

Body Condition of Mother and Calf Humpback Whales (*Megoptera novaeangiliae*) Over Temporal Scales

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```
tinytex::install_tinytex(force = TRUE)
```

```
## tlmgr --repository http://www.preining.info/tlgpg/ install tlgpg
```

```
## tlmgr option repository 'https://mirrors.mit.edu/CTAN/systems/texlive/tlnet'
```

```
## tlmgr update --list
```

```
library(dplyr)
```

```
##
```

```
## 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(tidyr)
```

```
library(ggplot2)
```

```
library(forcats)
```

Research Questions

1. How does the mother and calf body condition index vary by year?
2. How does the mother and calf body condition index vary seasonally?

Data Wrangling

Below is the code used to optimize and clean the dataset used to answer the research questions. `##` Install packages and organise sheets to be filled

```

# template to be filled
temp<-read.csv("lewis_temp.csv")
# data from master sheet to be transferred
data<-read.csv("Lewis_Raw_Sheet.csv")
# Pulling corrected altitude from master database to analysis data sheet
nm <- c("Corrected_height_m", "Pixel_length")
temp[nm] <- lapply(nm, function(x) data[[x]][match(temp$Filename,data$Filename)])
View(temp)
#write new data back to original temp csv file.
write.csv(temp,"lewis_temp.csv")

```

preparing to calculate body volumes for each row, need to clean data first:

```

data<-read.csv("Lewis_Raw_Sheet.csv")
head(data,20)

```

##	Region	Year	DOY	Grade_pass	Altitude_Source	Filename	Role
## 1	HI	2019	15	N	S_Alt	2019.01.15.03.01	Mother
## 2	HI	2019	15	Y	S_Alt	2019.01.15.03.02	Calf
## 3	HI	2019	15	N	S_Alt	2019.01.15.06.02	Mother
## 4	HI	2019	15	N	S_Alt	2019.01.15.08.01	Calf
## 5	HI	2019	16	N	S_Alt	2019.01.16.19.01	Mother
## 6	HI	2019	16	N	S_Alt	2019.01.16.19.02	Calf
## 7	HI	2019	16	Y	S_Alt	2019.01.16.20.01	Mother
## 8	HI	2019	16	Y	S_Alt	2019.01.16.20.02	Calf
## 9	HI	2019	16	Y	S_Alt	2019.01.16.28.03	Mother
## 10	HI	2019	16	Y	S_Alt	2019.01.16.28.04	Yearling
## 11	HI	2019	16	N	S_Alt	2019.01.16.29.01	Mother
## 12	HI	2019	16	N	S_Alt	2019.01.16.29.02	Calf
## 13	HI	2019	16	Y	S_Alt	2019.01.16.31.01	Mother
## 14	HI	2019	16	Y	S_Alt	2019.01.16.31.02	Calf
## 15	HI	2019	18	Y	S_Alt	2019.01.18.37.01	Mother
## 16	HI	2019	18	Y	S_Alt	2019.01.18.37.02	Calf
## 17	HI	2019	18	Y	S_Alt	2019.01.18.39.01	Mother
## 18	HI	2019	18	Y	S_Alt	2019.01.18.39.02	Calf
## 19	HI	2019	18	Y	S_Alt	2019.01.18.46.01	Mother
## 20	HI	2019	18	Y	S_Alt	2019.01.18.47.01	Calf
##	Corrected_height_m	Pixel_length	Pixel_Width_5	Pixel_Width_10	Pixel_Width_15		
## 1	32.97236219	0.3491373	9.214691	14.08607	16.75829		
## 2	29.66091393	0.1469100	9.168017	11.96253	14.89135		
## 3	35.1236886	0.3252343	9.235541	13.33296	15.24165		
## 4	33.1213199	0.1727700	8.592942	11.40709	13.43479		
## 5	28.41806378	0.4404700	7.601259	12.22899	13.32856		
## 6	28.3481908	0.1854800	8.151804	10.96770	12.79753		
## 7	26.92526647	0.4740500	7.264967	11.78561	13.53775		
## 8	27.23761989	0.1965600	7.527777	10.60096	12.77157		
## 9	44.31016642	0.2596200	7.488021	11.46235	12.95918		
## 10	40.52863803	0.2199700	7.357397	11.52921	13.42690		
## 11	35.51454667	0.3499500	7.934658	11.76965	11.13231		
## 12	35.44183216	0.1430300	9.196329	12.17870	13.53997		
## 13	33.51786646	0.4236100	7.551070	11.54780	13.30373		

## 14	32.12062813	0.1519900	6.906498	10.29645	13.14793
## 15	29.82653577	0.4328000	7.773092	11.93179	13.77891
## 16	30.91753566	0.1587100	7.774773	10.95052	12.63967
## 17	28.95496055	0.3999100	6.978168	10.54792	12.86602
## 18	30.95948877	0.1614000	7.535857	11.08413	12.26405
## 19	29.72669054	0.4367700	7.161791	10.72130	12.92166
## 20	33.40264928	0.1454500	9.667448	11.36653	13.47669
##	Pixel_Width_20	Pixel_Width_25	Pixel_Width_30	Pixel_Width_35	Pixel_Width_40
## 1	17.60272	18.97778	21.82566	21.32035	23.46663
## 2	19.27598	19.39924	20.14465	20.47707	20.60363
## 3	16.46303	20.91649	21.71981	22.57257	24.47837
## 4	17.99478	19.00087	20.61068	20.94254	20.53144
## 5	14.26289	17.53144	16.76094	17.62161	19.22495
## 6	17.40439	17.49475	17.82366	18.11683	18.59816
## 7	13.92794	17.20895	16.92749	17.47834	19.05466
## 8	17.10737	18.06163	18.82385	19.20491	18.99115
## 9	13.83876	17.44389	17.51684	17.76539	17.58225
## 10	15.19218	18.65696	19.46731	20.66172	21.92376
## 11	13.82885	17.48153	17.35476	17.63721	18.73034
## 12	17.00266	18.71652	20.14160	20.31278	19.31423
## 13	13.88924	16.89439	18.24686	18.37969	19.58700
## 14	16.11030	17.49982	18.51418	18.20086	17.98907
## 15	14.33013	17.92958	17.48693	17.90626	19.60360
## 16	17.10741	16.43856	18.56772	19.05737	18.97150
## 17	13.83772	17.00028	16.70581	16.42969	17.36708
## 18	16.50976	17.12640	18.65631	18.95578	19.53071
## 19	14.03786	17.13754	17.11963	17.11527	18.27278
## 20	18.04932	17.90279	19.60061	20.06176	19.21272
##	Pixel_Width_45	Pixel_Width_50	Pixel_Width_55	Pixel_Width_60	Pixel_Width_65
## 1	23.48878	23.24622	22.05670	20.48338	17.15620
## 2	20.52011	19.38956	17.30192	14.44496	11.64315
## 3	24.76568	23.72228	22.25214	19.60454	16.97563
## 4	20.42106	19.39355	18.11501	16.06948	13.12512
## 5	19.39205	19.03363	17.85561	16.04386	14.20165
## 6	18.36427	17.15453	15.43386	13.45949	11.13915
## 7	19.37626	19.05142	17.65981	16.34621	14.01598
## 8	18.83388	18.33518	17.08391	14.32996	12.05849
## 9	17.69819	17.55115	16.09979	14.18050	12.92683
## 10	22.04131	21.78012	19.30108	17.82342	16.05820
## 11	19.43507	18.97326	17.56442	15.76950	13.55491
## 12	18.70602	17.53451	16.28507	14.67773	13.02331
## 13	20.00920	20.23003	19.68546	18.35524	16.11702
## 14	17.63002	16.79251	15.70816	13.79602	11.28902
## 15	20.32834	20.06035	18.40953	16.57174	13.94073
## 16	18.21947	16.51763	14.11057	11.70644	10.15790
## 17	17.87276	17.38125	16.32448	14.47927	12.26478
## 18	18.80565	18.42439	15.99676	13.62290	11.30035
## 19	18.78152	18.47390	16.82046	15.25812	13.12270
## 20	19.19343	18.78801	16.40225	13.77020	11.13886
##	Pixel_Width_70	Pixel_Width_75	Pixel_Width_80	Pixel_Width_85	Pixel_Width_90
## 1	13.368451	9.313393	5.996423	4.145080	6.428957
## 2	9.400436	7.252516	5.628185	4.630932	7.018416
## 3	13.265143	9.806319	6.205202	3.880260	3.781384
## 4	10.408040	8.035108	5.839893	5.002380	7.944888

```
## 5      11.511003      7.885681      5.245174      3.469279      3.075581
## 6       9.107958      6.044240      3.718700      2.812207      7.884673
## 7      11.400634      8.498591      5.396030      3.718112      2.601100
## 8       9.445162      7.078139      4.690090      3.899297      7.493124
## 9      10.534293      8.485563      5.250565      3.108060      2.805712
## 10     12.431880      9.600389      6.004028      2.826976      4.630283
## 11     10.928039      7.677108      5.489817      3.713897      2.502679
## 12     10.196921      7.472869      4.762985      3.779840      9.420200
## 13     13.071048      9.824728      6.404522      3.051423      2.151714
## 14       9.349803      7.899898      6.515875      5.011698      6.906907
## 15     10.340296      7.439381      5.763816      3.246921      3.712072
## 16       8.412008      7.032644      5.787230      4.361447      5.207700
## 17     10.318540      7.615860      5.193292      3.288621      2.651242
## 18       8.461549      7.079675      5.254443      4.514248      5.923629
## 19     10.391854      7.994633      5.271805      3.200238      2.183869
## 20       9.179532      8.096080      5.616791      5.176974      7.508265
##      Pixel_Width_95
## 1      26.440150
## 2      19.082293
## 3      12.272840
## 4      18.171346
## 5      11.559919
## 6      17.642882
## 7      10.445093
## 8      19.441146
## 9      12.048172
## 10     17.471110
## 11     10.486013
## 12     18.765224
## 13     11.537238
## 14     19.155079
## 15       7.513404
## 16     16.646037
## 17     11.754325
## 18     18.803778
## 19     10.114084
## 20     18.330342
```

