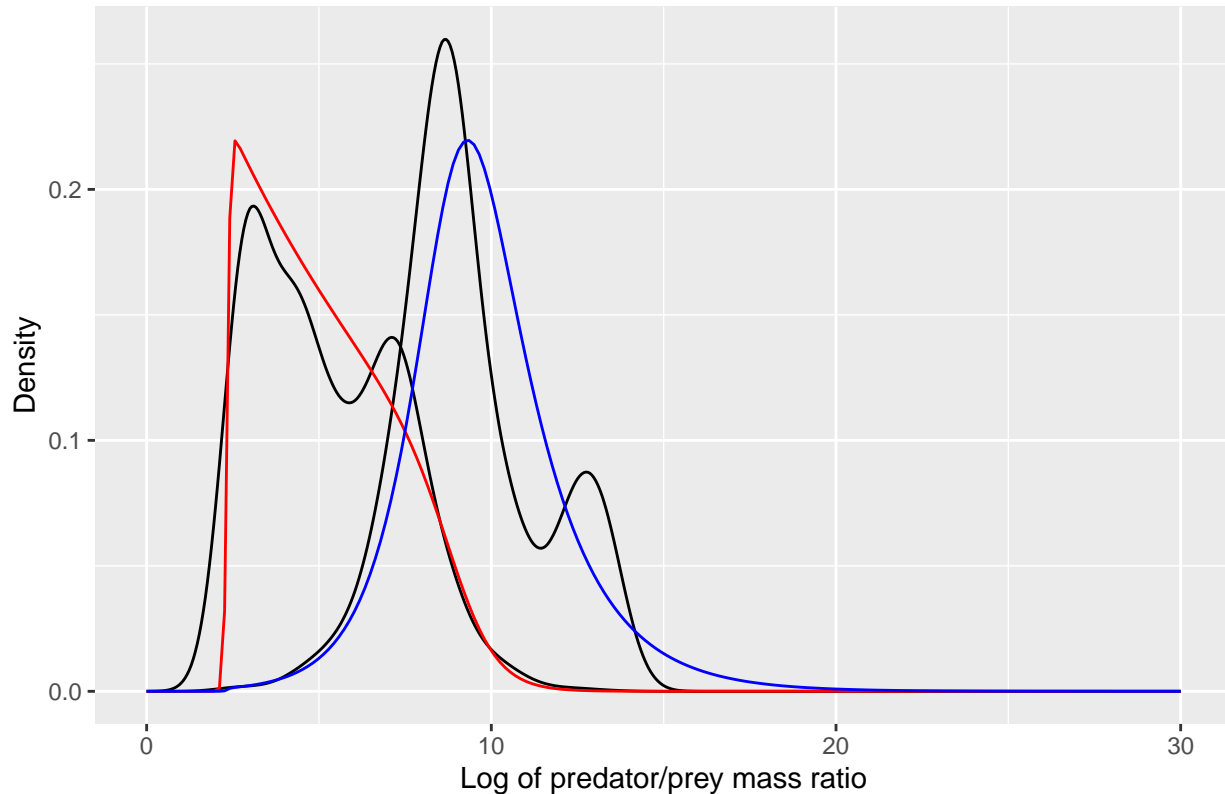
dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l = grid, Density = dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1] + 1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l = grid, Density = shiftdist)

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("Blue Whiting - Fitted to Biomass, shift to number")
```

### Blue Whiting – Fitted to Biomass, shift to number



##Common Dab

```
sprat <- stom_df%>%filter(pred_taxa=="Limanda limanda")
sprat <- sprat%>%filter(npred_perpred>0)
stomach <- sprat
stomach <- stomach%>%mutate(l=log(ppmr))%>%filter(!is.na(l))
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
stomach$biomass <- stomach$npred_perpred*stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

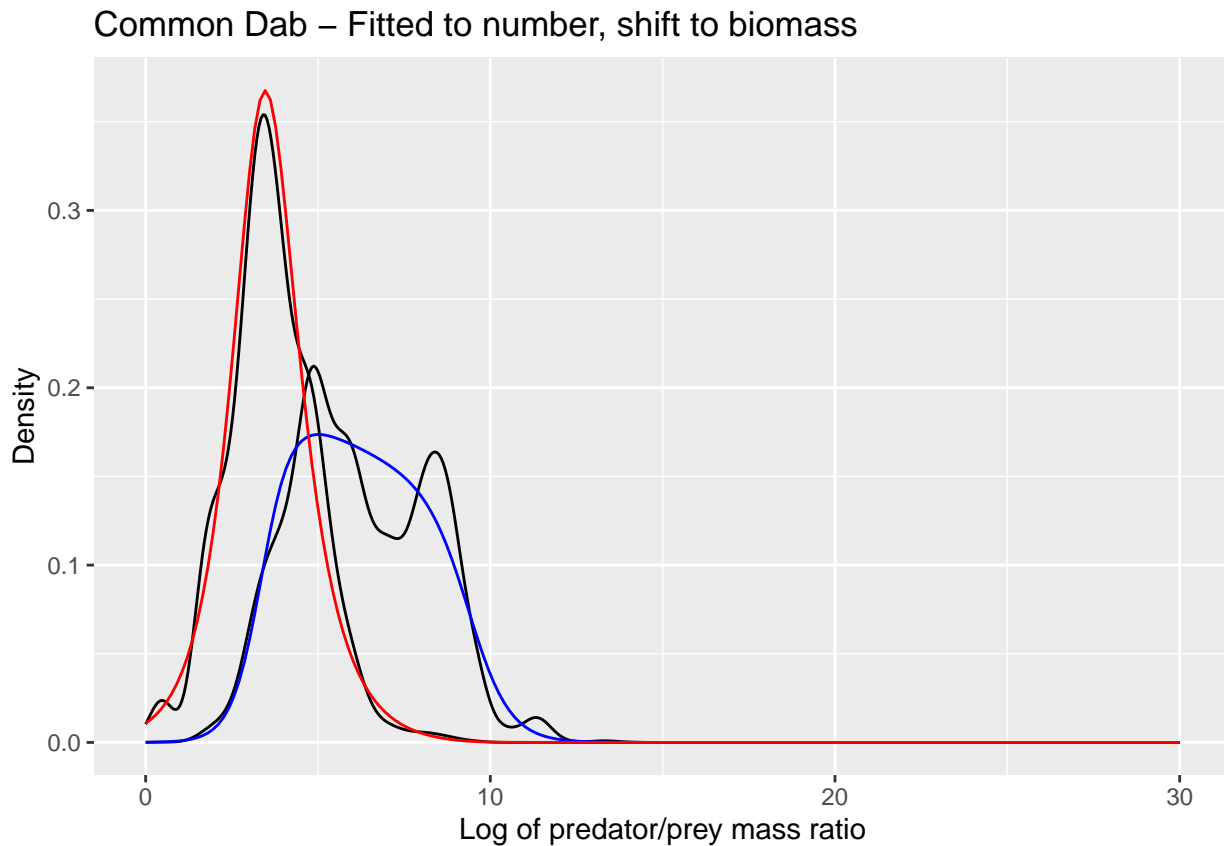
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l=grid, Density=dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1]-1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l=grid, Density=shiftdist)

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 = "blue")+
geom_line(aes(l, Density), data = shiftbiomassdist, color = "red")+
ggtitle("Common Dab – Fitted to number, shift to biomass")
```



```
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])

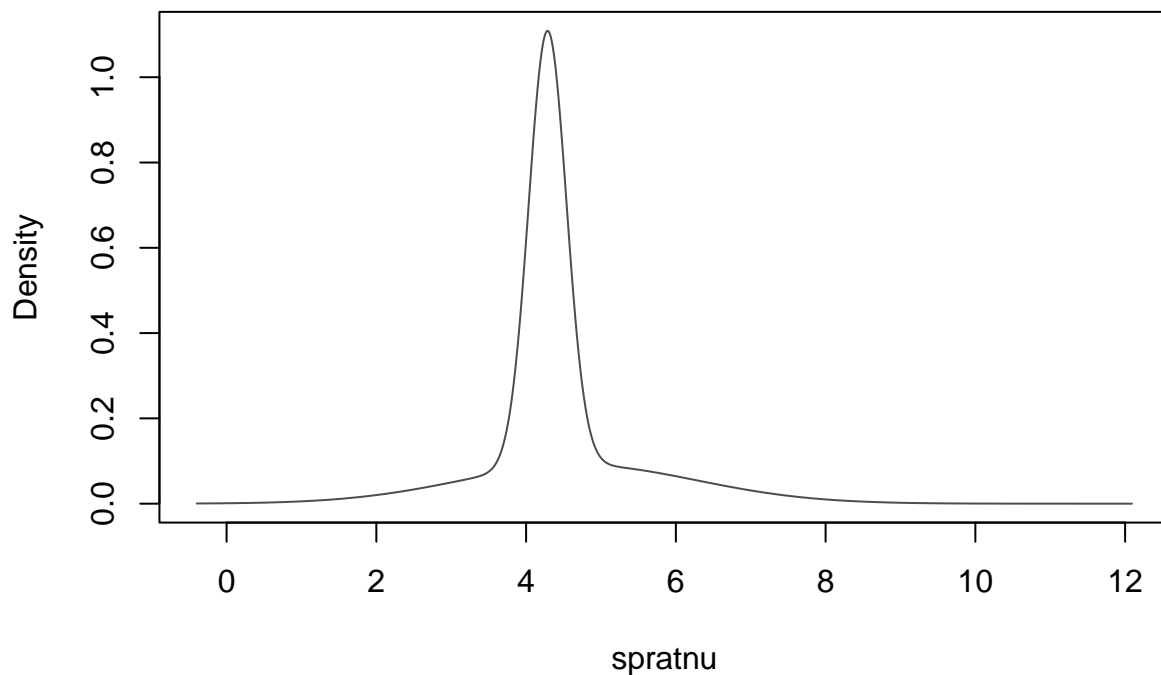
    repeated_values <- rep(data[i], times = rounded_weight)

    final_vector <- c(final_vector, repeated_values)
  }

  return(final_vector)
}
```

```
##European Hake
```

```
sprat <- stom_df%>%filter(pred_taxa=="Merluccius merluccius")
spratnu <- repeat_elements(log(sprat$ppmr), sprat$npred_perpred)
sprat$weight_numbers <- sprat$npred_perpred
sprat$weight_biomass <- sprat$npred_perpred*sprat$pred_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=2)
```



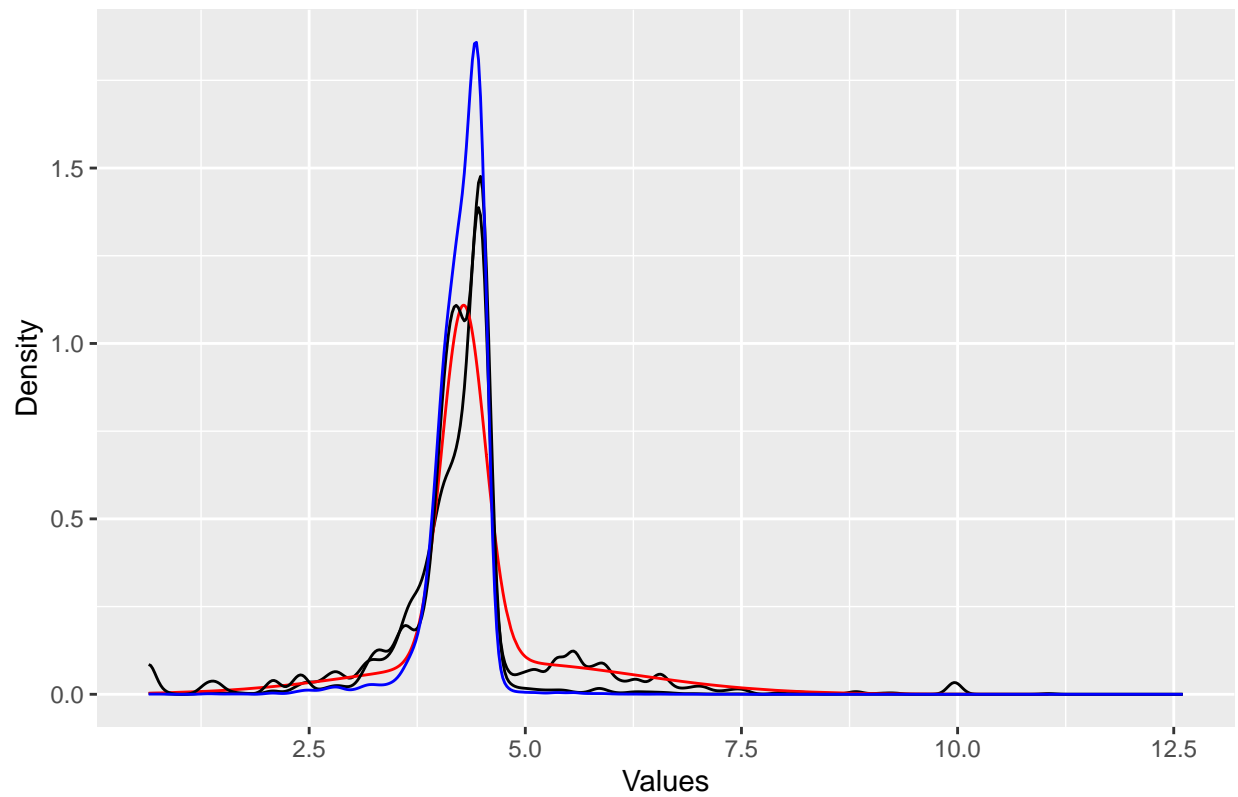
```
dplot <- data.frame(x=gmm[["data"]], density=gmm[["density"]])

