OGC-biomass

Primary Analyses

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Contents

Data Management

Raw data were imported and compiled for each of the two sampling periods, 1980s and 2010s. Subsets were merged or cast as needed for later analyses. Raw data were initially managed in the R environment, but final data management tasks were performed in Microsoft Excel after exporting the data; final data files are imported from csv files.

```
## Read in raw data files
raw.biomass.1982  <- read_csv("data/OGC_biomass_data-1982.csv", show_col_types = FALSE)
raw.biomass.1983  <- read_csv("data/OGC_biomass_data-1983.csv", show_col_types = FALSE)
raw.biomass.2010s <- read_csv("data/OGC_biomass_data-2010s.csv", show_col_types = FALSE)

## Set column structure for the raw data
raw.biomass.1982$Date  <- as_factor(raw.biomass.1982$Date)
raw.biomass.1982$Snag  <- as_factor(raw.biomass.1982$Snag)
raw.biomass.1983$Date  <- as_factor(raw.biomass.1983$Date)
raw.biomass.1983$Snag  <- as_factor(raw.biomass.1983$Snag)
raw.biomass.2010s$Date <- as_factor(raw.biomass.2010s$Date)
raw.biomass.2010s$Snag <- as_factor(raw.biomass.2010s$Snag)
```

```r
## Biomass data management

## Create date-by-taxa matrices for biomass values
# 1982 raw biomass by taxa matrix
OGC.biomass.1982 <- dcast(
    raw.biomass.1982, Date ~ Genus, sum, value.var = "Biomass_Estimate"
    )
# 1983 raw biomass by taxa matrix
OGC.biomass.1983 <- dcast(
    raw.biomass.1983, Date ~ Genus, sum, value.var = "Biomass_Estimate"
    )
# 2010s raw biomass by taxa matrix
OGC.biomass.2010s <- dcast(
    raw.biomass.2010s, Date ~ Genus, sum, value.var = "Biomass_Estimate"
    )

## Create dataframe of biomass values for each dataset
OGC.biomass.1982.values  <- tibble(OGC.biomass.1982[, 2:59])
OGC.biomass.1983.values  <- tibble(OGC.biomass.1983[, 2:48])
OGC.biomass.2010s.values <- tibble(OGC.biomass.2010s[, 2:64])

## Average by number of snags
OGC.biomass.1982.snag.correction      <- OGC.biomass.1982.values/20
# Correct for 19 snags instead of 20 in first sample
OGC.biomass.1982.snag.correction[1, ] <- ((OGC.biomass.1982.snag.correction[1, ] * 20)/19)
OGC.biomass.1983.snag.correction      <- OGC.biomass.1983.values/10
OGC.biomass.2010s.snag.correction     <- OGC.biomass.2010s.values/10

## Add Date to the biomass data
OGC.biomass.1982.final  <- OGC.biomass.1982.snag.correction %>%
    add_column(OGC.biomass.1982$Date) %>%
    rename(UID = "OGC.biomass.1982$Date")
OGC.biomass.1983.final  <- OGC.biomass.1983.snag.correction %>%
    add_column(OGC.biomass.1983$Date) %>%
    rename(UID = "OGC.biomass.1983$Date")
OGC.biomass.2010s.final <- OGC.biomass.2010s.snag.correction %>%
    add_column(OGC.biomass.2010s$Date) %>%
    rename(UID = "OGC.biomass.2010s$Date")

## Export biomass data files
write_csv(OGC.biomass.1982.final, file = "data/OGC_1982_biomass_by_taxa.csv")
write_csv(OGC.biomass.1983.final, file = "data/OGC_1983_biomass_by_taxa.csv")
write_csv(OGC.biomass.2010s.final, file = "data/OGC_2010s_biomass_by_taxa.csv")
```

```r
## Density data management

## Create date-by-taxa matrices for density values
# 1982 density by taxa matrix
OGC.density.1982 <- dcast(
    raw.biomass.1982, Date ~ Genus, sum, value.var = "Density"
    )
# 1983 density by taxa matrix
OGC.density.1983 <- dcast(
    raw.biomass.1983, Date ~ Genus, sum, value.var = "Density"
    )
# 2010s density by taxa matrix
OGC.density.2010s <- dcast(
    raw.biomass.2010s, Date ~ Genus, sum, value.var = "Density"
    )

## Create dataframe of density values for each dataset
OGC.density.1982.values  <- OGC.density.1982[, 2:59]
OGC.density.1983.values  <- OGC.density.1983[, 2:48]
OGC.density.2010s.values <- OGC.density.2010s[, 2:64]

## Average by number of snags
OGC.density.1982.snag.correction      <- OGC.density.1982.values/20
# Correct for 19 snags instead of 20 in first sample
OGC.density.1982.snag.correction[1, ] <-((OGC.density.1982.snag.correction[1, ] * 20)/19)
OGC.density.1983.snag.correction      <- OGC.density.1983.values/10
OGC.density.2010s.snag.correction     <- OGC.density.2010s.values/10

## Add UID to density values
OGC.density.1982.final  <- OGC.density.1982.snag.correction %>%
    add_column(OGC.density.1982$Date) %>%
    rename(UID = "OGC.density.1982$Date")
OGC.density.1983.final  <- OGC.density.1983.snag.correction %>%
    add_column(OGC.density.1983$Date) %>%
    rename(UID = "OGC.density.1983$Date")
OGC.density.2010s.final <- OGC.density.2010s.snag.correction %>%
    add_column(OGC.density.2010s$Date) %>%
    rename(UID = "OGC.density.2010s$Date")

## Export density data files
write_csv(OGC.density.1982.final, file = "data/OGC_1982_density_by_taxa.csv")
write_csv(OGC.density.1983.final, file = "data/OGC_1983_density_by_taxa.csv")
write_csv(OGC.density.2010s.final, file = "data/OGC_2010s_density_by_taxa.csv")
```