```
dim(data)
```

```
## [1] 2686  28
```

```
#remove rows containg NA value
```

```
data <- data %>% drop_na()
```

```
dim(data)
```

```
## [1] 2671  28
```

```
# Only keep rows containing S_Alt altitude source
```

```
data<-subset(data, Altitude_Source == 'S_Alt')
```

```
dim(data)
```

```
## [1] 2446  28
```

```
#Remove any measuremetns that didnt pass grading (N)
data<-subset(data, Grade_pass != 'N')
dim(data)
```

```
## [1] 2166 28
```

```
#Check value class and change to numeric
class(data$Corrected_height_m)
```

```
## [1] "character"
```

```
data$Corrected_height_m <- as.numeric(data$Corrected_height_m)
class(data$Pixel_length)
```

```
## [1] "numeric"
```

Calculate Total length of whale and length of 5% intervals

```
# Calculate TL
data$TL <- data$Corrected_height_m*data$Pixel_length

#check range to see for anomolies
range(data$TL)
```

```
## [1] 3.753996 14.787516
```

```
#equation to change 5% intervals from pixel length to absolute length
data<-data %>% mutate(across(c("Pixel_Width_5","Pixel_Width_10","Pixel_Width_15","Pixel_Width_20","Pixel_Width_25"),
View(data)
```

isolating 5 % intervals

```
colnames(data)[10:28] <- c("Width.5.proc.m","Width.10.proc.m","Width.15.proc.m","Width.20.proc.m","Width.25.proc.m")
```

```
#Renaming TL and Role.
```

```
data <- data %>%
  rename("Total.length.m" = "TL",
         "Rep.class" = "Role")
```

reorganisng/subsetting and reprganisng columns of interest. changename to BM

```
BM<-as.data.frame(data[,c("Filename","Total.length.m","Rep.class","Width.5.proc.m","Width.10.proc.m","Width.15.proc.m","Width.20.proc.m","Width.25.proc.m")])

#confirming widths are numeric
class(BM$Width.5.proc.m)
```

```
## [1] "numeric"
```

choosing 5% intervals from 5%-85% of the whale.

```
HW.ratios<-data.frame(
  Measurement.site=seq(5,85,5),
  All.HW.ratio=c(0.89,0.78,0.90,0.97,0.91,0.92,0.93,0.92,0.94,1.00,1.08,1.19,1.34,1.51,1.75,2.03,2.26))

for(i in 1:length(BM[,1])){
  temp.widths<-BM[i,c(which(colnames(BM)=="Width.5.proc.m"):which(colnames(BM)=="Width.85.proc.m"))] #Ru
  temp.heights<-temp.widths*HW.ratios$All.HW.ratio #...calculate the height of whale
  colnames(temp.heights)<-c("Height.5.proc.m","Height.10.proc.m","Height.15.proc.m","Height.20.proc.m",
  ifelse(i==1,temp.output<-temp.heights,temp.output<-rbind(temp.output,temp.heights)) #
}
BM<-cbind(BM,temp.output)
```

Set width and height at 0 and 100%BL from rostrum to be 0

```
BM$Width.0.proc.m<-0
BM$Height.0.proc.m<-0
BM$Width.100.proc.m<-0
BM$Height.100.proc.m<-0
```

Calculate the body width and height at 90 and 95%BL from rostrum based on linear interpolation between 85 and 100%BL from rostrum

```
BM$Width.90.proc.m<-BM$Width.85.proc.m-(1*(BM$Width.85.proc.m/3))
BM$Width.95.proc.m<-BM$Width.85.proc.m-(2*(BM$Width.85.proc.m/3))
BM$Height.90.proc.m<-BM$Height.85.proc.m-(1*(BM$Height.85.proc.m/3))
BM$Height.95.proc.m<-BM$Height.85.proc.m-(2*(BM$Height.85.proc.m/3))
```

Re-order data frame (necessary for the next step)

```
BM<-BM[,c(which(colnames(BM)=="Width.0.proc.m"),which(colnames(BM)=="Width.5.proc.m"):which(colnames(BM)
Width.col.start<-which(colnames(BM)=="Width.0.proc.m") #Extracts the column number of the starti
Height.col.start<-which(colnames(BM)=="Height.0.proc.m") #Extracts the column number of the starti
```

Calculate the body volume of the whales

```
BM$Volume.m3<-NA #Creates an empty storage vector for body volume
for(y in 1:length(BM[,1])){ #Runs a loop for every individual in the data frame
  for(k in 1:(length(seq(0,100,5))-1)){ #Runs a loop for every body segment (volume between two mea
    f.ellipse<-function(x){ #Formula to calculate the volume of an ellipse
      (BM[y,Width.col.start+(k-1)]+(BM[y,(Width.col.start+k)]-BM[y,Width.col.start+(k-1)])*x)/2*(BM[y
    }
    Volume.temp<-integrate(f.ellipse,lower=0,upper=1)$value*BM$Total.length.m[y]*0.05 #Multiplies the
```

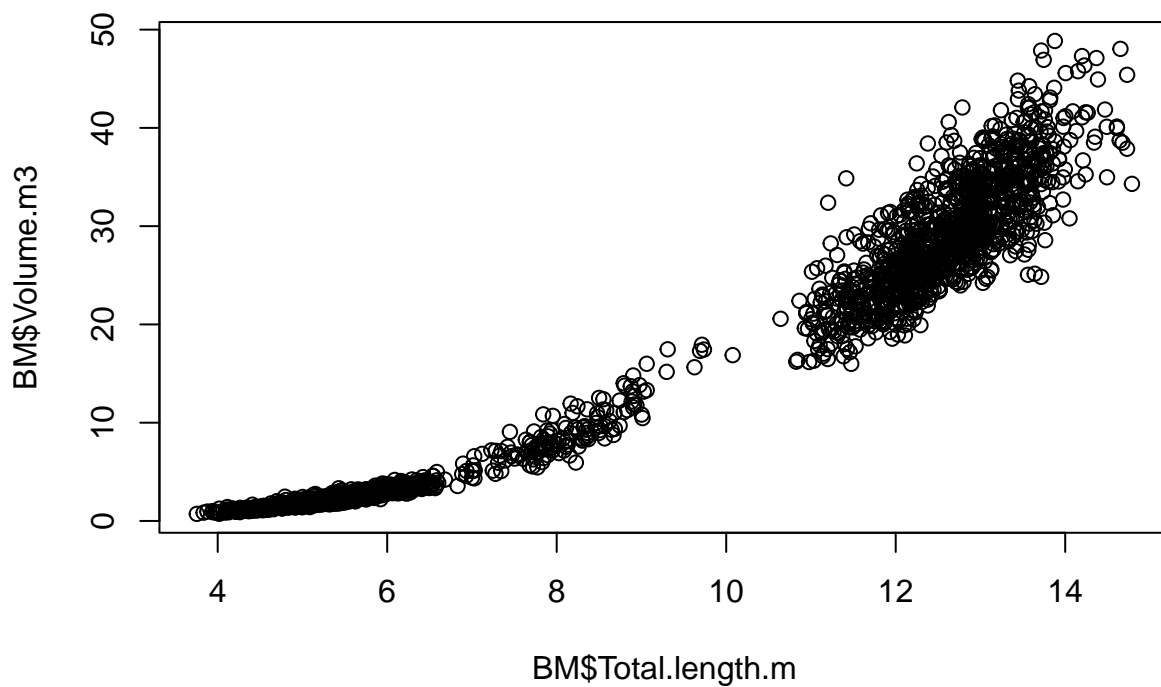
```

    ifelse(k==1,Store1<-Volume.temp,Store1<-c(Store1,Volume.temp))      #Stores the out,
  }
  BM$Volume.m3[y]<-sum(Store1)                                           #Calculates the
}

```

check data

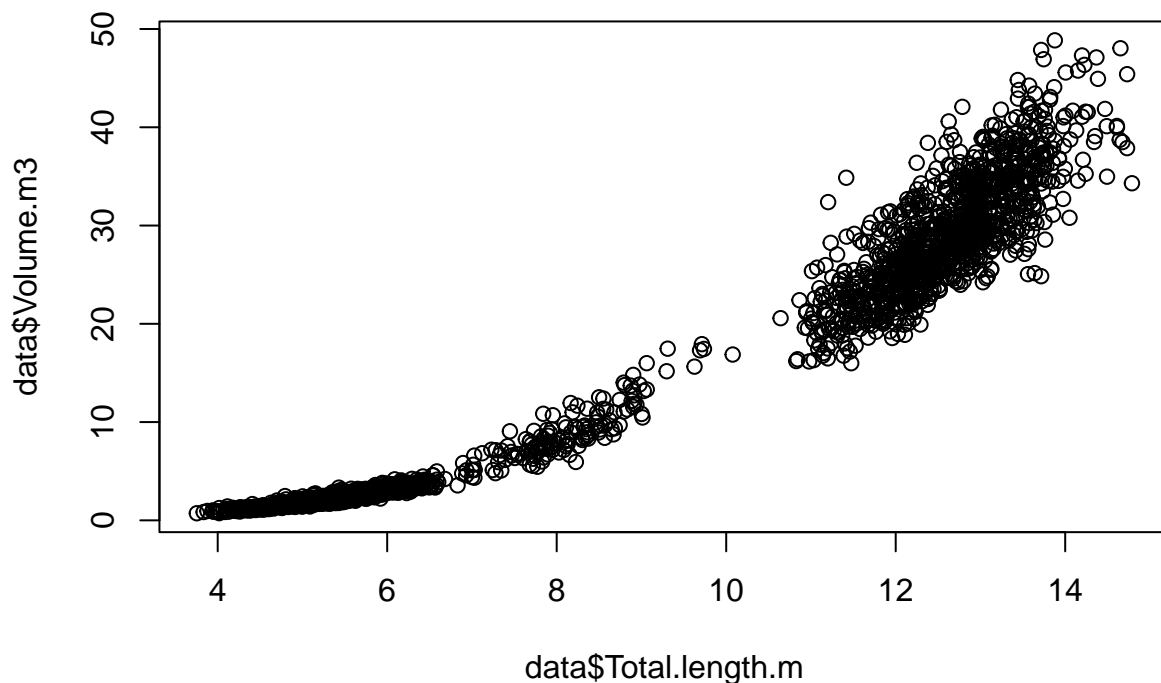
```
plot(BM$Total.length.m,BM$Volume.m3)
```