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

#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

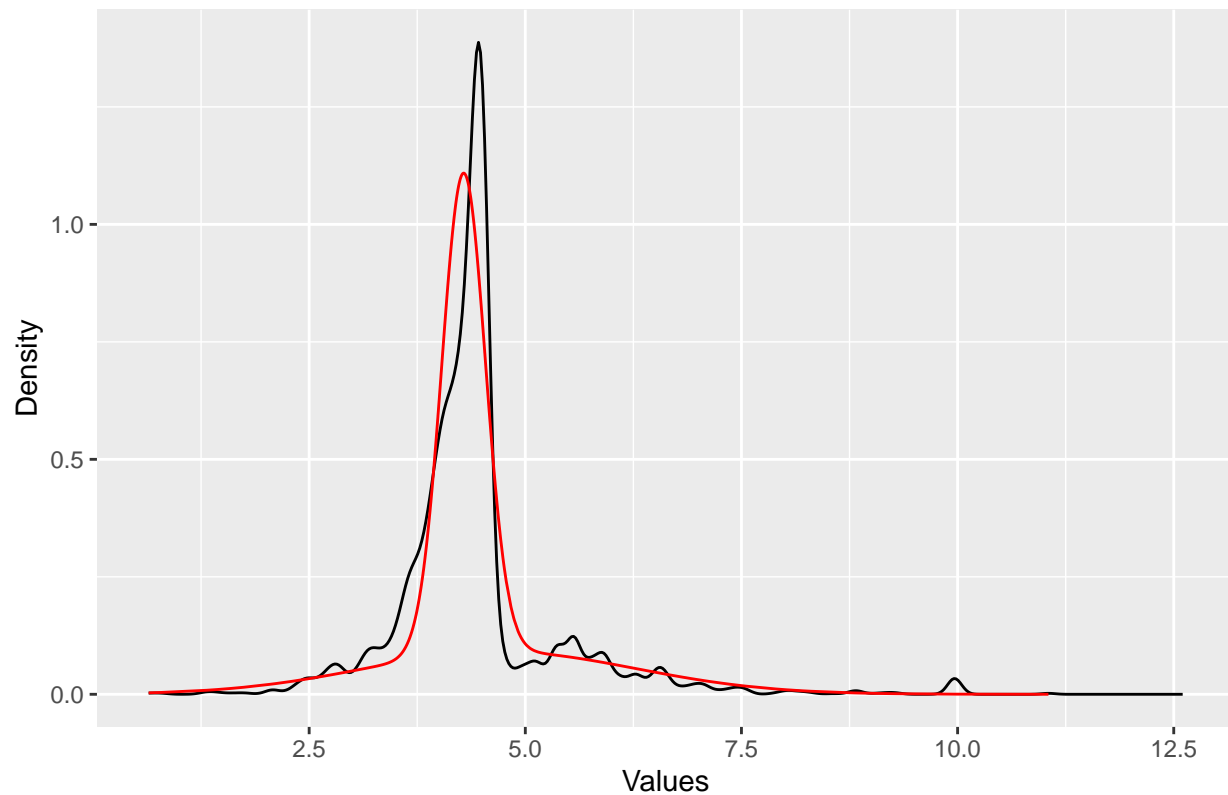
(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("European Hake - Fitted to number, shifted to biomass"))
```

## European Hake – Fitted to number, shifted to biomass



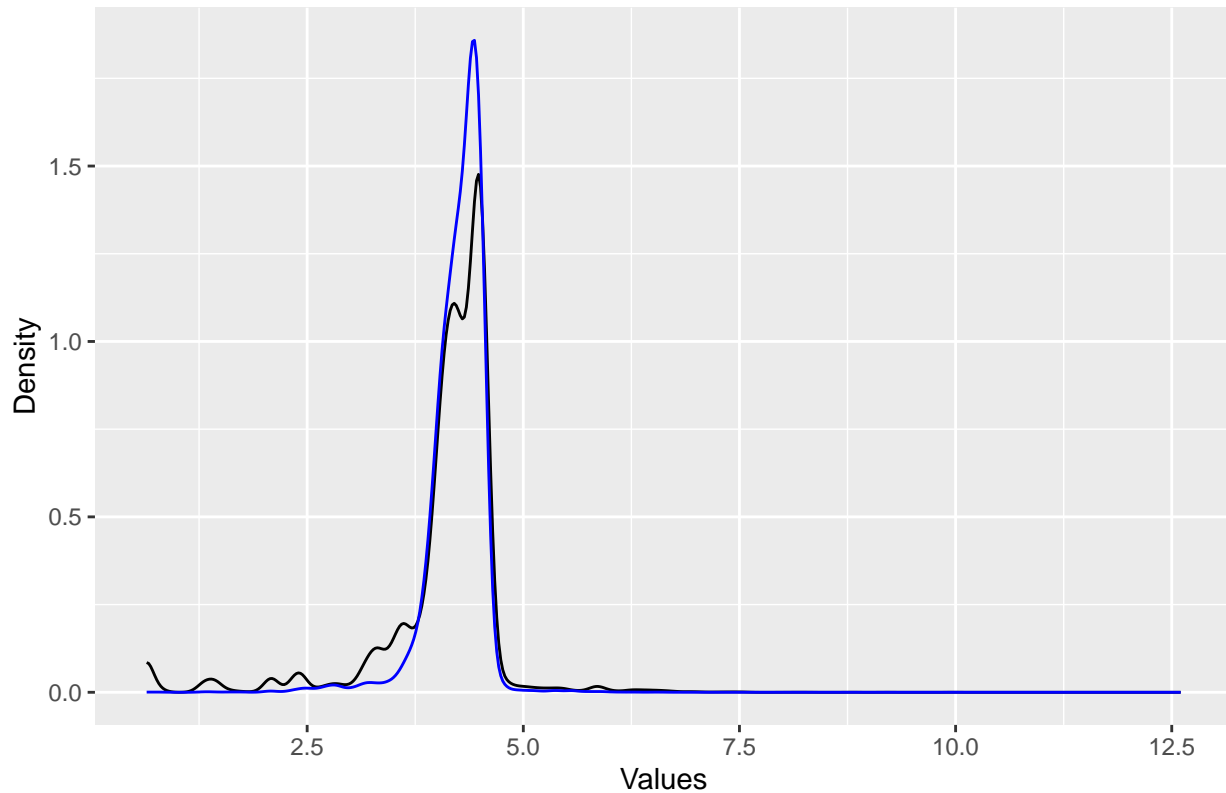
```
#only number
(numbfitt <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers)) +
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  labs(x = "Values", y = "Density") +
  ggtitle("Number Density Plot from Number Distribution"))
```

Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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"))
```

Diet Density Plot from Number Distribution



##Haddock

```
sprat <- stom_df %>% filter(pred_taxa == "Melanogrammus aeglefinus")
sprat <- sprat %>% filter(npred_perpred > 0)
stomach <- sprat
stomach <- stomach %>% mutate(l = log(ppmr)) %>% filter(!is.na(l))
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
stomach$biomass <- stomach$npred_perpred * stomach$prey_ind_weight_g
stomach <- stomach %>% filter(npred_perpred < 2000)

est <- mle_texp(stomach)
biomassestco <- est@coef

stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l = grid, Density = dist)

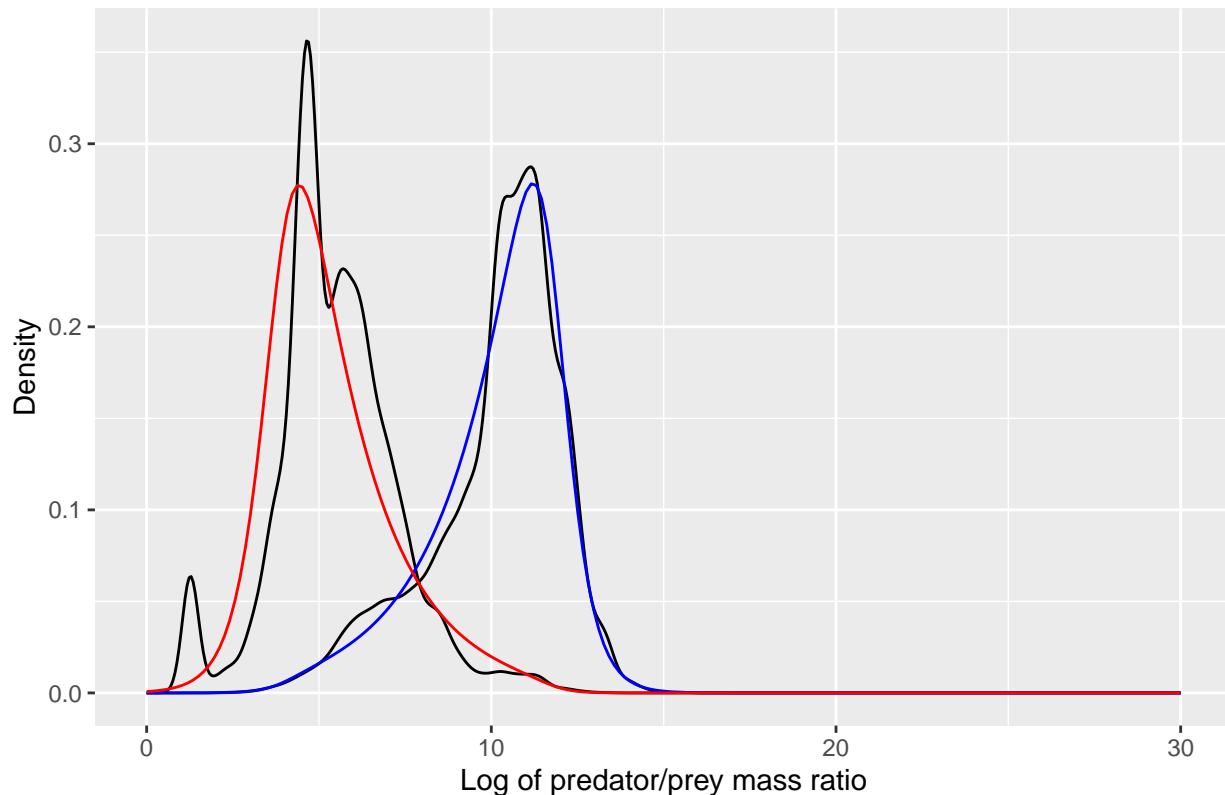
shiftdist <- dtexp(grid, alpha = (biomassestco[1] - 1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l = grid, Density = shiftdist)

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 = "blue")+
geom_line(aes(l, Density), data = shiftbiomassdist, color = "red")+
ggtitle("Haddock - Fitted to number, shift to biomass")
```

### Haddock – Fitted to number, shift to biomass



##Horse Mackerel

```
sprat <- stom_df %>% filter(pred_species=="Trachurus trachurus")
sprat <- sprat %>% filter(npred_perpred>0)
stomach <- sprat
stomach <- stomach %>% mutate(l=log(ppmr)) %>% filter(!is.na(l), l>0)
stomach <- stomach %>% mutate(weight_numbers = npred_perpred*stomach$prey_ind_weight_g)
stomach$biomass <- stomach$npred_perpred*stomach$prey_ind_weight_g
stomach <- stomach[-884,]

est <- mle_texp(stomach)
biomassestco <- est@coef

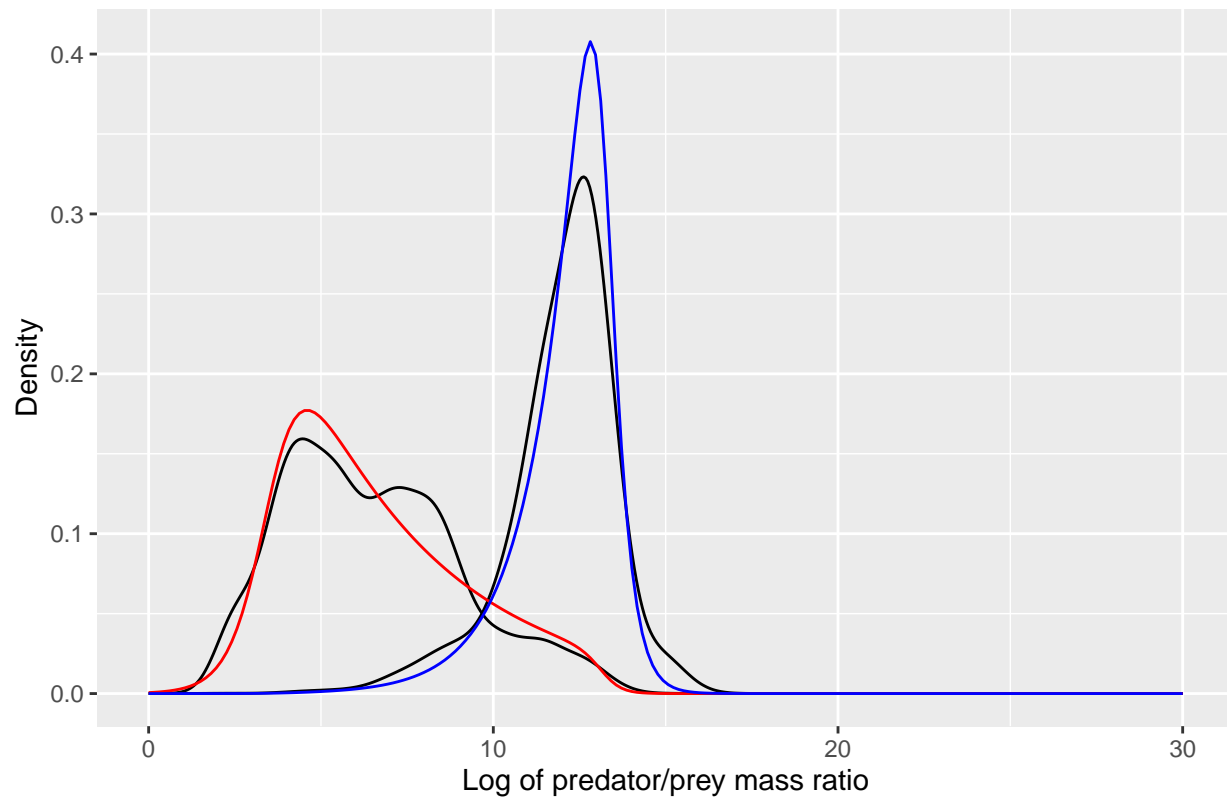
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l=grid, Density=dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1]+1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l=grid, Density=shiftdist)
```

```
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("Horse Mackerel - Fitted to biomass, shift to number")
```