Load Data

```
## Read in data
biomass.data <- read_csv("data/OGC_final_biomass_data.csv", show_col_types = FALSE)
density.data <- read_csv("data/OGC_final_density_data.csv", show_col_types = FALSE)

## Set variables as factors
# Biomass data
biomass.data$UID            <- as_factor(biomass.data$UID)
biomass.data$Year           <- as_factor(biomass.data$Year)
biomass.data$Year_Recoded   <- as_factor(biomass.data$Year_Recoded)
biomass.data$Season         <- as_factor(biomass.data$Season)
biomass.data$Season_Recoded <- as_factor(biomass.data$Season_Recoded)
biomass.data$Period         <- as_factor(biomass.data$Period)

# Density data
density.data$UID            <- as_factor(density.data$UID)
density.data$Year           <- as_factor(density.data$Year)
density.data$Year_Recoded   <- as_factor(density.data$Year_Recoded)
density.data$Season         <- as_factor(density.data$Season)
density.data$Season_Recoded <- as_factor(density.data$Season_Recoded)
density.data$Period         <- as_factor(density.data$Period)

## Dataframe of sampling info
sampling.info <- biomass.data[, 1:6]

## Matrices of invertebrate biomass and density
invertebrate.biomass.matrix <- biomass.data[, 16:87]
invertebrate.density.matrix <- density.data[, 16:87]

## Filter biomass and density data by sampling period; no further subsetting
# Biomass data
biomass.1980s <- invertebrate.biomass.matrix[1:25, ]
biomass.2010s <- invertebrate.biomass.matrix[26:49, ]

# Density data
density.1980s <- invertebrate.density.matrix[1:25, ]
density.2010s <- invertebrate.density.matrix[26:49, ]
```

Biomass & Density ANOVAs

Biomass and density were compared by sampling period, season, and the interaction using an ANOVA with Type II sums-of-squares [`Anova()`]. ANOVA assumptions were inspected graphically using `check_model()`, and effect sizes for the ANOVAs were calculated as η_P^2 using `eta_squared()`.

Biomass ANOVA

```
biomass.anova <- lm(
    Summed_Biomass ~ Period * Season, data = biomass.data
    )
```