```

#Check data makes sense/that there arent many outliers
data$Volume.m3 <- NA
nm <- c("Volume.m3")
data[nm] <- lapply(nm, function(x) BM[[x]][match(data$Filename,BM$Filename)])
View(data)
plot(data$Total.length.m,data$Volume.m3)

```



```
#write the CSV file
write.csv(data, "Lewis_Raw_Sheet.csv")
```

Data Analysis

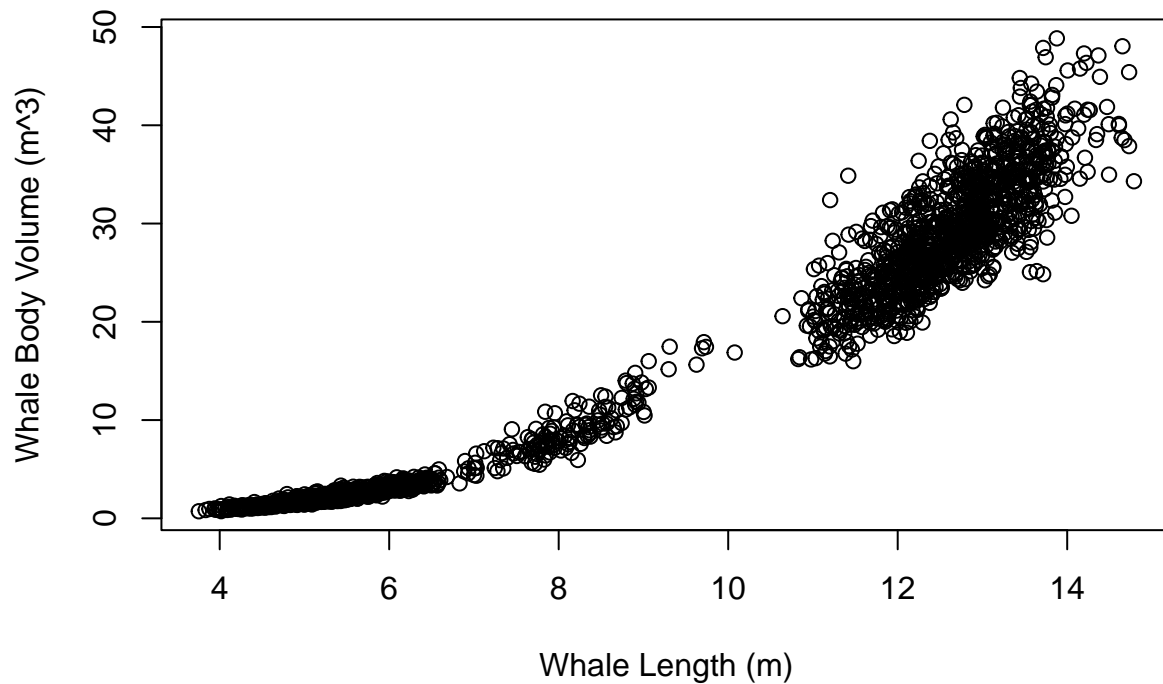
Below is the code and plots used to analyze our data with the corresponding statistical analysis.

```
###Create regression###
whales <- read.csv("Lewis_Raw_Sheet.csv")
model <- lm(Volume.m3 ~ Total.length.m, data = whales)
model

##
## Call:
## lm(formula = Volume.m3 ~ Total.length.m, data = whales)
##
## Coefficients:
## (Intercept) Total.length.m
## -18.322 3.771

whale_plot <- plot(whales$Total.length.m, whales$Volume.m3, main = "Whale Length vs. Volume",
  xlab = "Whale Length (m)", ylab = "Whale Body Volume (m^3)")
```


Whale Length vs. Volume



```
summary_result <- summary(model)
summary_result
```

```
##
## Call:
## lm(formula = Volume.m3 ~ Total.length.m, data = whales)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.9548 -1.8605 -0.1104  1.6421 14.8411
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -18.32208    0.18839   -97.26  <2e-16 ***
## Total.length.m   3.77054    0.01905  197.95  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.176 on 2164 degrees of freedom
## Multiple R-squared:  0.9477, Adjusted R-squared:  0.9476
## F-statistic: 3.919e+04 on 1 and 2164 DF, p-value: < 2.2e-16
```

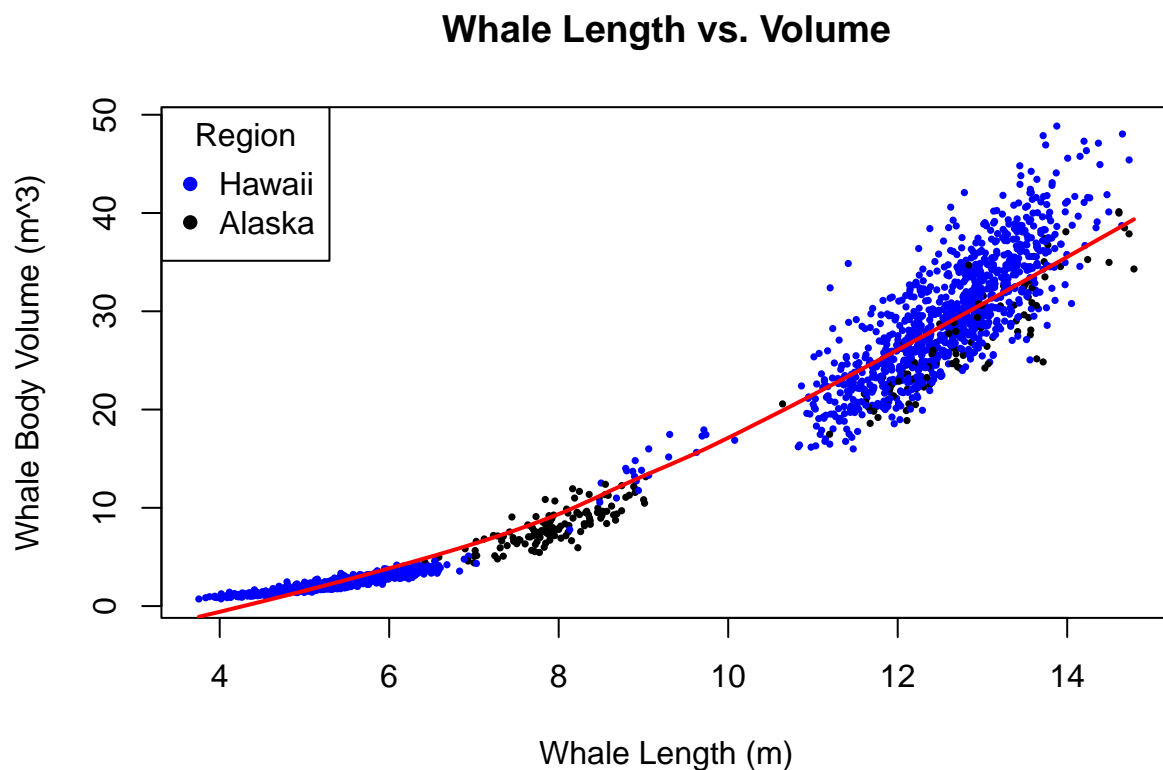
```
r_squared <- summary_result$r.squared
r_squared
```

```
## [1] 0.9476658
```

```
# Plot with points of different colors based on Region
colors <- ifelse(whales$Region == "HI", "blue", "black")
whale_plot <- plot(
  whales$Total.length.m, whales$Volume.m3,
  main = "Whale Length vs. Volume",
  xlab = "Whale Length (m)", ylab = "Whale Body Volume (m^3)",
  col = colors, pch = 16, cex = 0.5
)
whale_plot
```

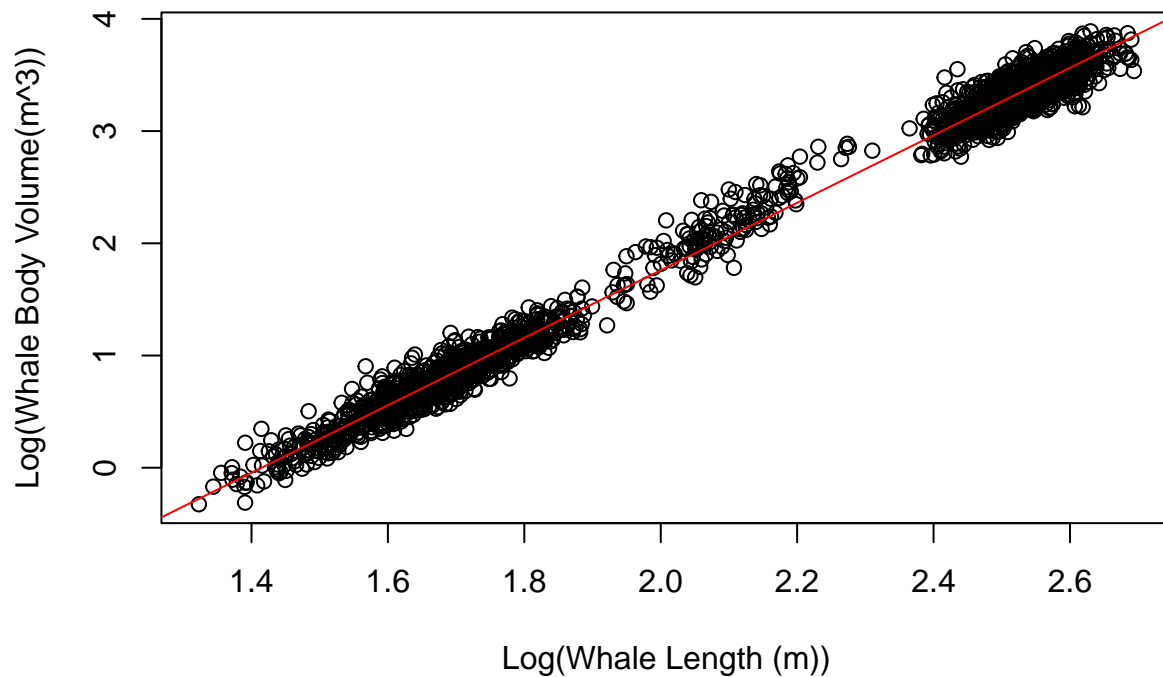
```
## NULL
```