Horse Mackerel – Fitted to biomass, shift to number



##Mackerel

```
sprat <- stom_df%>%filter(pred_taxa=="Scomber scombrus")
sprat <- sprat%>%filter(npred_perpred>0)
stomach <- sprat
stomach <- stomach%>%mutate(l=log(ppmr))%>%filter(!is.na(l), l>0)
stomach <- stomach %>% mutate(weight_numbers = npred_perpred*stomach$prey_ind_weight_g)
stomach$biomass <- stomach$npred_perpred*stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l=grid, Density=dist)
```

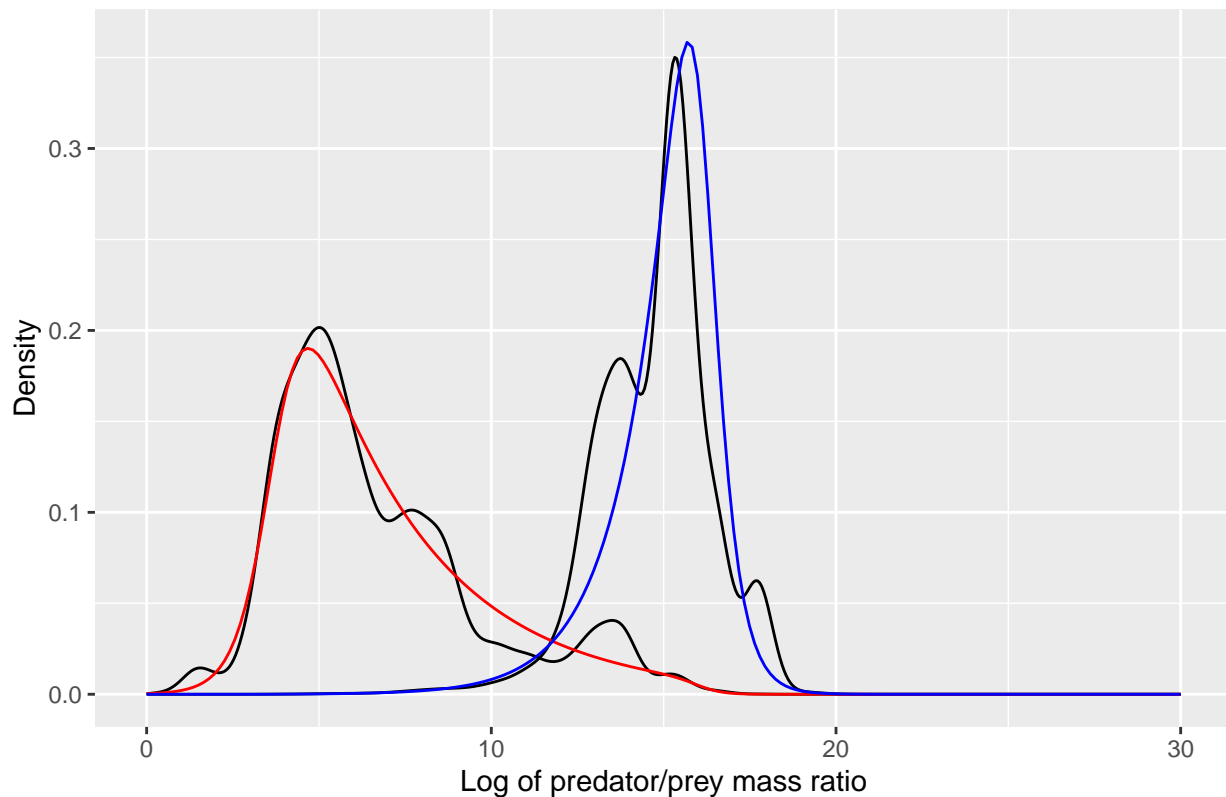
```

shiftdist <- dtexp(grid, alpha = (biomassestco[1]+1), ll = biomassestco[2], ul = biomassestco[3], lr = 1)
shiftbiomassdist <- data.frame(l=grid, Density=shiftdist)

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("Mackerel - Fitted to biomass, shift to number")

```

Mackerel – Fitted to biomass, shift to number



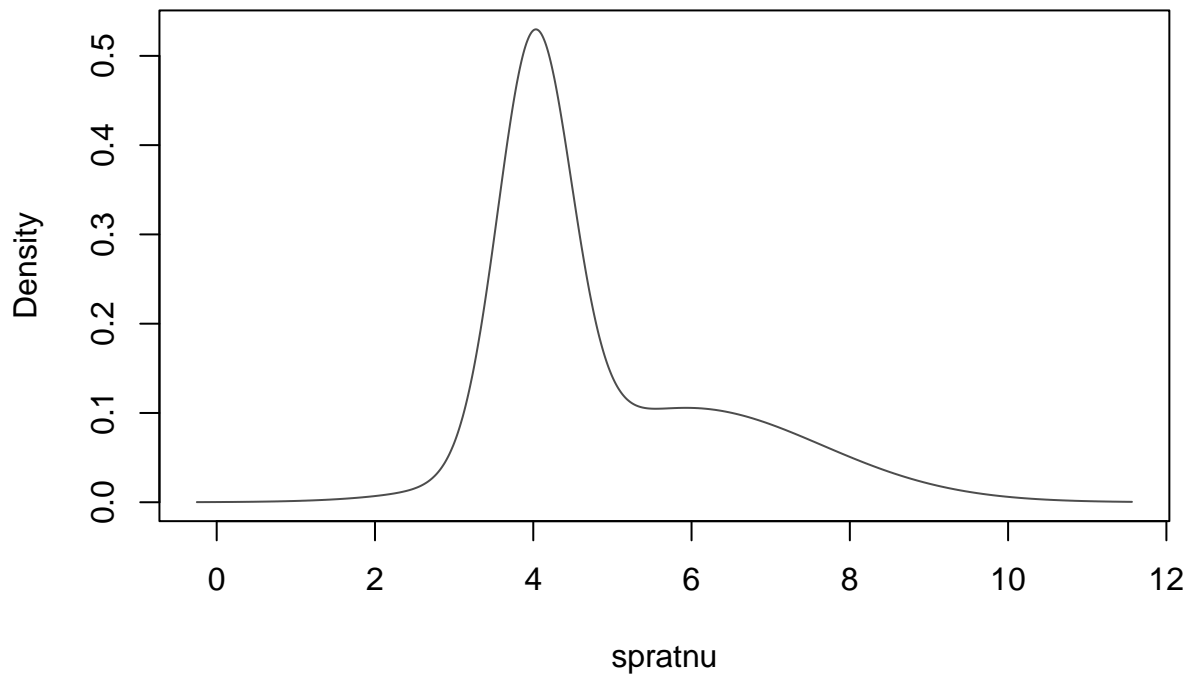
##Megrin

```

sprat <- stom_df %>% filter(pred_taxa=="Lepidorhombus whiffiagonis")

spratnu <- repeat_elements(log(sprat$ppmr), sprat$npred_perpred)
sprat$weight_numbers <- sprat$npred_perpred
sprat$weight_biomass <- sprat$npred_perpred*sprat$prey_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=2)

```



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

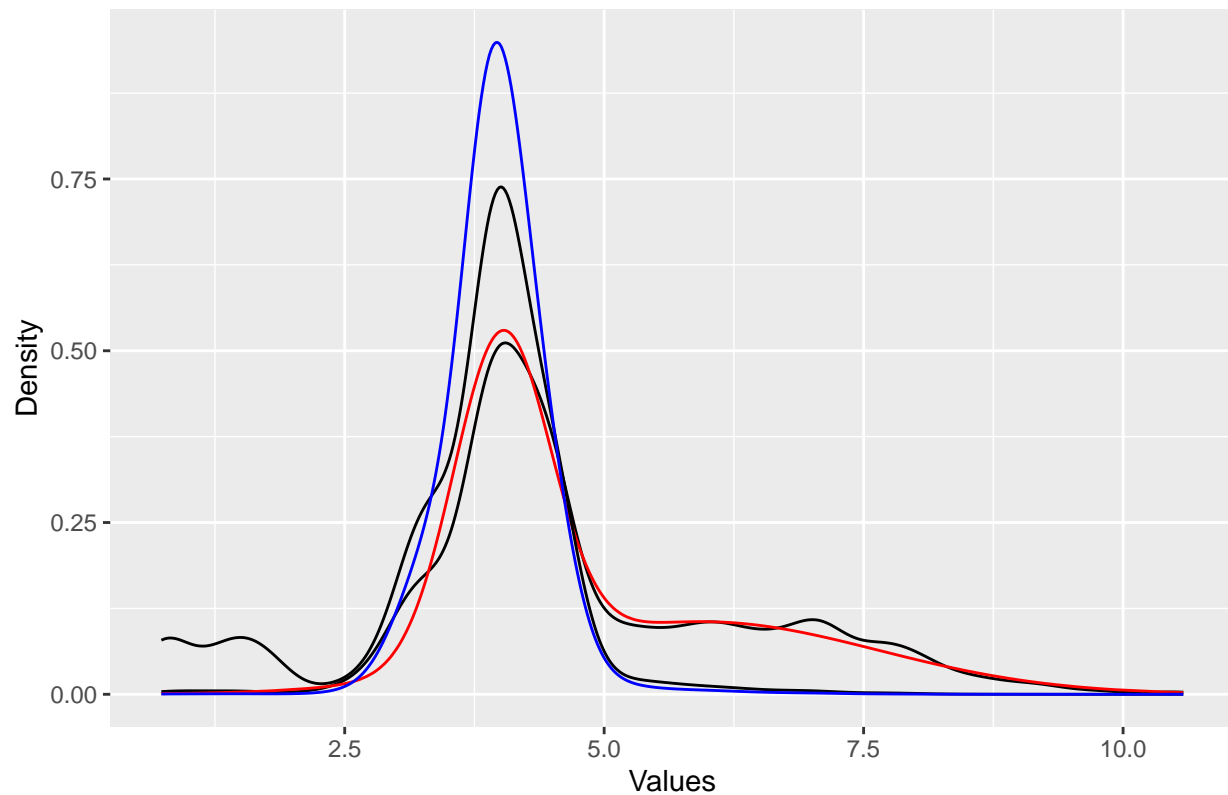
newspratdens <- gmm[["density"]]*exp(-dig*gmm[["data"]])
shifted_pdf_normalized <- newspratdens / sum(newspratdens)

#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("Megrim - Fitted to number, shifted to biomass"))
```

```
## Warning: Removed 1 row containing non-finite outside the scale range ('stat_density()').
## Removed 1 row containing non-finite outside the scale range ('stat_density()').
```

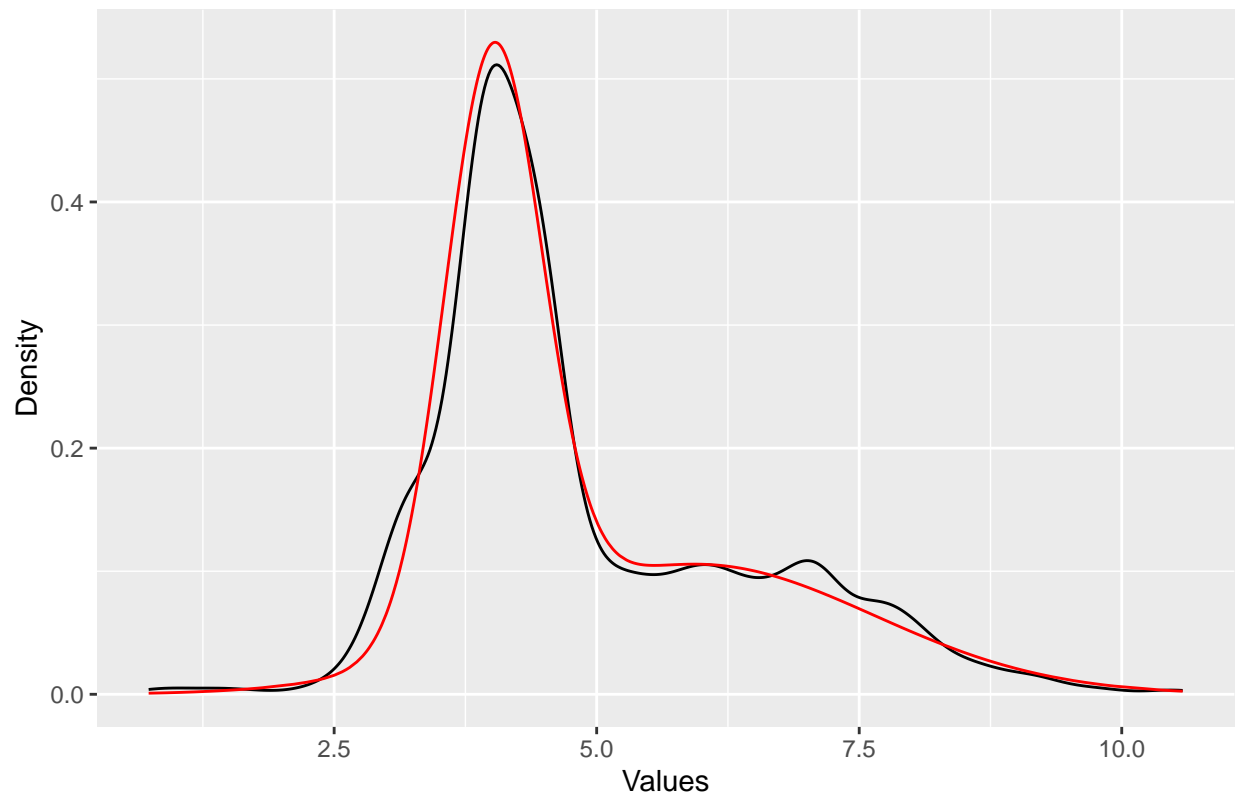
## Megrim – Fitted to number, shifted to biomass