```
smoothed_data <- lowess(whales$Total.length.m, whales$Volume.m3)
lines(smoothed_data, col = "red", lwd = 2)
legend("topleft", legend = c("Hawaii", "Alaska"), col = c("blue", "black"), pch = 16, cex = 1, title = "Region")
```



```
###Transform Data###
whales$log_length <- log(whales$Total.length.m)
whales$log_volume <- log(whales$Volume.m3)
log_regression <- lm(log_volume ~ log_length, data = whales)
plot(whales$log_length, whales$log_volume, main = "Log-Transformed Whale Length vs. Volume",
      xlab = "Log(Whale Length (m))", ylab = "Log(Whale Body Volume(m^3))")
abline(log_regression, col = "red")
```

Log-Transformed Whale Length vs. Volume



```
summary_result_log <- summary(log_regression)
summary_result_log
```

```
##
## Call:
## lm(formula = log_volume ~ log_length, data = whales)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.40714 -0.08384 -0.00541  0.07253  0.48363
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.254489   0.013381  -317.9   <2e-16 ***
## log_length   3.007065   0.006145   489.4   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1216 on 2164 degrees of freedom
## Multiple R-squared:  0.991, Adjusted R-squared:  0.991
## F-statistic: 2.395e+05 on 1 and 2164 DF, p-value: < 2.2e-16
```

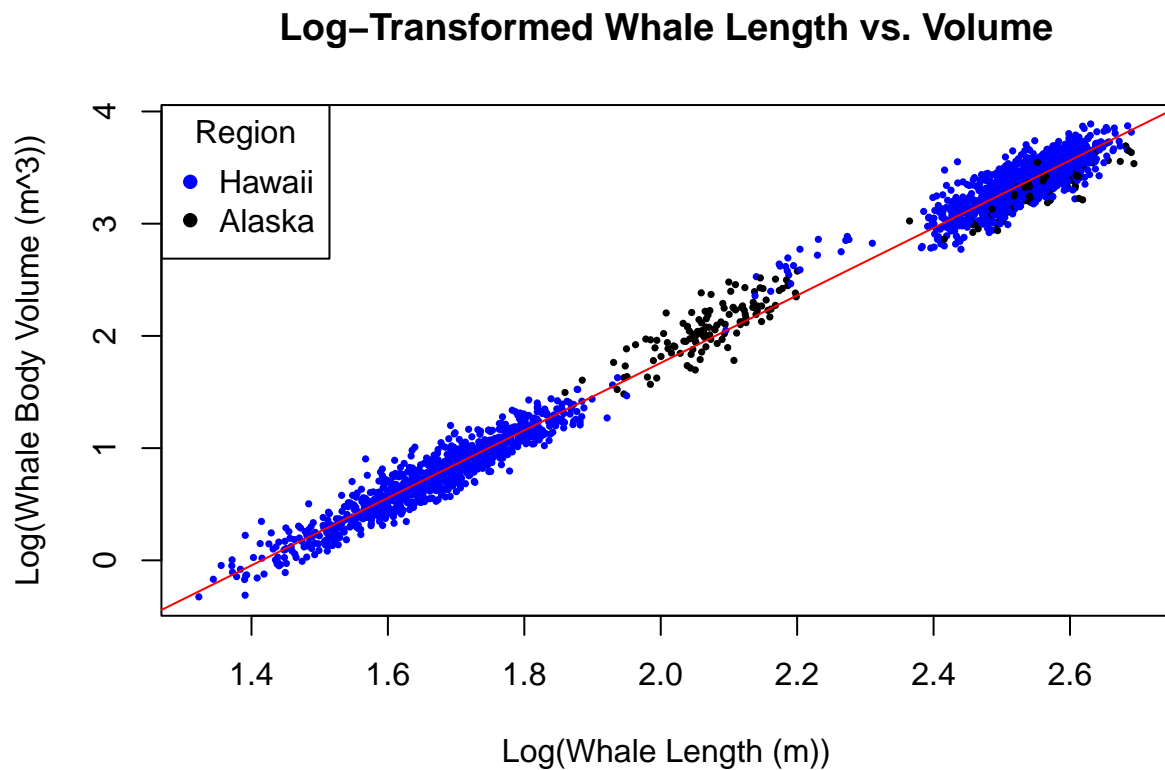
```
r_squared_log <- summary_result_log$r.squared
r_squared_log
```

```
## [1] 0.991045
```

```
# Plot with points of different colors based on Region
colors <- ifelse(whales$Region == "HI", "blue", "black")
whale_plot <- plot(
  whales$log_length, whales$log_volume,
  main = "Log-Transformed Whale Length vs. Volume",
  xlab = "Log(Whale Length (m))", ylab = "Log(Whale Body Volume (m^3))",
  col = colors, pch = 16, cex = 0.5
)
whale_plot
```

```
## NULL
```

```
legend("topleft", legend = c("Hawaii", "Alaska"), col = c("blue", "black"), pch = 16, cex = 1, title = "Region")
abline(log_regression, col = "red")
```



```
summary_result_log <- summary(log_regression)
summary_result_log
```

```
##
## Call:
## lm(formula = log_volume ~ log_length, data = whales)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.40714 -0.08384 -0.00541  0.07253  0.48363
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.254489   0.013381  -317.9   <2e-16 ***
## log_length   3.007065   0.006145   489.4   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1216 on 2164 degrees of freedom
## Multiple R-squared:  0.991, Adjusted R-squared:  0.991
## F-statistic: 2.395e+05 on 1 and 2164 DF, p-value: < 2.2e-16
```

```
r_squared_log <- summary_result_log$r.squared
r_squared_log
```

```
## [1] 0.991045
```

```
###Calculating residuals###
```

```
residuals_vector <- residuals(log_regression)
head(residuals_vector)
```

```
##           1           2           3           4           5           6
## 0.117148607 0.006315415 -0.018770543 -0.097434808 0.219220464 0.133003399
```

```
residual_variance <- var(residuals_vector)
head(residual_variance)
```

```
## [1] 0.01476808
```

```
whales$BCI <- residuals_vector
head(whales)
```

```
##      X Region Year DOY Grade_pass Altitude_Source      Filename Rep.class
## 1  2      HI 2019  15         Y          S_Alt 2019.01.15.03.02      Calf
## 2  7      HI 2019  16         Y          S_Alt 2019.01.16.20.01      Mother
## 3  8      HI 2019  16         Y          S_Alt 2019.01.16.20.02      Calf
## 4  9      HI 2019  16         Y          S_Alt 2019.01.16.28.03      Mother
## 5 10      HI 2019  16         Y          S_Alt 2019.01.16.28.04      Yearling
## 6 13      HI 2019  16         Y          S_Alt 2019.01.16.31.01      Mother
##      Corrected_height_m Pixel_length Width.5.proc.m Width.10.proc.m
## 1          29.66091      0.14691      0.3994949      0.5212653
## 2          26.92527      0.47405      0.9272948      1.5043068
## 3          27.23762      0.19656      0.4030241      0.5675568
## 4          44.31017      0.25962      0.8614074      1.3186065
## 5          40.52864      0.21997      0.6559182      1.0278384
## 6          33.51787      0.42361      1.0721390      1.6396154
##      Width.15.proc.m Width.20.proc.m Width.25.proc.m Width.30.proc.m
## 1          0.6488881      0.8399478      0.8453190      0.877800
```

```
## 2      1.7279477      1.7777515      2.1965369      2.160612
## 3      0.6837677      0.9158989      0.9669881      1.007797
## 4      1.4907987      1.5919845      2.0067111      2.015104
## 5      1.1970195      1.3543958      1.6632835      1.735527
## 6      1.8889308      1.9720644      2.3987504      2.590781
## Width.35.proc.m Width.40.proc.m Width.45.proc.m Width.50.proc.m
## 1      0.8922854      0.897800      0.8941606      0.8448973
## 2      2.2309215      2.432123      2.4731709      2.4317089
## 3      1.0281975      1.016753      1.0083333      0.9816338
## 4      2.0436958      2.022627      2.0359649      2.0190499
## 5      1.8420096      1.954522      1.9650014      1.9417163
## 6      2.6096411      2.781060      2.8410066      2.8723615
## Width.55.proc.m Width.60.proc.m Width.65.proc.m Width.70.proc.m
## 1      0.7539285      0.6294370      0.5073486      0.4096226
## 2      2.2540847      2.0864176      1.7889882      1.4551682
## 3      0.9146428      0.7672011      0.6455904      0.5056776
## 4      1.8520885      1.6312966      1.4870776      1.2118446
## 5      1.7207080      1.5889729      1.4316019      1.1083126
## 6      2.7950413      2.6061701      2.2883757      1.8558932
## Width.75.proc.m Width.80.proc.m Width.85.proc.m Width.90.proc.m
## 1      0.3160273      0.2452473      0.2017922      0.3058264
## 2      1.0847535      0.6887451      0.4745769      0.3320024
## 3      0.3789513      0.2510993      0.2087616      0.4011689
## 4      0.9761627      0.6040148      0.3575452      0.3227636
## 5      0.8558828      0.5352642      0.2520273      0.4127937
## 6      1.3949643      0.9093462      0.4332564      0.3055112
## Width.95.proc.m Total.length.m Volume.m3 log_length log_volume      BCI
## 1      0.831508      4.357485  1.334750  1.471895  0.2887440  0.117148607
## 2      1.333204      12.763923 30.255767  2.546623  3.4096868  0.006315415
## 3      1.040845      5.353827  2.164153  1.677812  0.7720293 -0.018770543
## 4      1.385998      11.503805 19.952769  2.442678  2.9933679 -0.097434808
## 5      1.557564      8.915085 12.723143  2.187745  2.5434226  0.219220464
## 6      1.638115      14.198503 47.307513  2.653137  3.8566691  0.133003399
```