```
#only number
(numbfitt <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers)) +
  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 1 row containing non-finite outside the scale range
## ('stat_density()').
```

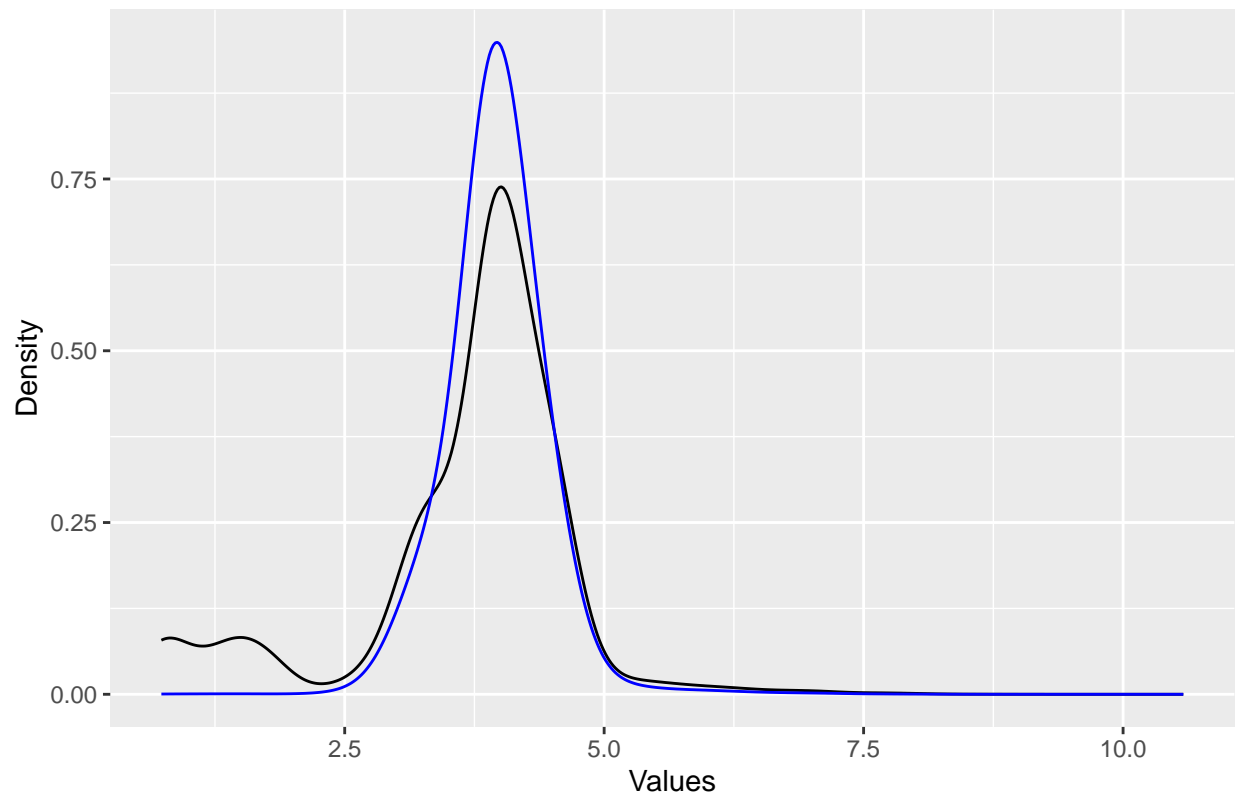
Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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 1 row containing non-finite outside the scale range
## ('stat_density()').
```

## Diet Density Plot from Number Distribution



##Monkfish

```
sprat <- stom_df %>% filter(pred_taxa == "Lophius piscatorius")
sprat <- sprat %>% filter(npred_perpred > 0)
stomach <- sprat
stomach <- stomach %>% mutate(l = log(ppmr)) %>% filter(!is.na(l), l > 0)
stomach <- stomach %>% mutate(weight_numbers = npred_perpred * stomach$prey_ind_weight_g)
stomach$biomass <- stomach$npred_perpred * stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

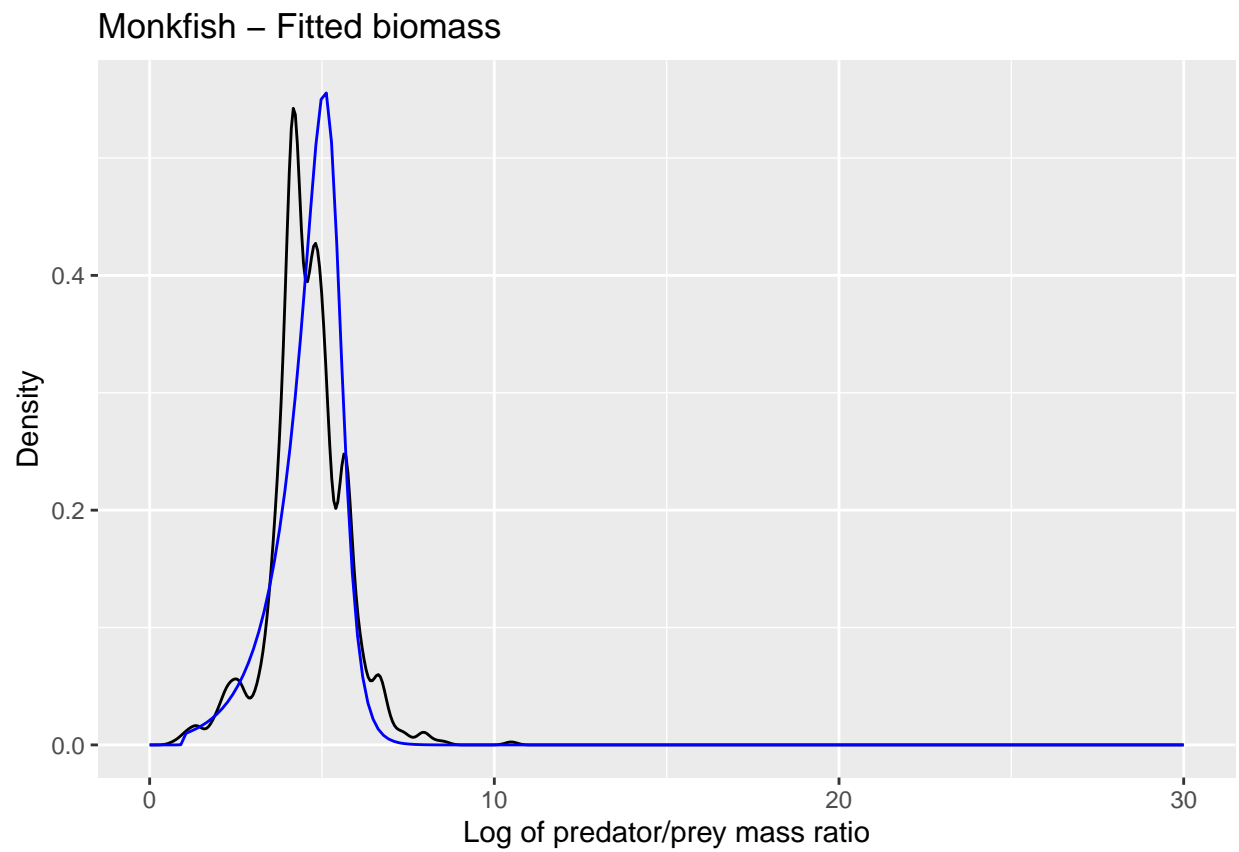
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l = grid, Density = dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1] + 1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l = grid, Density = shiftdist)

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

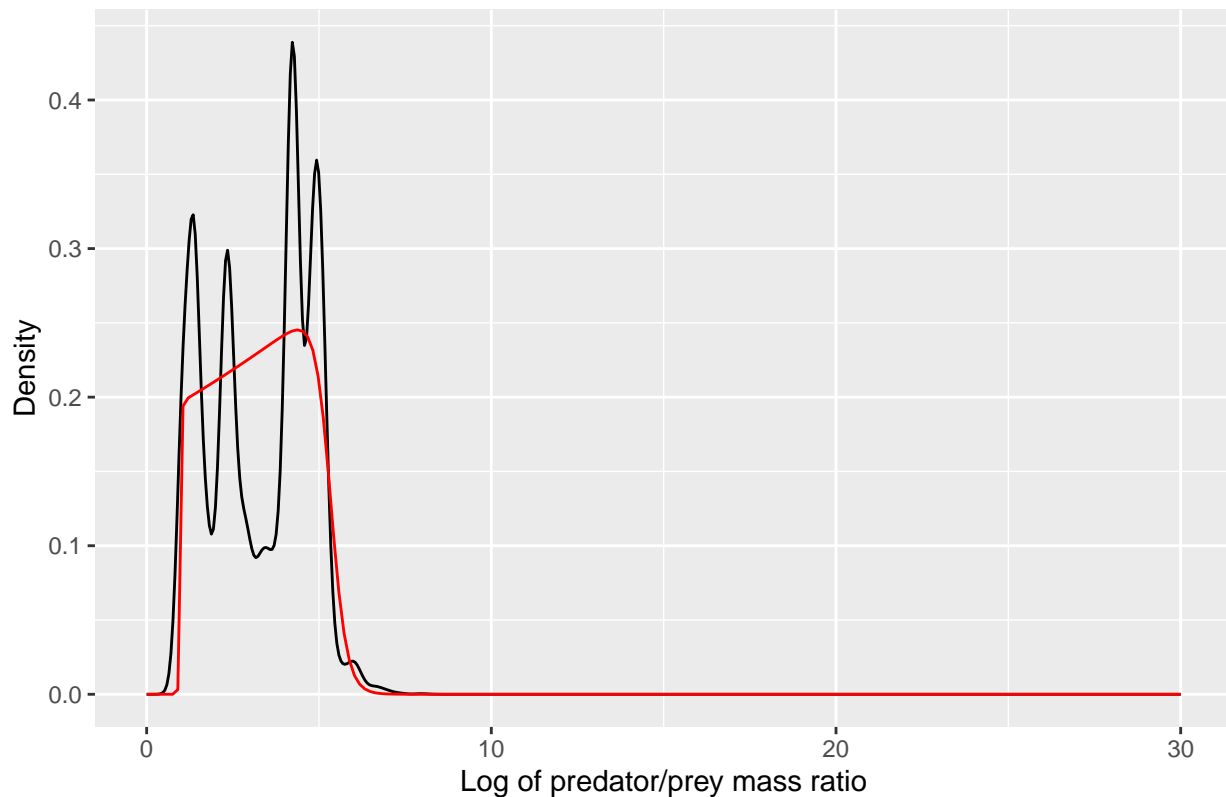
```
ggtitle("Monkfish - Fitted biomass")
```



```
ggplot(stomach) +  
  geom_density(aes(l, weight=biomass))+  
  xlab("Log of predator/prey mass ratio") +  
  geom_line(aes(l, Density), data = biomassdist, color = "red")+  
  ggtitle("Monkfish - shifted to number")
```



## Monkfish – shifted to number



##Norway pout

```
sprat <- stom_df %>% filter(pred_taxa == "Trisopterus esmarkii")
sprat <- sprat %>% filter(npred_perpred > 0)
stomach <- sprat
stomach <- stomach %>% mutate(l = log(ppmr)) %>% filter(!is.na(l), l > 0)
stomach <- stomach %>% mutate(weight_numbers = npred_perpred * stomach$prey_ind_weight_g)
stomach$biomass <- stomach$npred_perpred * stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

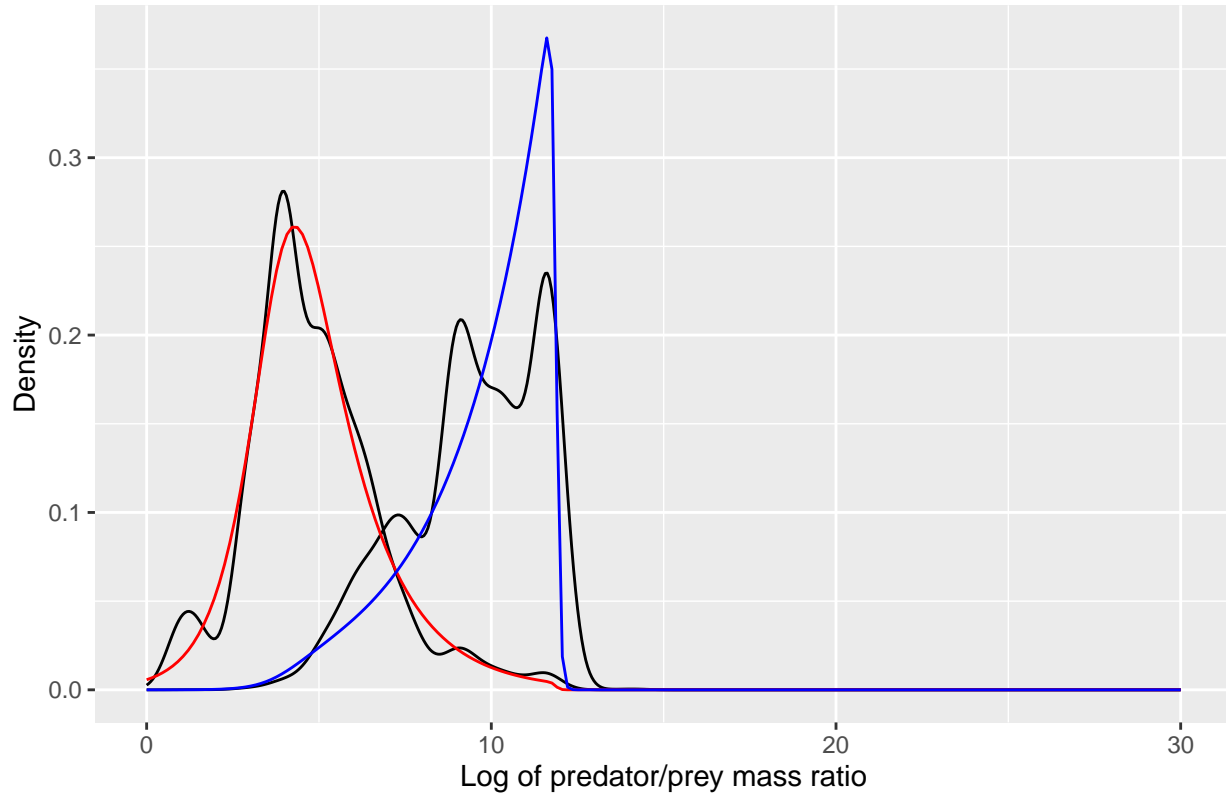
dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l = grid, Density = dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1] + 1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l = grid, Density = shiftdist)

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("Norway Pout - Fitted to biomass, shift to number")
```

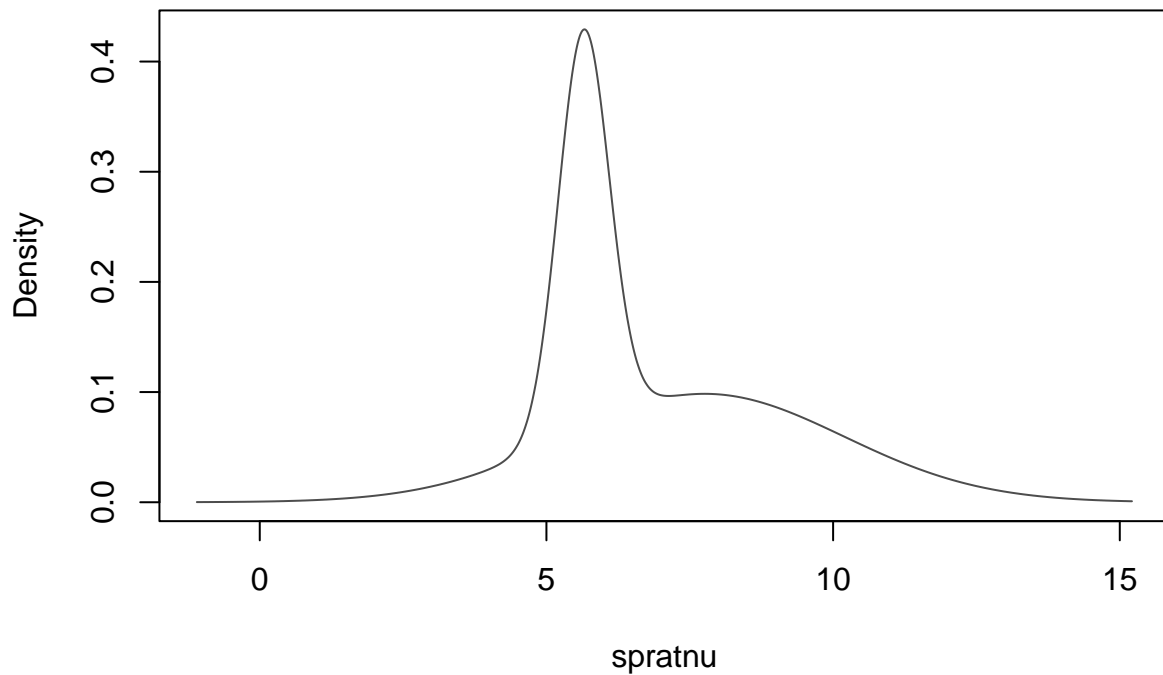
Norway Pout – Fitted to biomass, shift to number



##Plaice

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

spratnu <- repeat_elements(log(sprat$ppmr), sprat$nprey_perpred)
sprat$weight_numbers <- sprat$nprey_perpred
sprat$weight_biomass <- sprat$nprey_perpred*sprat$prey_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=2)
```



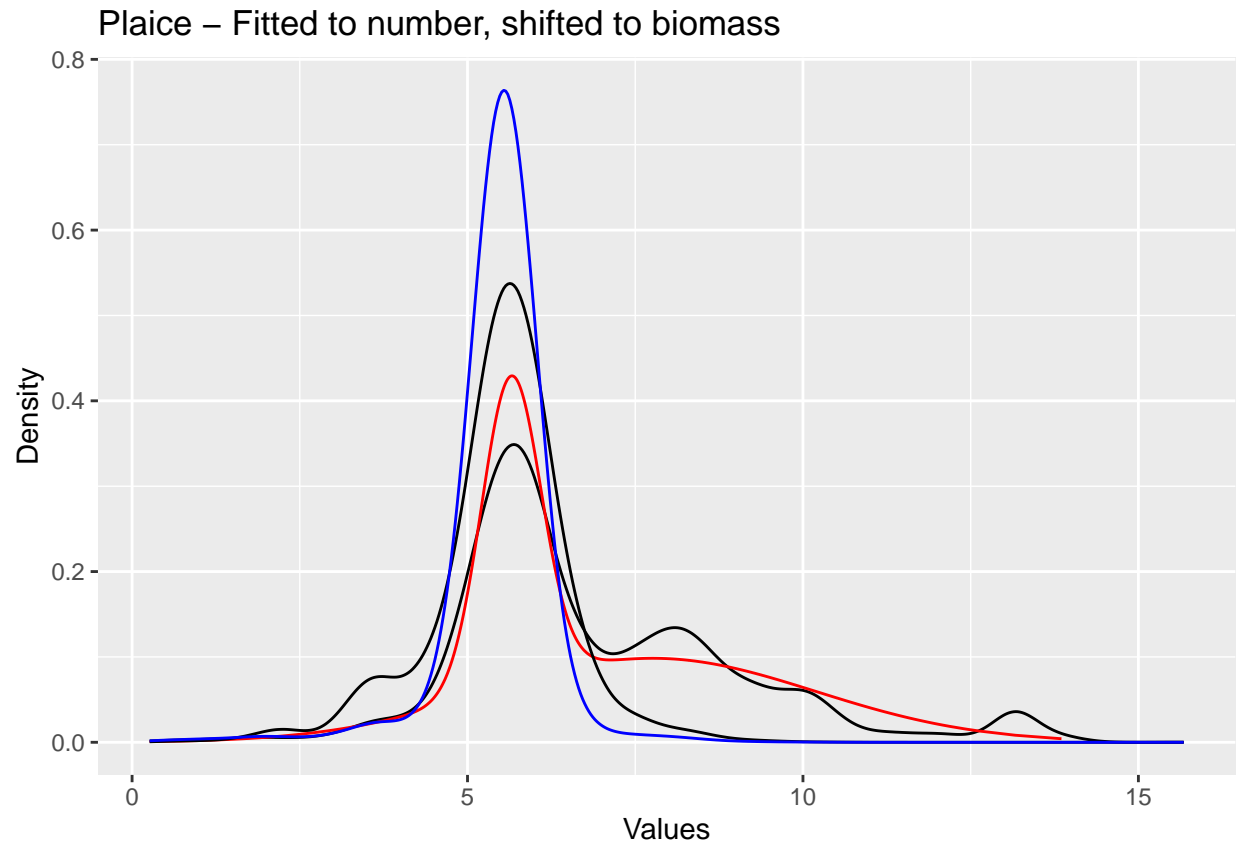
```
dplot <- data.frame(x=gmm[["data"]], density=gmm[["density"]])

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

#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("Plaice - Fitted to number, shifted to biomass"))
```

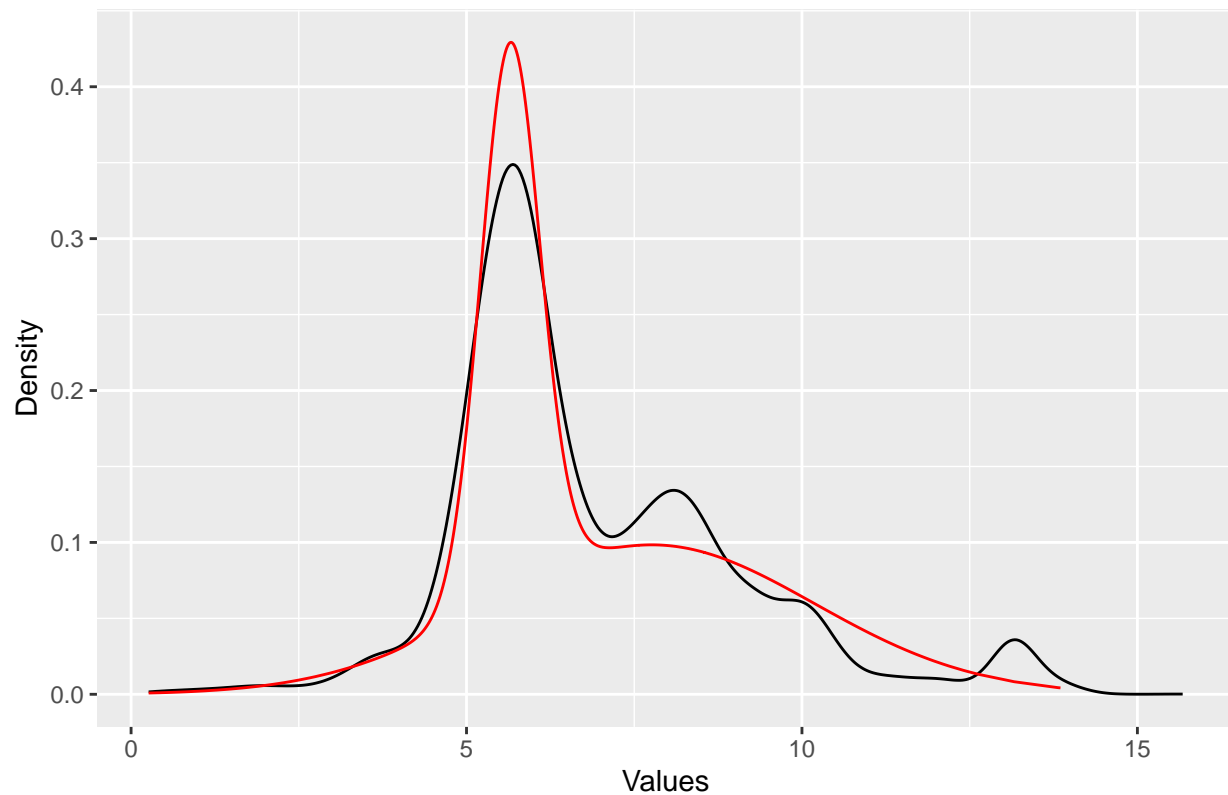
```
## Warning: Removed 111 rows containing non-finite outside the scale range
## ('stat_density()').
## Removed 111 rows containing non-finite outside the scale range
## ('stat_density()').
```



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

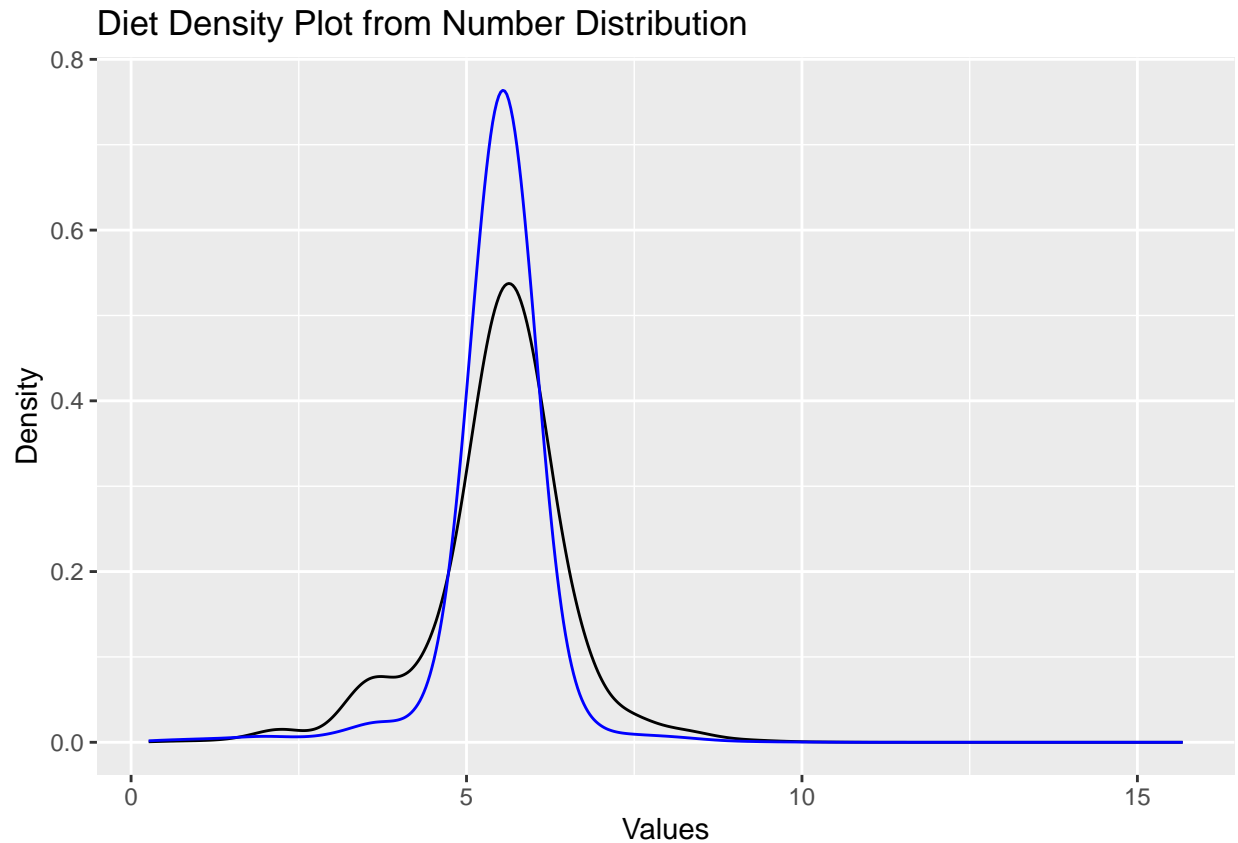
```
## Warning: Removed 111 rows containing non-finite outside the scale range
## ('stat_density()').
```

Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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()').
```



##Poor Cod

```
sprat <- stom_df %>% filter(pred_taxa == "Trisopterus minutus")
sprat <- sprat %>% filter(npred_perpred > 0)
stomach <- sprat
stomach <- stomach %>% mutate(l = log(ppmr)) %>% filter(!is.na(l), l > 0)
stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
stomach$biomass <- stomach$npred_perpred * stomach$prey_ind_weight_g

est <- mle_texp(stomach)
biomassestco <- est@coef

stomach <- stomach %>% mutate(weight_numbers = npred_perpred)
grid = seq(0, 30, length.out = 200)

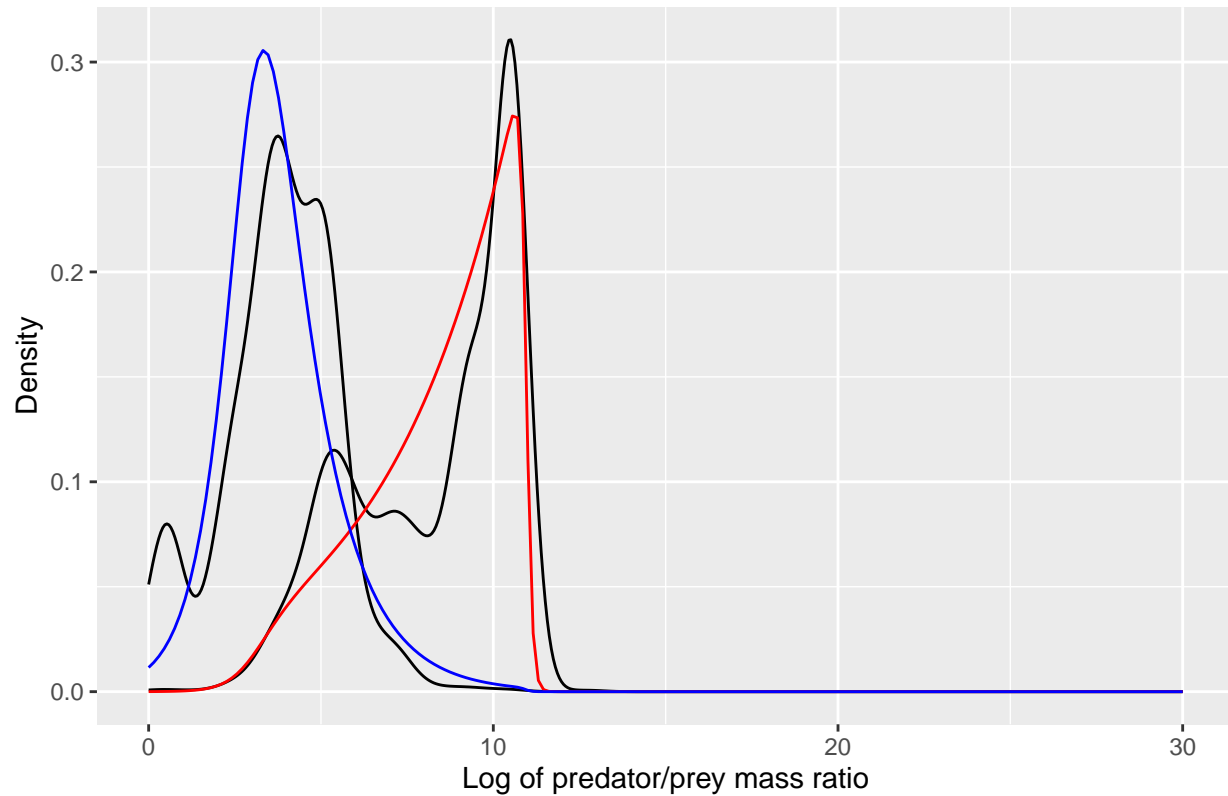
dist <- dtexp(grid, alpha = (biomassestco[1]), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
biomassdist <- data.frame(l = grid, Density = dist)

shiftdist <- dtexp(grid, alpha = (biomassestco[1] - 1), ll = biomassestco[2], ul = biomassestco[3], lr = biomassestco[4])
shiftbiomassdist <- data.frame(l = grid, Density = shiftdist)

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("Poor Cod – Fitted to biomass, shift to number")
```

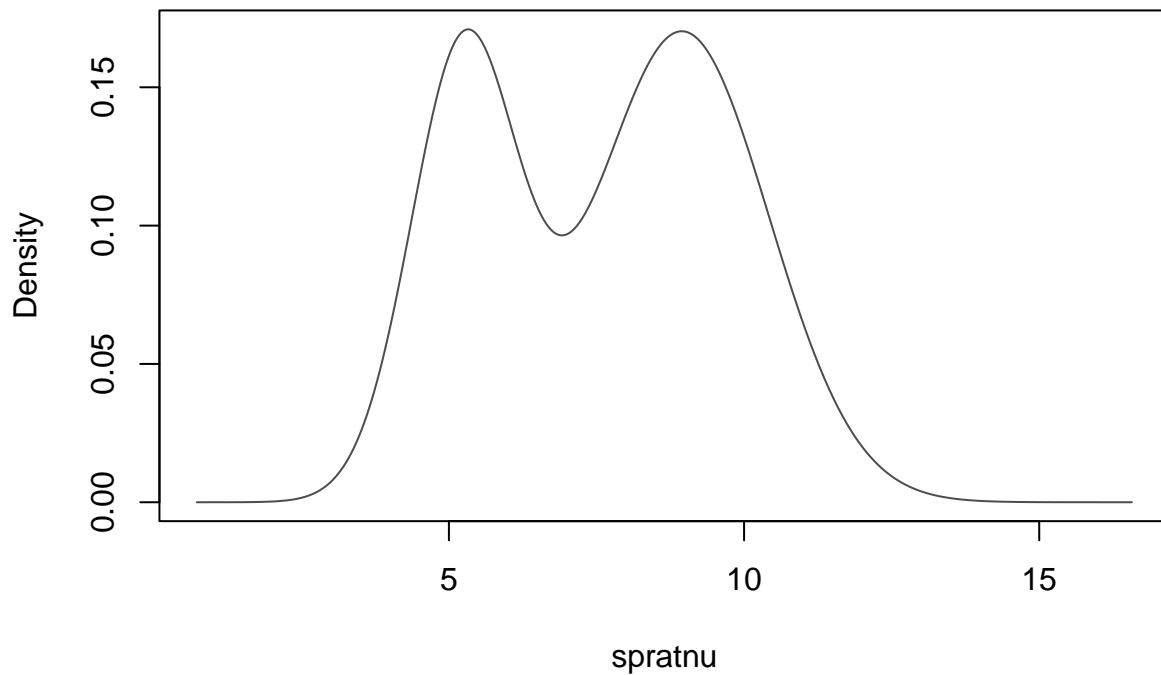
Poor Cod – Fitted to biomass, shift to number



##Sole

```
sprat <- stom_df %>% filter(pred_taxa=="Solea solea")

spratnu <- repeat_elements(log(sprat$ppmr), sprat$npred_perpred)
sprat$weight_numbers <- sprat$npred_perpred
sprat$weight_biomass <- sprat$npred_perpred*sprat$prey_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=2)
```



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

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

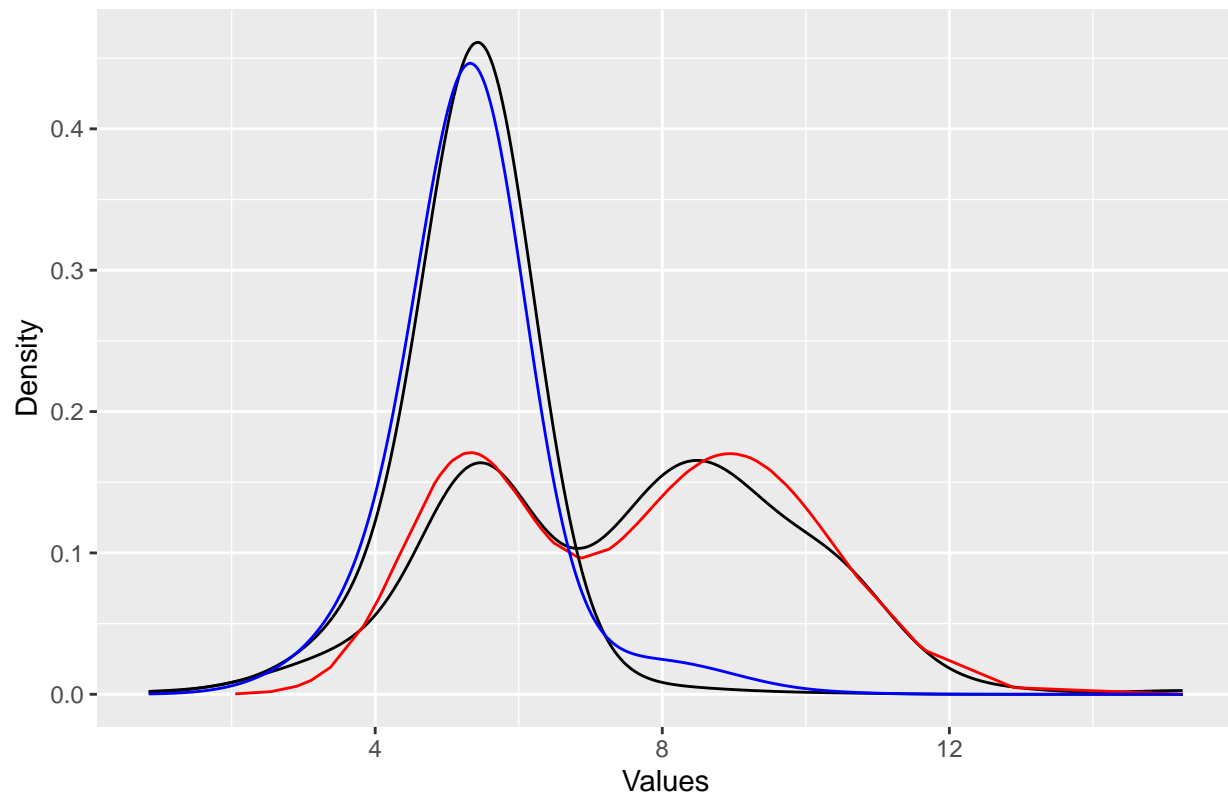
#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("Sole - Fitted to number, shifted to biomass"))
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_density()').
## Removed 10 rows containing non-finite outside the scale range
## ('stat_density()').
```



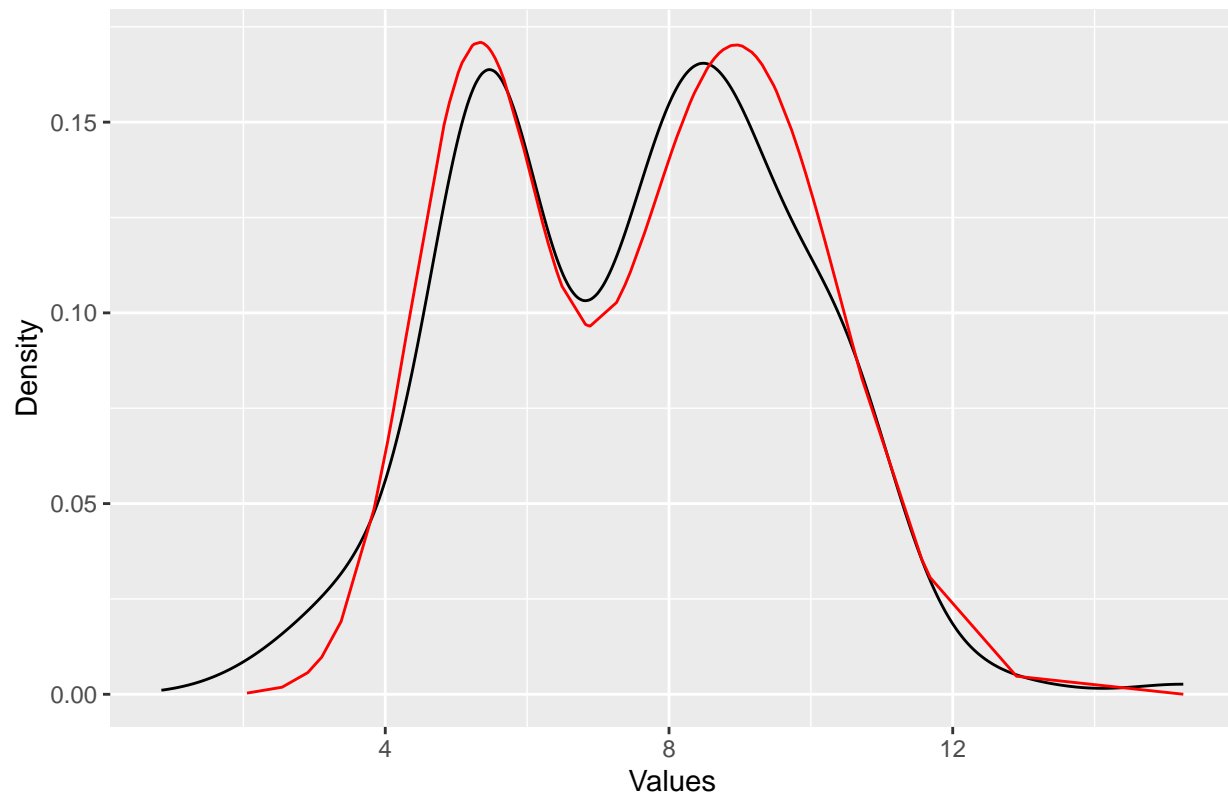
### Sole – Fitted to number, shifted to biomass



```
#only number
(numbfitt <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers)) +
  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 10 rows containing non-finite outside the scale range
## ('stat_density()').
```