```
###Create month column###
```

```
whales <- whales %>%
  mutate(Date = as.Date(paste(Year, DOY, sep = "-"), format = "%Y-%j"))
whales <- whales %>%
  mutate(Month = format(Date, "%m"))
avg_bv_per_month <- whales %>%
  group_by(Year, Month, Rep.class) %>%
  summarise(Avg_BV = mean(Volume.m3))
```

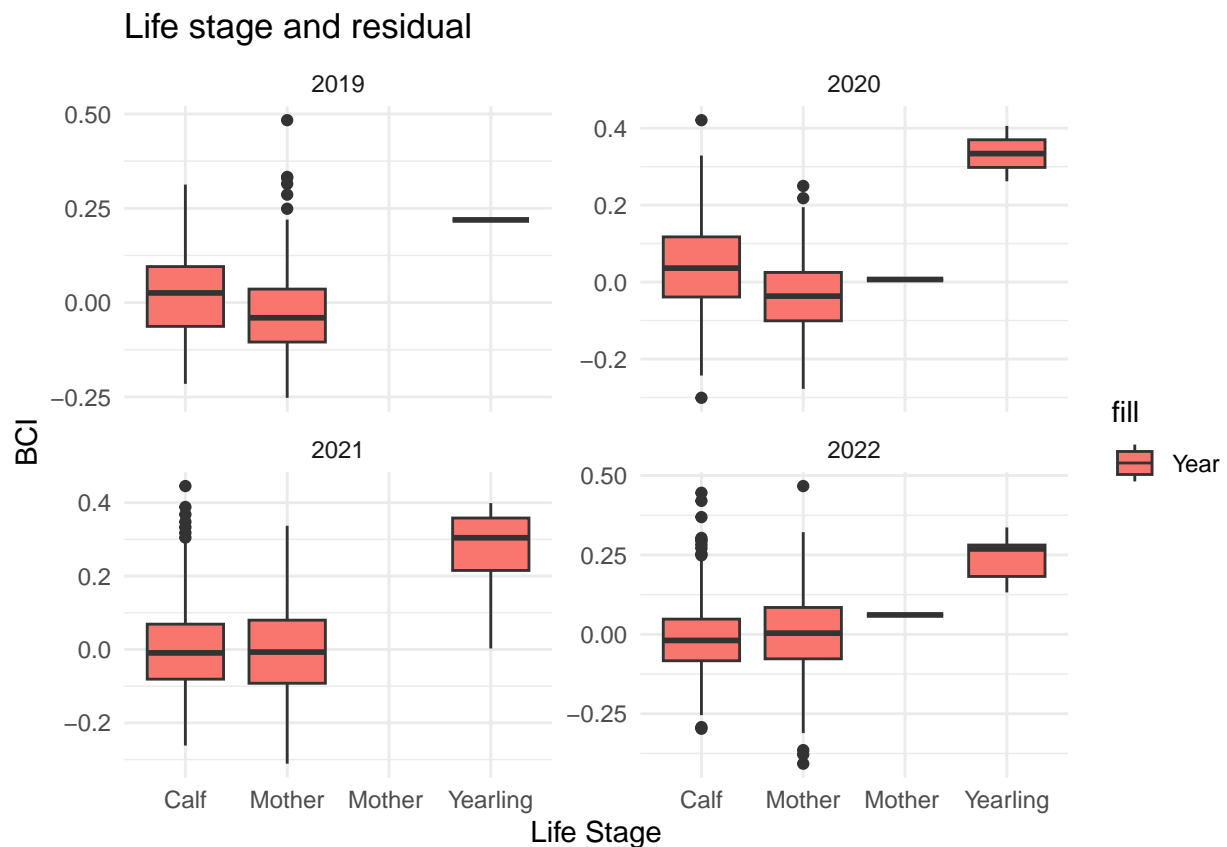
```
## 'summarise()' has grouped output by 'Year', 'Month'. You can override using the
## '.groups' argument.
```

```
print(avg_bv_per_month)
```

```
## # A tibble: 63 x 4
## # Groups:   Year, Month [27]
##   Year Month Rep.class Avg_BV
##   <int> <chr> <chr>      <dbl>
## 1  2019 01    Calf        1.75
```

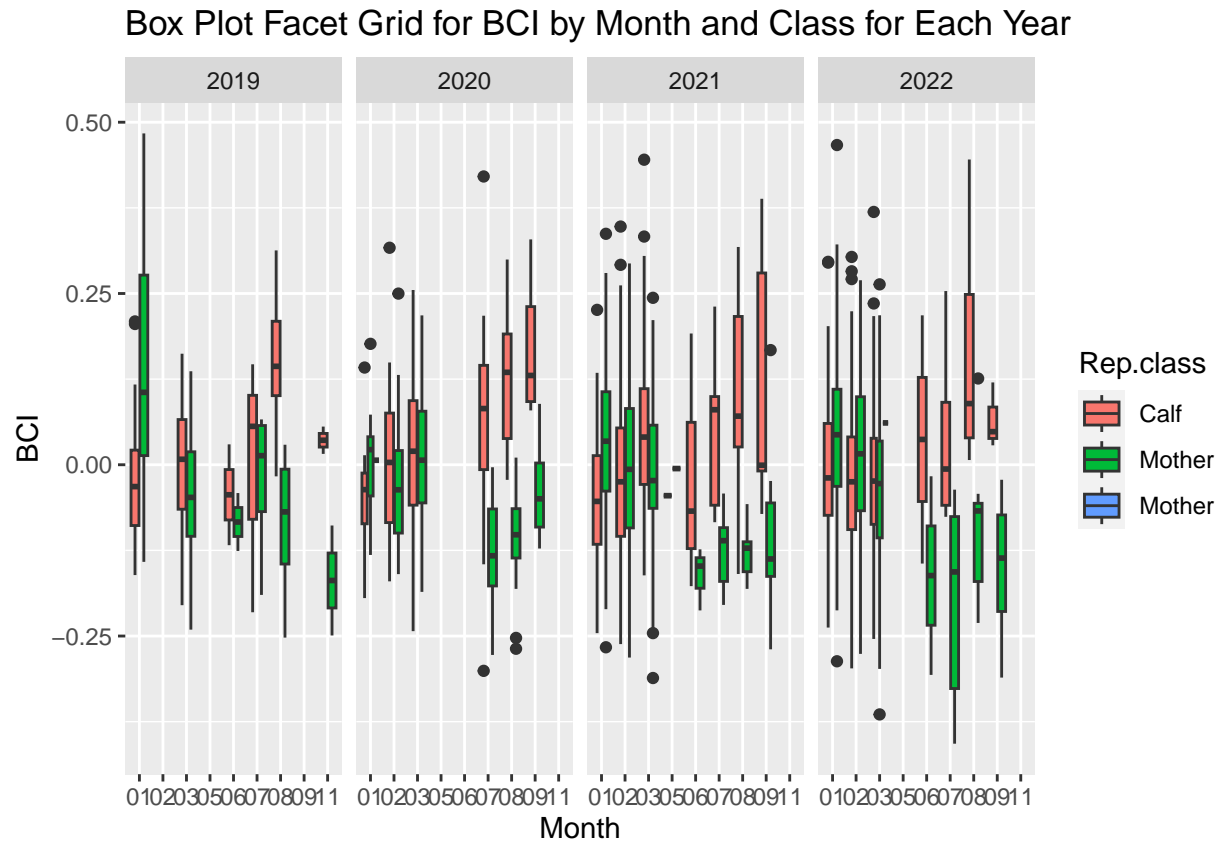
```
## 2 2019 01 Mother 33.3
## 3 2019 01 Yearling 12.7
## 4 2019 03 Calf 2.10
## 5 2019 03 Mother 24.6
## 6 2019 06 Calf 5.08
## 7 2019 06 Mother 26.6
## 8 2019 07 Calf 7.09
## 9 2019 07 Mother 28.4
## 10 2019 08 Calf 7.59
## # i 53 more rows
```

```
###Create a facet grid###
whale_grid <- ggplot(whales, aes(x = Rep.class, y = BCI, fill = "Year")) +
  geom_boxplot() +
  facet_wrap(~Year, scales = "free_y") +
  labs(title = "Life stage and residual",
       x = "Life Stage",
       y = "BCI") +
  theme_minimal()
whale_grid
```



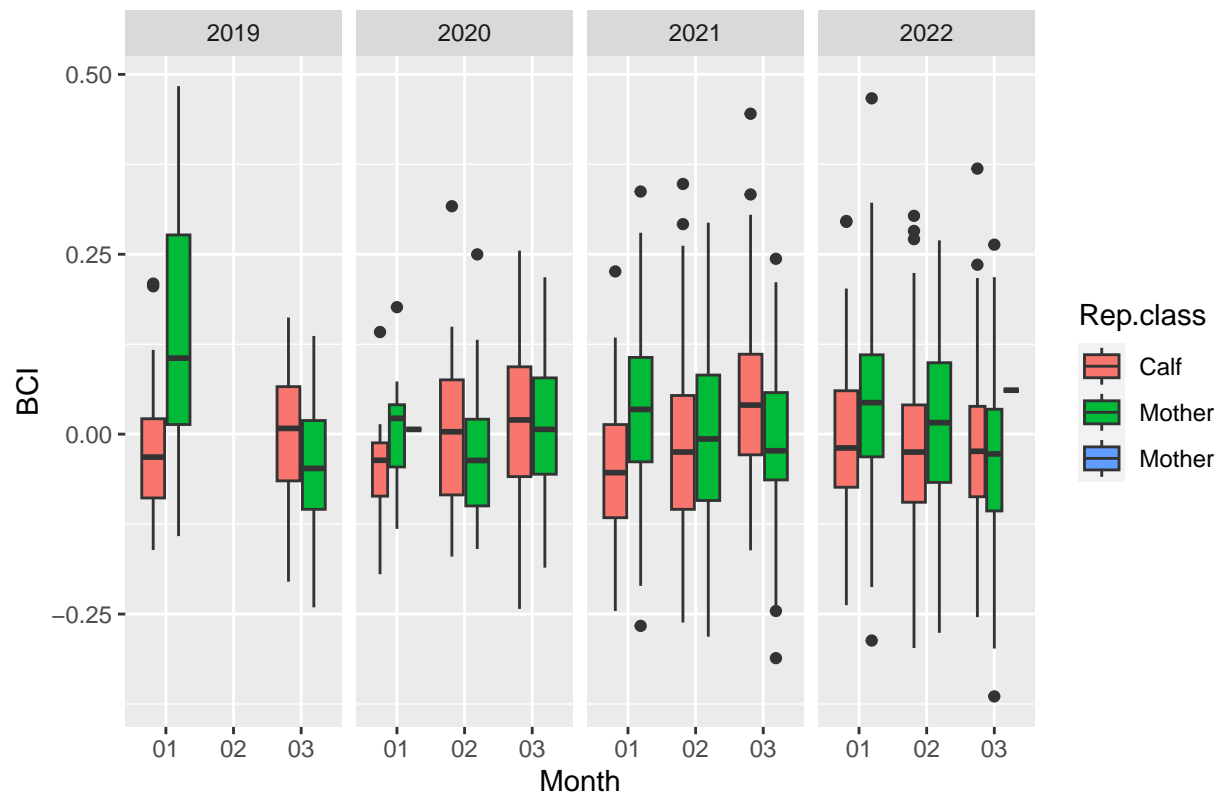
```
###Facet grid with month###
#omit yearling#
whales_filtered1 <- whales %>%
  filter(Rep.class != "Yearling")
```