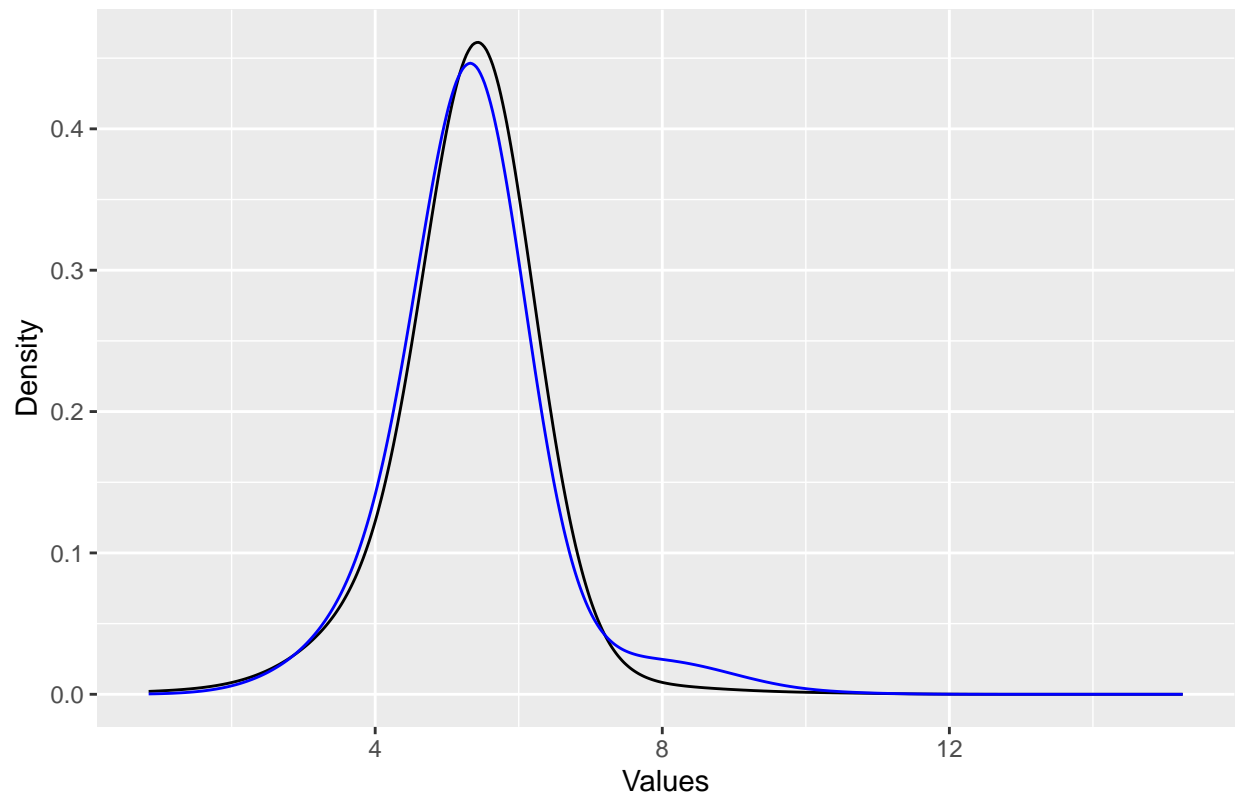
Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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"))
```

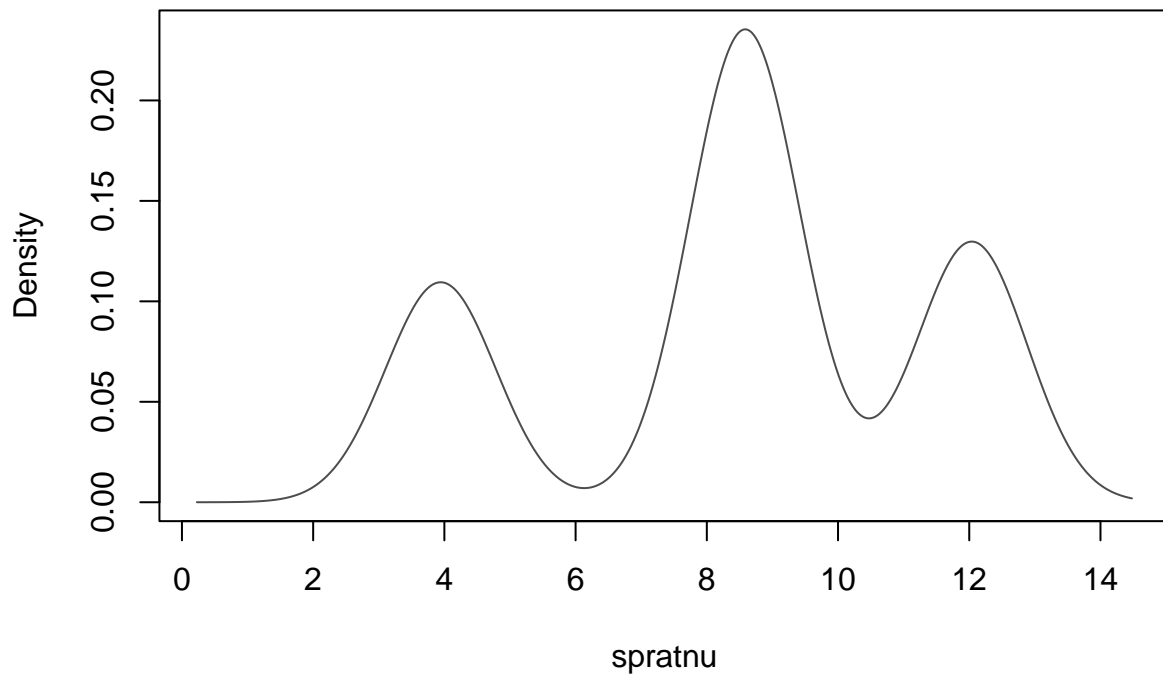
```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_density()').
```

Diet Density Plot from Number Distribution



##Sprat

```
sprat <- stom_df%>%filter(pred_taxa=="Sprattus sprattus")
spratnu <- repeat_elements(log(sprat$ppmr), sprat$nprey_perpred)
sprat$weight_numbers <- sprat$nprey_perpred
sprat$weight_biomass <- sprat$nprey_perpred*sprat$prey_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=3)
```



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

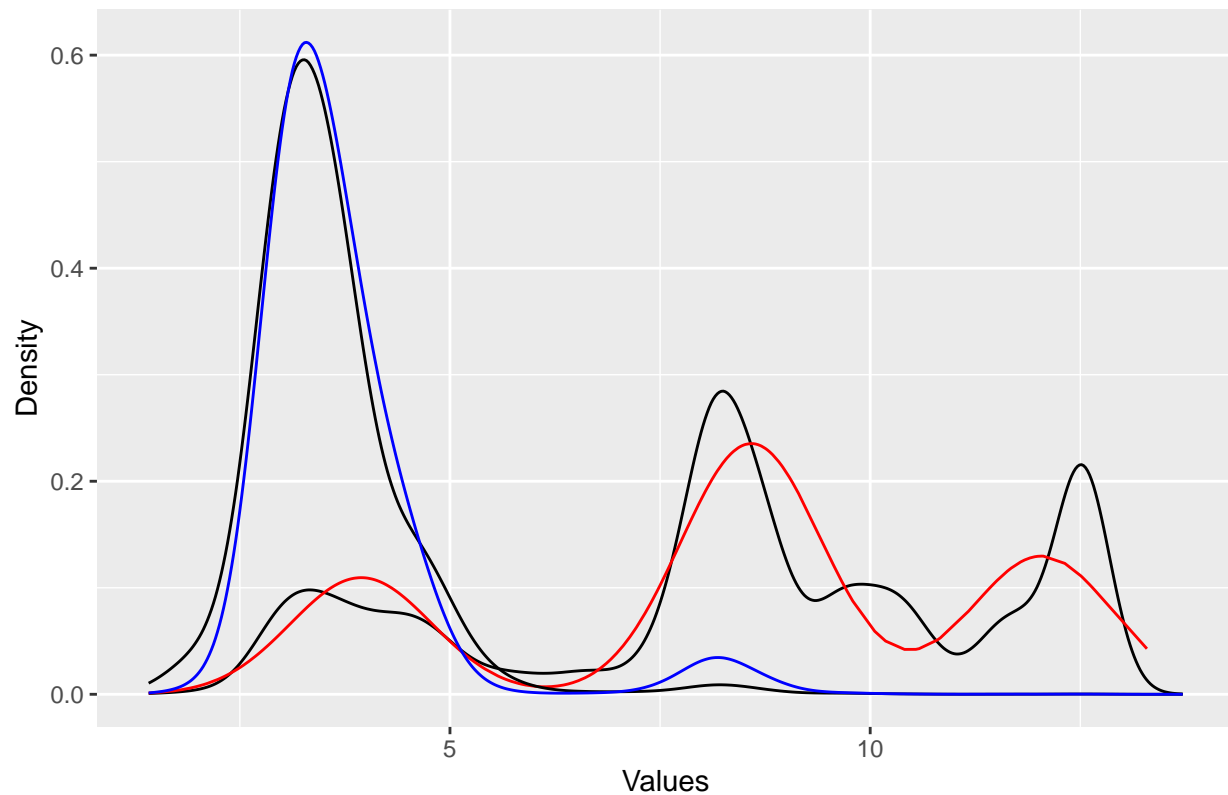
newspratdens <- gmm[["density"]]*exp(-dig*gmm[["data"]])
shifted_pdf_normalized <- newspratdens / sum(newspratdens)

#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("Sole - Fitted to number, shifted to biomass"))
```

```
## Warning: Removed 6 rows containing non-finite outside the scale range
## ('stat_density()').
## Removed 6 rows containing non-finite outside the scale range
## ('stat_density()').
```

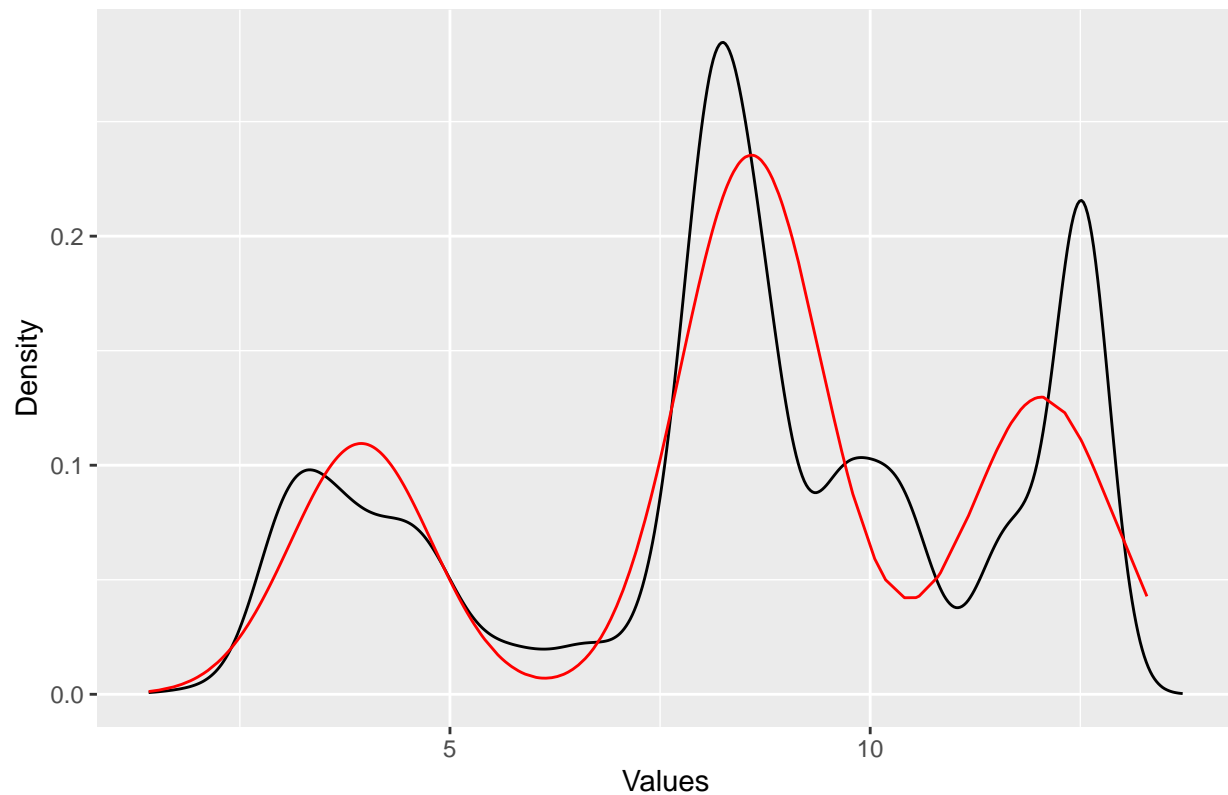
Sole – Fitted to number, shifted to biomass



```
#only number
(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers)) +
  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 6 rows containing non-finite outside the scale range
## ('stat_density()').
```