```
ggplot(whales_filtered1, aes(x = Month, y = BCI, fill = Rep.class)) +
  geom_boxplot() +
  facet_grid(~Year) +
  labs(x = "Month", y = "BCI", fill = "Rep.class") +
  ggtitle("Box Plot Facet Grid for BCI by Month and Class for Each Year")
```



```
###Facet grid with month 1,2, and 3###
whales_subset <- whales %>% filter(Month %in% c("01", "02", "03"))
whales_filtered <- whales_subset %>%
  filter(Rep.class != "Yearling")
ggplot(whales_filtered, aes(x = as.factor(Month), y = BCI, fill = Rep.class)) +
  geom_boxplot() +
  facet_grid(~Year) +
  labs(x = "Month", y = "BCI", fill = "Rep.class") +
  ggtitle("Box Plot Facet Grid for BCI by Month and Class for Each Year")
```


Box Plot Facet Grid for BCI by Month and Class for Each Year



```
###Perform a t-test to compare BCI of calf and mother###
```

```
# Exclude 'yearling' class
```

```
#####whales_filtered <- whales %>%
```

```
whales_filtered <- whales %>%
```

```
  filter(Rep.class != "Yearling")
```

```
table(whales_filtered$Rep.class)
```

```
##
```

```
##   Calf  Mother Mother
```

```
##  1046   1097      2
```

```
whales_filtered$Rep.class <- fct_collapse(whales_filtered$Rep.class, Mother = c('Mother', 'Mother '))
```

```
table(whales_filtered$Rep.class)
```

```
##
```

```
##   Calf Mother
```

```
##  1046   1099
```

```
t_test_result <- t.test(BCI ~ Rep.class, data = whales_filtered)
```

```
print(t_test_result)
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
## data: BCI by Rep.class
## t = 1.6244, df = 2141.8, p-value = 0.1044
## alternative hypothesis: true difference in means between group Calf and group Mother is not equal to
## 95 percent confidence interval:
## -0.001728381 0.018409689
## sample estimates:
## mean in group Calf mean in group Mother
## 0.001745506 -0.006595148
```

```
#T-test for Hawaii
t_test_hawaii <- t.test(BCI ~ Rep.class, data = whales_filtered[whales_filtered$Region == "HI", ])
print("T-Test for Hawaii:")
```

```
## [1] "T-Test for Hawaii:"
```

```
print(t_test_hawaii)
```

```
##
## Welch Two Sample t-test
##
## data: BCI by Rep.class
## t = -3.1041, df = 1903, p-value = 0.001937
## alternative hypothesis: true difference in means between group Calf and group Mother is not equal to
## 95 percent confidence interval:
## -0.026202972 -0.005912059
## sample estimates:
## mean in group Calf mean in group Mother
## -0.01075828 0.00529924
```

```
#T-test for Alaska
t_test_alaska <- t.test(BCI ~ Rep.class, data = whales_filtered[whales_filtered$Region == "AK", ])
print("T-Test for Alaska:")
```

```
## [1] "T-Test for Alaska:"
```

```
print(t_test_alaska)
```

```
##
## Welch Two Sample t-test
##
## data: BCI by Rep.class
## t = 13.145, df = 215.44, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group Calf and group Mother is not equal to
## 95 percent confidence interval:
## 0.1724013 0.2332230
## sample estimates:
## mean in group Calf mean in group Mother
## 0.09733226 -0.10547985
```

```
###Creating a time series plot###
```

```
##TIME SERIES
```

```
##First, find the average BV of calves and mothers per month
```

```
#convert year and DOY to date format
```

```
###make avg per month
```

```
whales <- whales %>%  
  mutate(Date = as.Date(paste(Year, DOY, sep = "-"), format = "%Y-%j"))
```

```
# Extract month from the date
```

```
whales <- whales %>%  
  mutate(Month = format(Date, "%m"))
```

```
# Group by Year, Month, and class, then calculate the average body volume
```

```
avg_bv_per_month <- whales %>%  
  group_by(Year, Month, Rep.class) %>%  
  summarise(Avg_BV = mean(Volume.m3))
```

```
## 'summarise()' has grouped output by 'Year', 'Month'. You can override using the  
## '.groups' argument.
```

```
# View the resulting dataset with average body volume per month for each year and Rep.class
```

```
print(avg_bv_per_month)
```

```
## # A tibble: 63 x 4  
## # Groups:   Year, Month [27]  
##   Year Month Rep.class Avg_BV  
##   <int> <chr> <chr>      <dbl>  
## 1  2019 01    Calf        1.75  
## 2  2019 01    Mother       33.3  
## 3  2019 01   Yearling    12.7  
## 4  2019 03    Calf        2.10  
## 5  2019 03    Mother       24.6  
## 6  2019 06    Calf        5.08  
## 7  2019 06    Mother       26.6  
## 8  2019 07    Calf        7.09  
## 9  2019 07    Mother       28.4  
## 10 2019 08    Calf        7.59  
## # i 53 more rows
```

```
##NEXT, prepare data by excluding yearling class to focus on mothers and calves,  
#then group by year, month and class to calculate avg body volume for each year
```

```
# Exclude 'yearling' class
```

```
whales_filtered <- whales %>%  
  filter(Rep.class != "Yearling")
```

```
# Group by Year, Month, and Rep.class, then calculate the average BCI
```

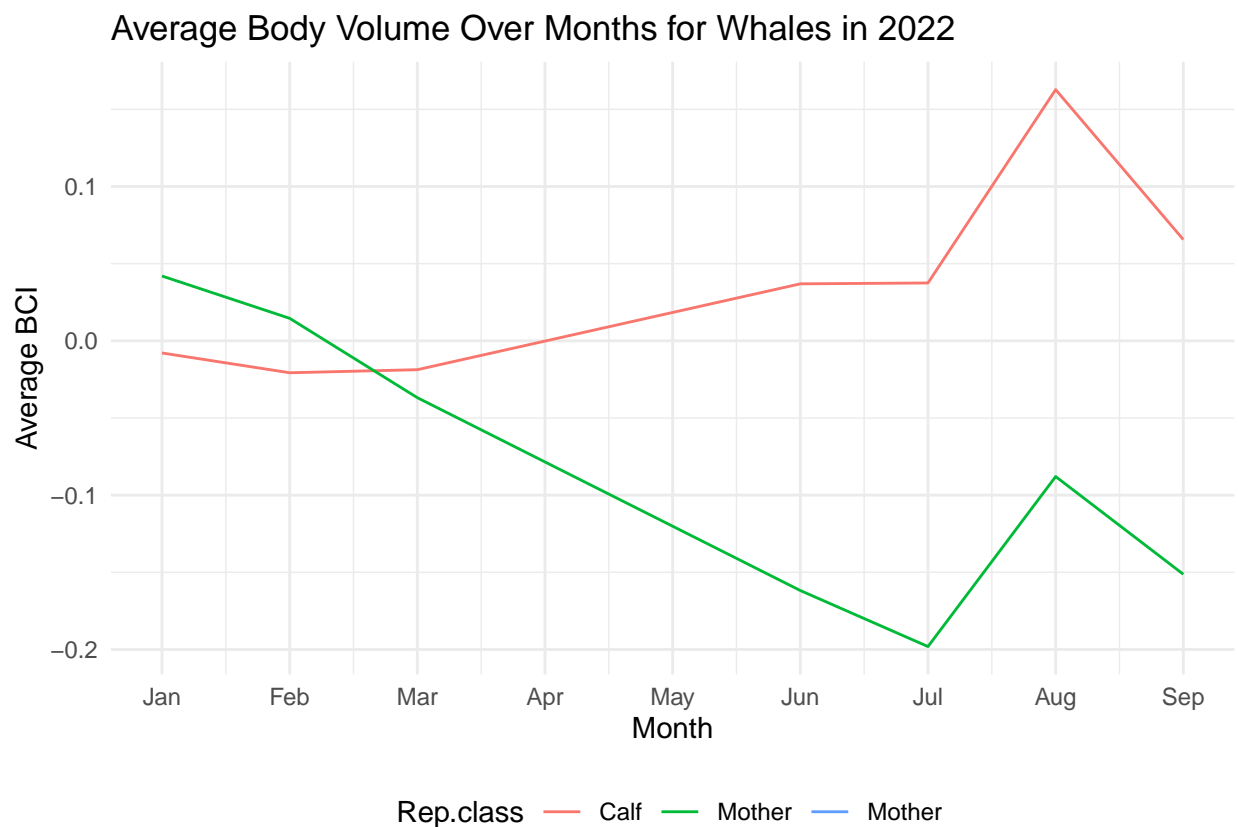
```
avg_BCI_per_month <- whales_filtered %>%  
  group_by(Year, Month, Rep.class) %>%  
  summarise(Avg_BCI = mean(BCI))
```

```
## 'summarise()' has grouped output by 'Year', 'Month'. You can override using the
## '.groups' argument.
```

```
# Plotting for each year
for (year in 2019:2022) {
  # Subset data for the current year
  year_data <- avg_BCI_per_month %>%
    filter(Year == year) %>%
    filter(Rep.class != "Yearling") # Filter out 'yearling' within each year

  # Plotting average body volume over months for each Rep.class
  ggplot(year_data, aes(x = as.numeric(Month), y = Avg_BCI, group = Rep.class, color = Rep.class)) +
    geom_line() +
    labs(title = paste("Average Body Volume Over Months for Whales in", year),
         x = "Month", y = "Average BCI") +
    scale_x_continuous(breaks = 1:12, labels = month.abb) +
    theme_minimal() +
    theme(legend.position = "bottom")
  #Doesnt print all years, only 2022. So Next codes will plot each separately

  # You can save the plot here or use any preferred method to display it
  # ggsave(filename = paste("Avg_BV_over_months_", year, ".png"), plot = last_plot())
}
print(last_plot())
```



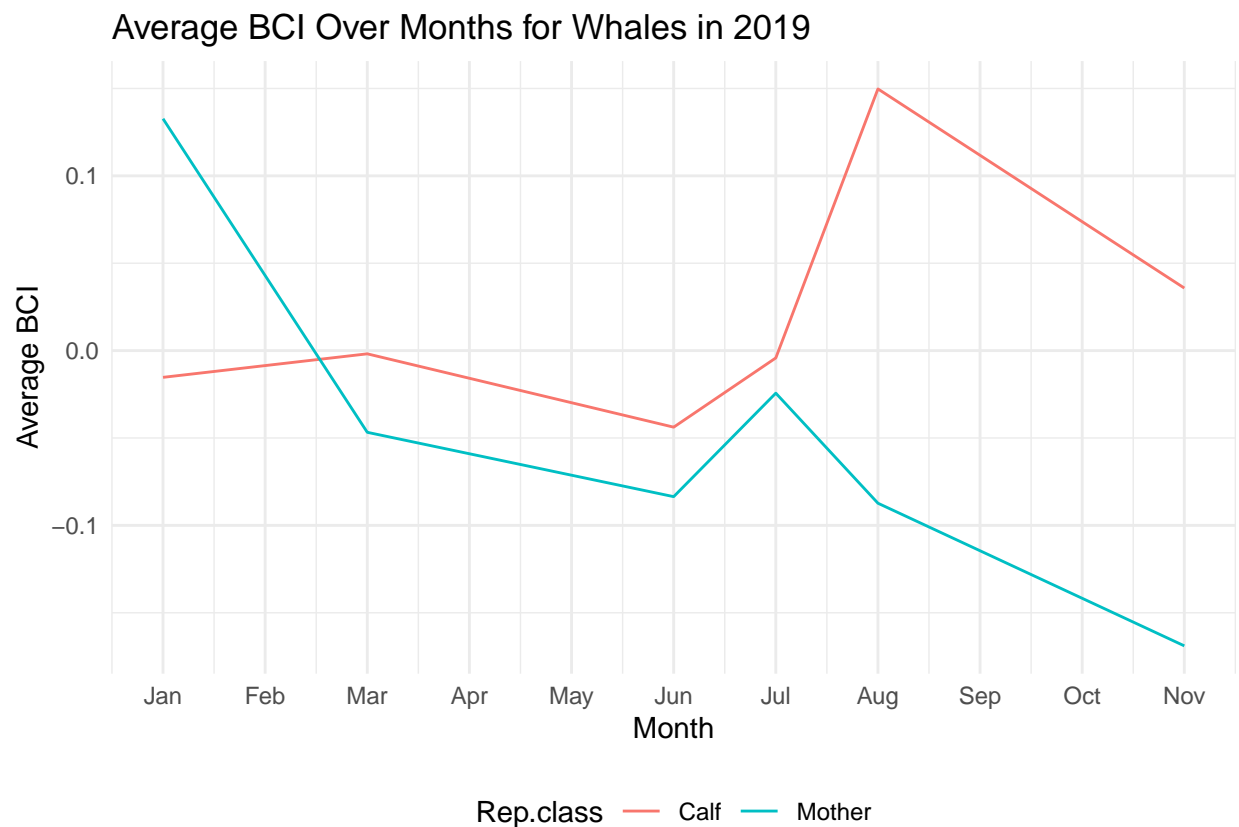
```

# Convert 'Year' and 'Month' to numeric for plotting
avg_BCI_per_month <- avg_BCI_per_month %>%
  mutate(Year = as.numeric(Year),
         Month = as.numeric(Month))

# Filter data for year 2019
data_2019 <- avg_BCI_per_month %>%
  filter(Year == 2019)

# Plotting for 2019
ggplot(data_2019, aes(x = Month, y = Avg_BCI, group = Rep.class, color = Rep.class)) +
  geom_line() +
  labs(title = "Average BCI Over Months for Whales in 2019",
       x = "Month", y = "Average BCI") +
  scale_x_continuous(breaks = 1:12, labels = month.abb) +
  theme_minimal() +
  theme(legend.position = "bottom")

```



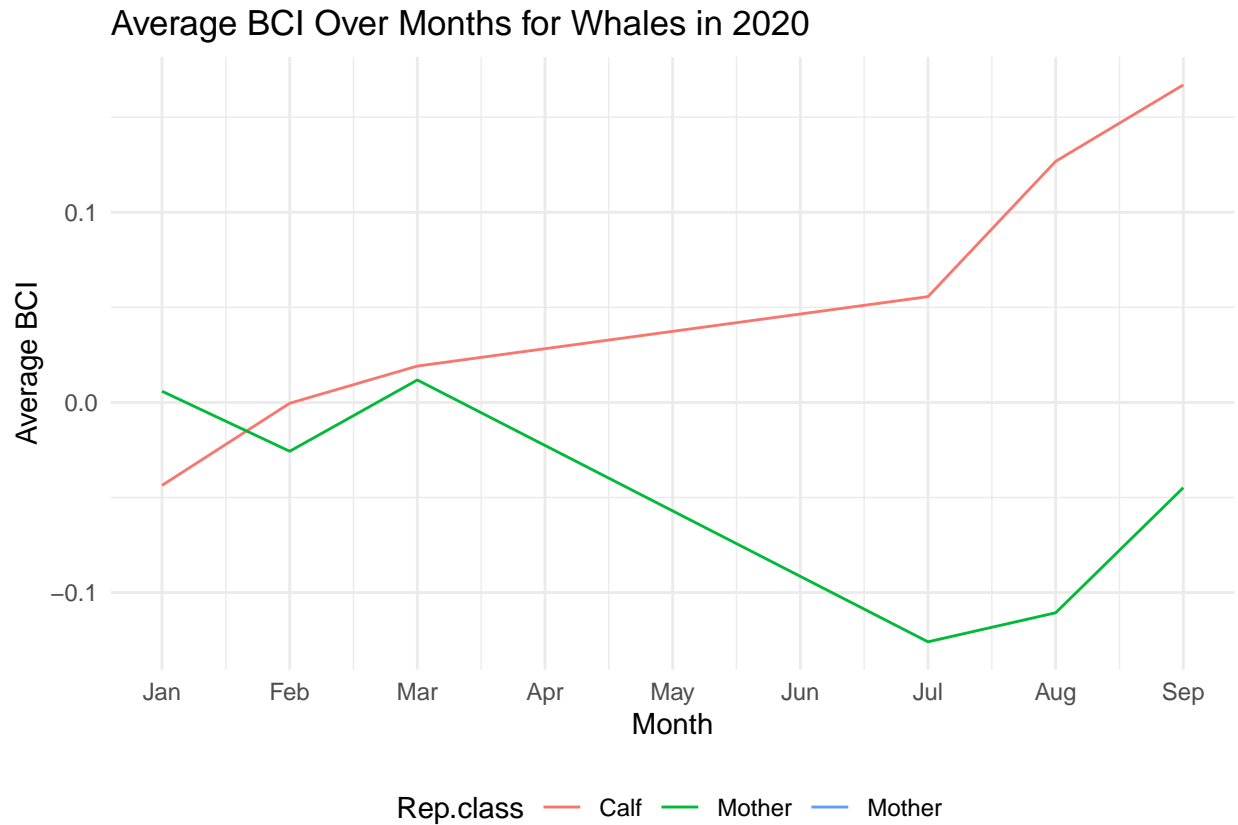
```

# Filter data for year 2020
data_2020 <- avg_BCI_per_month %>%
  filter(Year == 2020)

# Plotting for 2020
ggplot(data_2020, aes(x = Month, y = Avg_BCI, group = Rep.class, color = Rep.class)) +
  geom_line() +

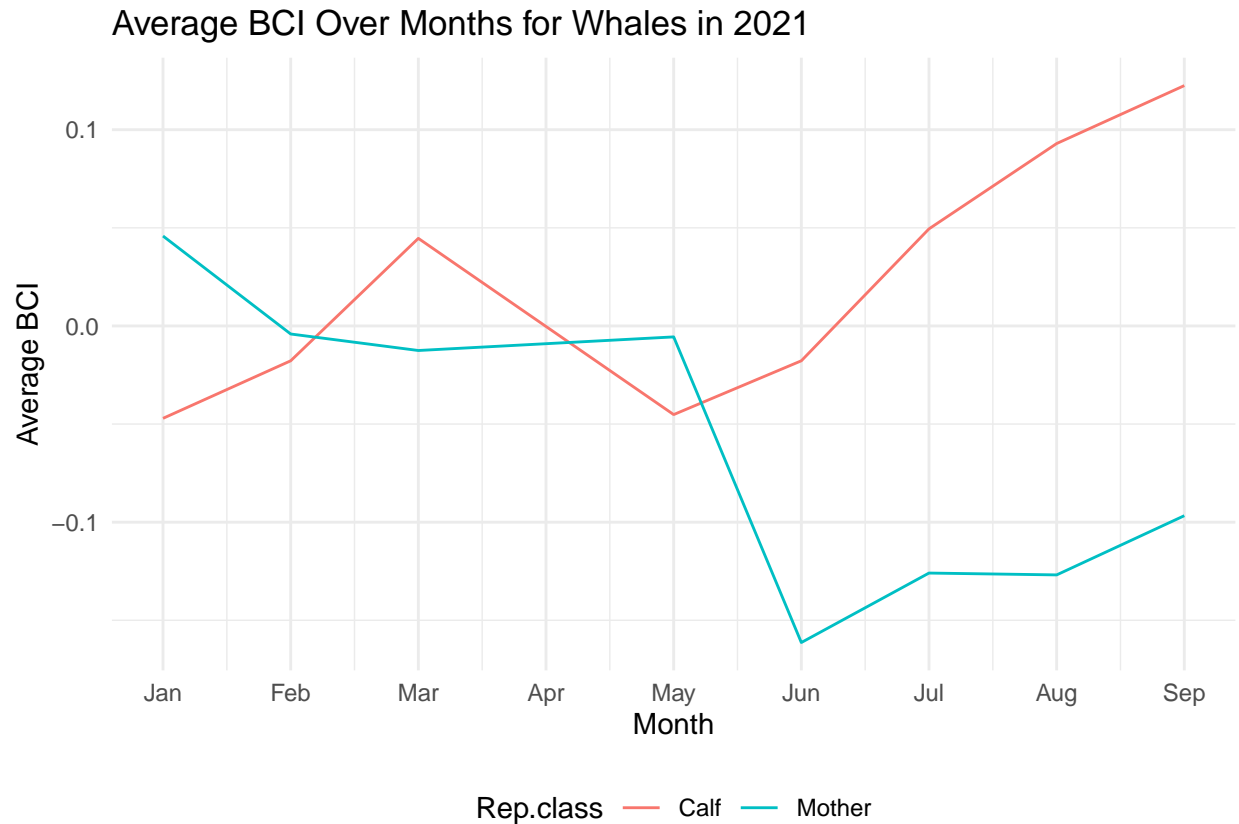
```

```
labs(title = "Average BCI Over Months for Whales in 2020",
     x = "Month", y = "Average BCI") +
scale_x_continuous(breaks = 1:12, labels = month.abb) +
theme_minimal() +
theme(legend.position = "bottom")
```