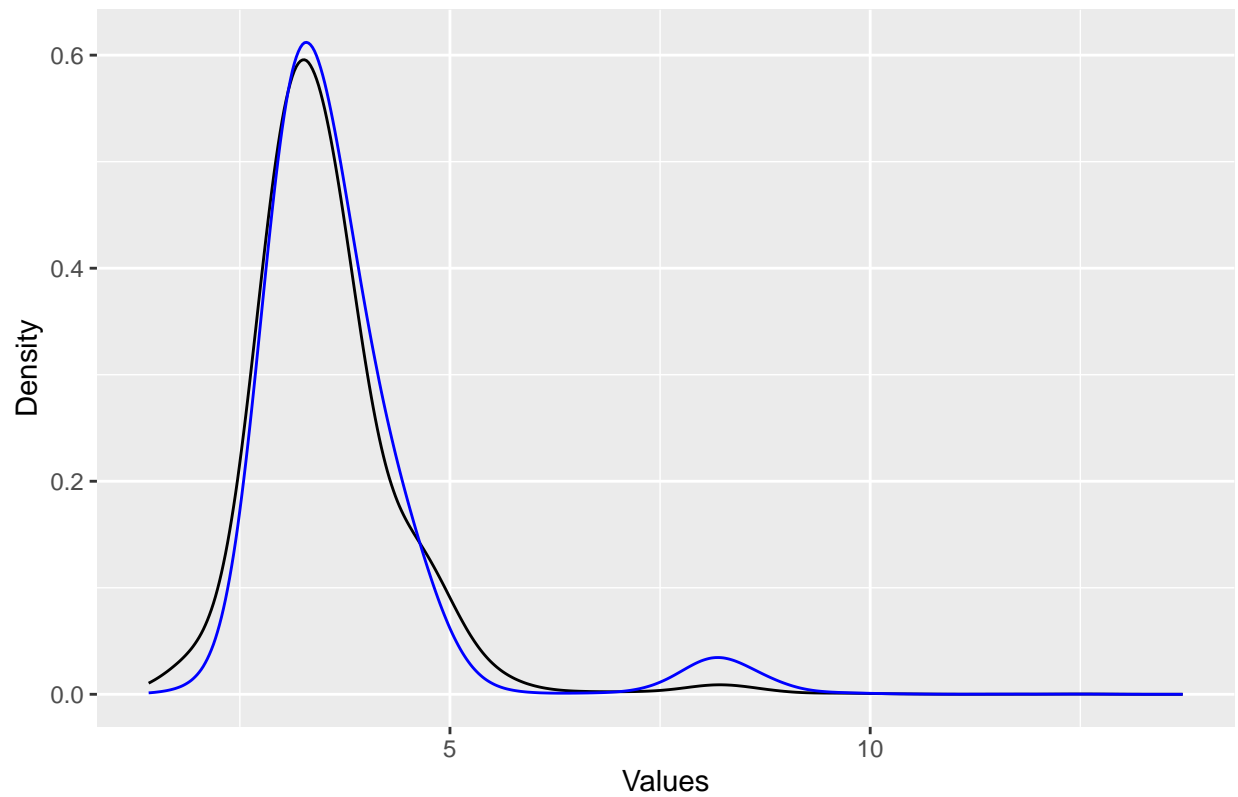
Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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"))
```

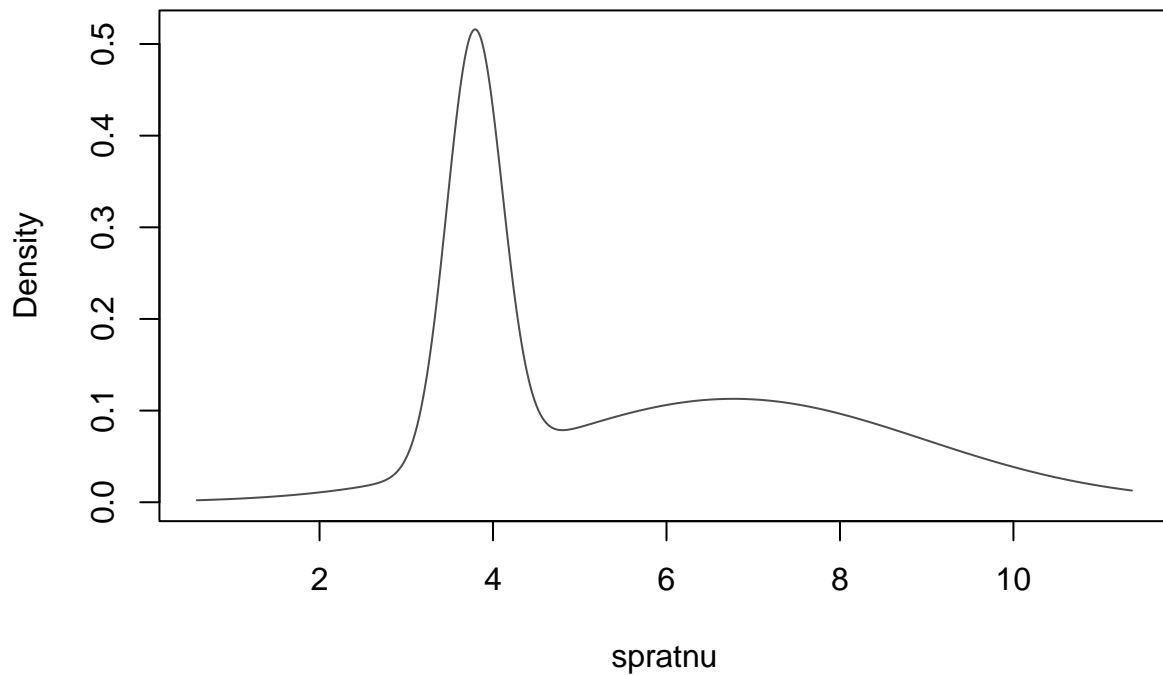
```
## Warning: Removed 6 rows containing non-finite outside the scale range
## ('stat_density()').
```

Diet Density Plot from Number Distribution



##Spurdog

```
sprat <- stom_df%>%filter(pred_taxa=="Squalus acanthias")
sprat <- sprat%>%filter(npred_perpred<200)
spratnu <- repeat_elements(log(sprat$ppmr), sprat$npred_perpred)
sprat$weight_numbers <- sprat$npred_perpred
sprat$weight_biomass <- sprat$npred_perpred*sprat$pred_ind_weight_g^dig
gmm <- densityMclust(spratnu, G=2)
```



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

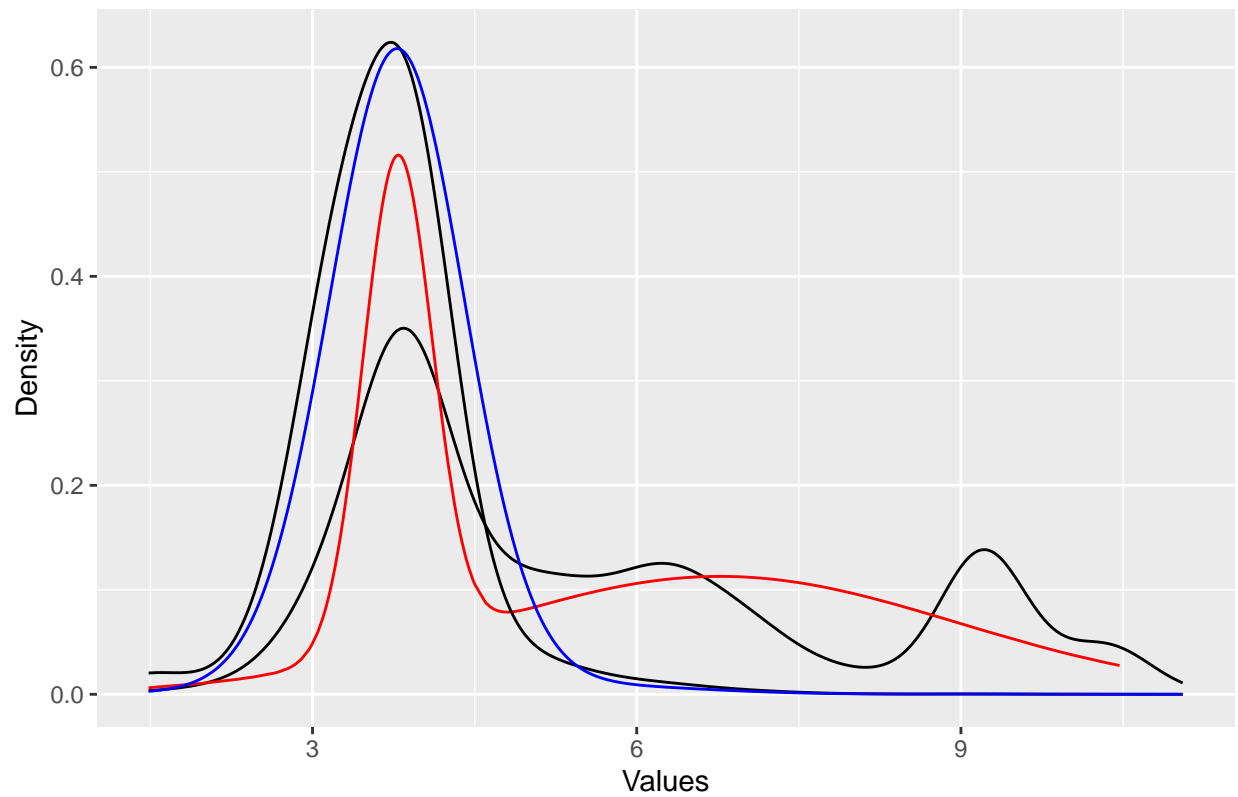
newspratdens <- gmm[["density"]]*exp(-dig*gmm[["data"]])
shifted_pdf_normalized <- newspratdens / sum(newspratdens)

#making new dataframe
dplot2 <- data.frame(x=gmm[["data"]], density=shifted_pdf_normalized)

(numbfit <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_numbers))+
  geom_line(data=dplot, aes(x = x, y = density), color="red") +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue")+
  labs(x = "Values", y = "Density") +
  ggtitle("Spurdog - Fitted to number, shifted to biomass"))
```

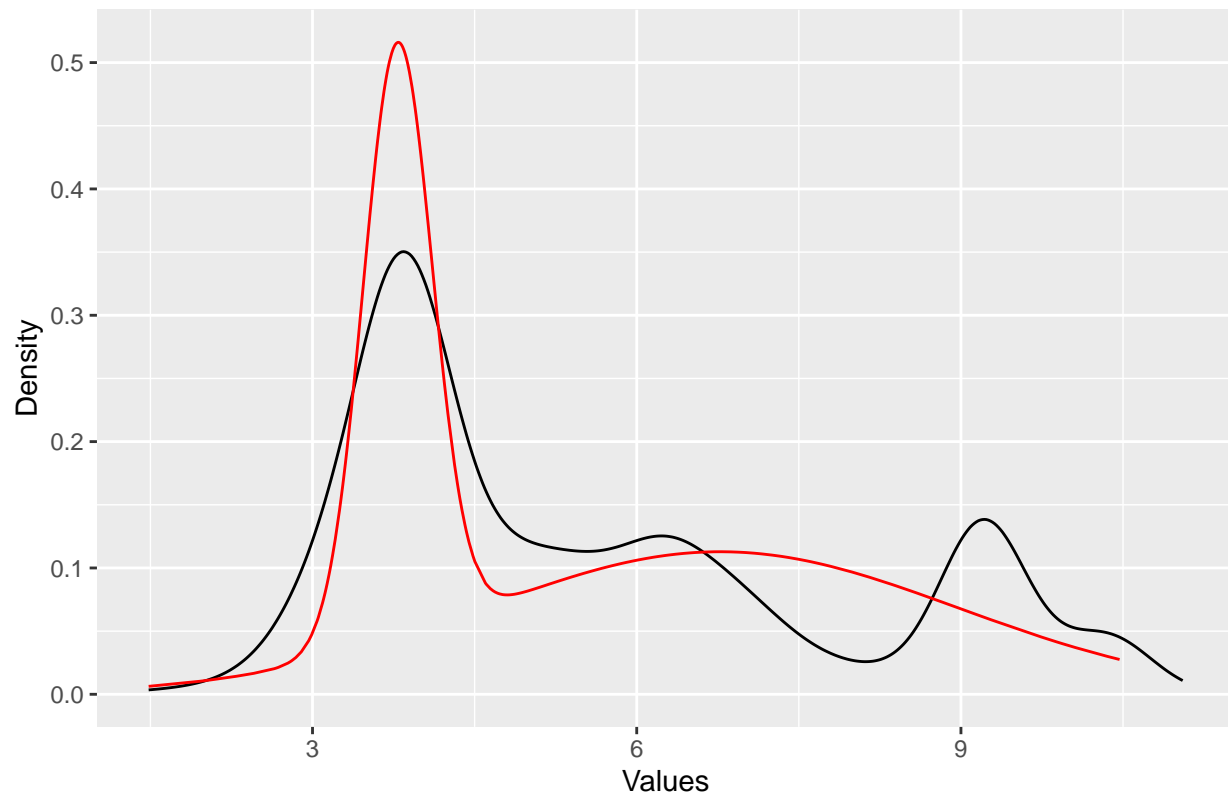


### Spurdog – Fitted to number, shifted to biomass



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

Number Density Plot from Number Distribution



```
#only biomass
(numbfittbio <- ggplot() +
  geom_density(data=sprat, aes(log(ppmr), weight=weight_biomass))+
  geom_density(data=dplot2, aes(x, weight=shifted_pdf_normalized), color="blue", 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"))
```

Diet Density Plot from Number Distribution