```
# Filter data for year 2021
data_2021 <- avg_BCI_per_month %>%
  filter(Year == 2021)

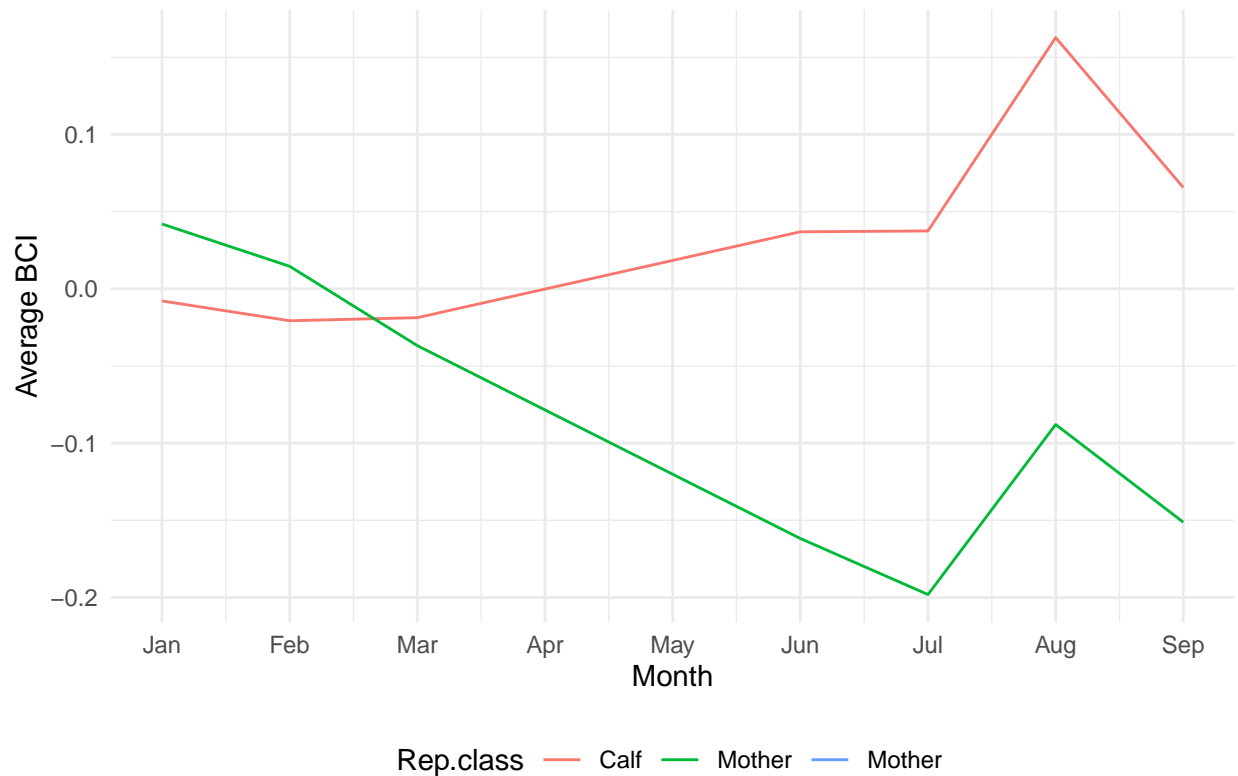
# Plotting for 2021
ggplot(data_2021, aes(x = Month, y = Avg_BCI, group = Rep.class, color = Rep.class)) +
  geom_line() +
  labs(title = "Average BCI Over Months for Whales in 2021",
       x = "Month", y = "Average BCI") +
  scale_x_continuous(breaks = 1:12, labels = month.abb) +
  theme_minimal() +
  theme(legend.position = "bottom")
```



```
# Filter data for year 2022
data_2022 <- avg_BCI_per_month %>%
  filter(Year == 2022)

# Plotting for 2022
ggplot(data_2022, aes(x = Month, y = Avg_BCI, group = Rep.class, color = Rep.class)) +
  geom_line() +
  labs(title = "Average BCI Over Months for Whales in 2019",
       x = "Month", y = "Average BCI") +
  scale_x_continuous(breaks = 1:12, labels = month.abb) +
  theme_minimal() +
  theme(legend.position = "bottom")
```

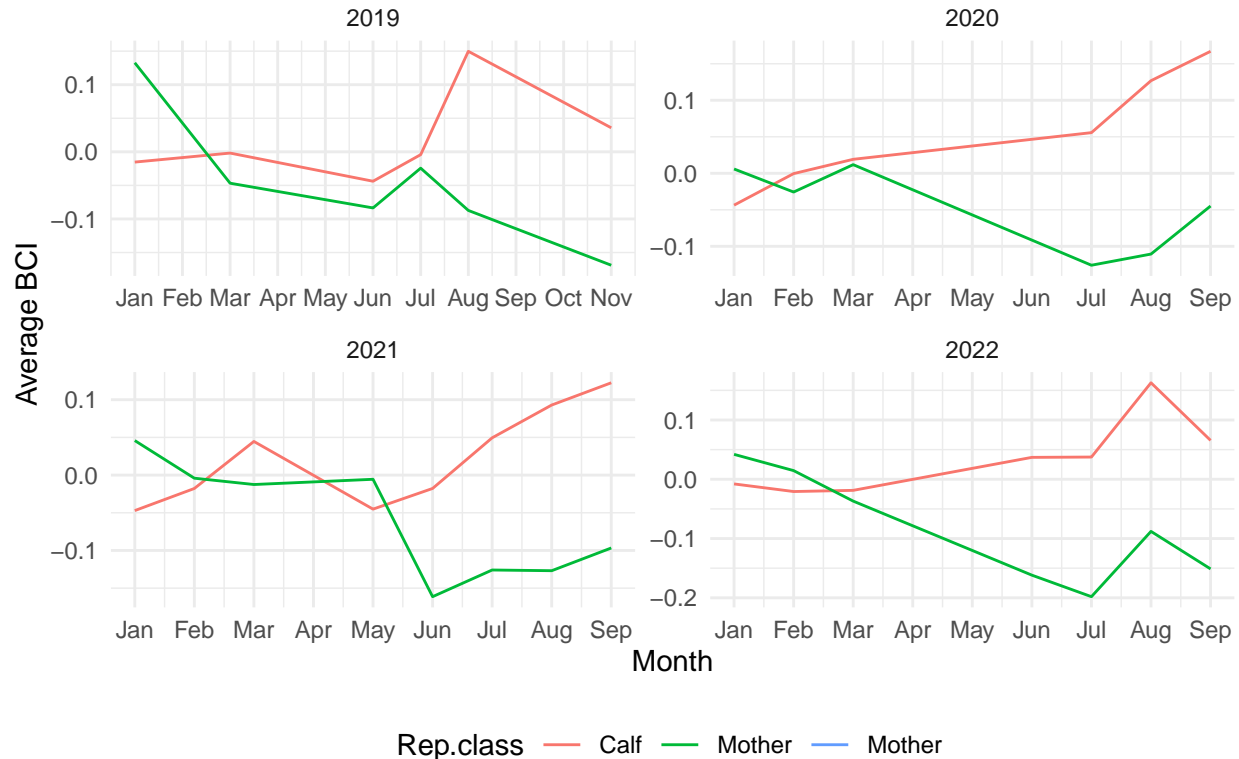
Average BCI Over Months for Whales in 2019



```
# Filter data for years 2019 to 2022
data_years <- avg_BCI_per_month %>%
  filter(Year %in% c(2019, 2020, 2021, 2022))

# Plotting for all years in one panel
ggplot(data_years, aes(x = Month, y = Avg_BCI, group = Rep.class, color = Rep.class)) +
  geom_line() +
  labs(title = "Average Over BCI for Whales (2019-2022)",
       x = "Month", y = "Average BCI") +
  scale_x_continuous(breaks = 1:12, labels = month.abb) +
  facet_wrap(~Year, scales = "free") +
  theme_minimal() +
  theme(legend.position = "bottom")
```


Average Over BCI for Whales (2019–2022)



```
summary(lm(Avg_BCI~Month*Year, data_years))
```

```
##
## Call:
## lm(formula = Avg_BCI ~ Month * Year, data = data_years)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.174353 -0.048193 -0.002956  0.053466  0.189335
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  11.4515878  43.5106655   0.263   0.793
## Month        -0.4125044   6.9919074  -0.059   0.953
## Year         -0.0056655   0.0215338  -0.263   0.794
## Month:Year    0.0002026   0.0034606   0.059   0.954
##
## Residual standard error: 0.08721 on 52 degrees of freedom
## Multiple R-squared:  0.01491,    Adjusted R-squared:  -0.04192
## F-statistic: 0.2624 on 3 and 52 DF,  p-value: 0.8522
```