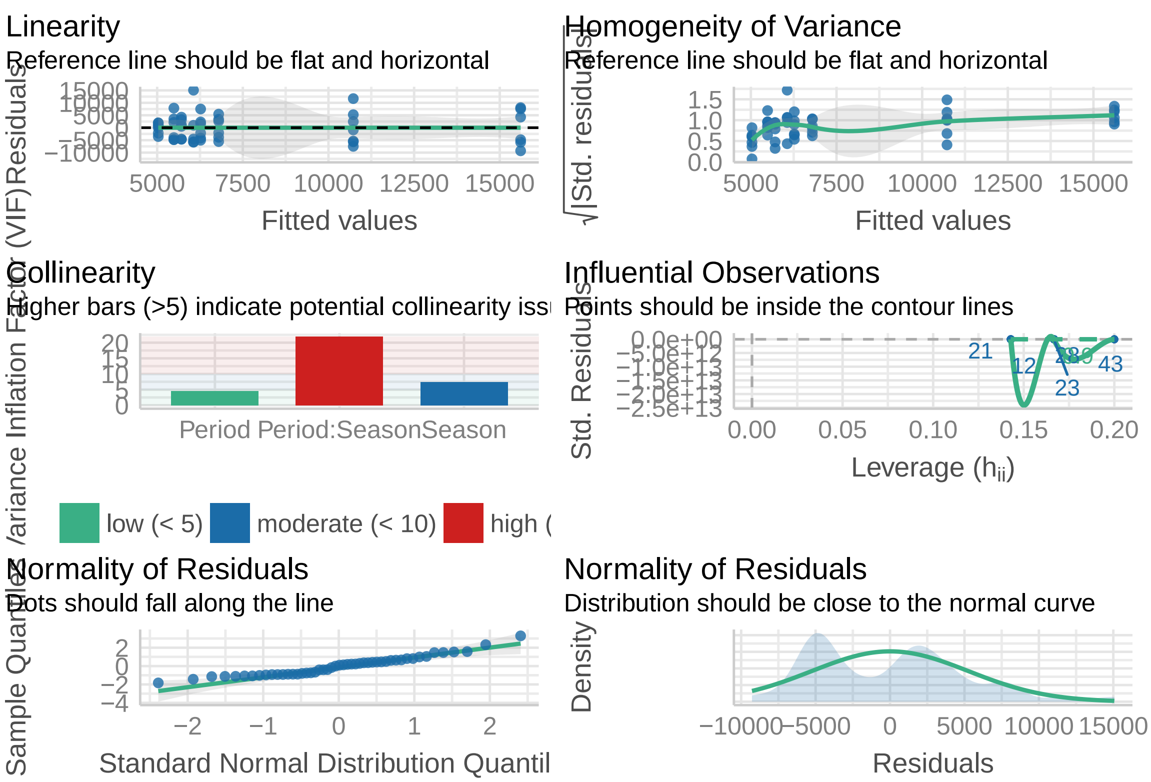


Figure 1: Diagnostic plots of the biomass ANOVA.

Table 1: ANOVA results for biomass by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	186450328	1	5.728	0.021
Season	158525193	3	1.623	0.199
Period:Season	235509414	3	2.412	0.081
Residuals	1334471006	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the biomass ANOVA
biomass.anova.eta.squared <- eta_squared(
    Anova(biomass.anova, type = "II"),
    partial = TRUE
    )
```

Table 2: Table of the effect sizes in the biomass ANOVA.

Term	Eta-squared	CI	CI_Low	CI_High
Period	0.123	0.95	0.011	1
Season	0.106	0.95	0.000	1
Period:Season	0.150	0.95	0.000	1

Density ANOVA

```
density.anova <- lm(
    log(Summed_Density) ~ Period * Season, data = density.data
    )
```

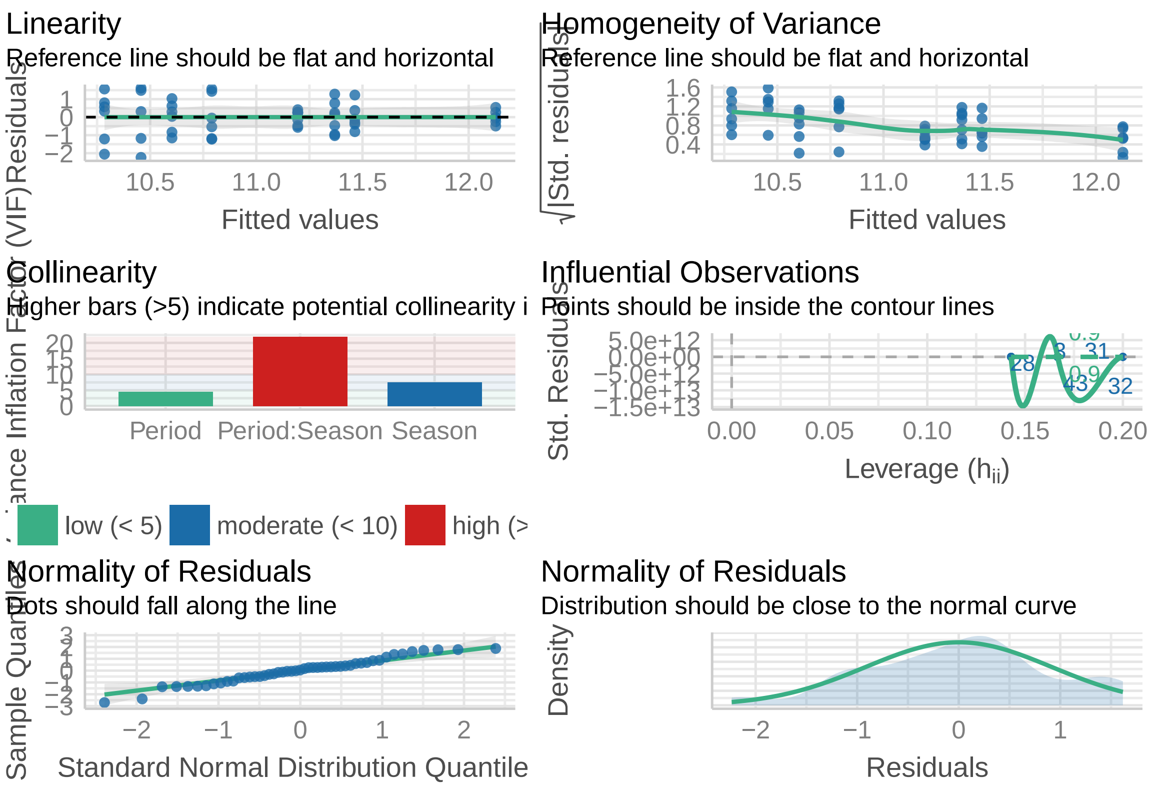


Figure 2: Diagnostic plots of the density ANOVA.

Table 3: ANOVA result for density by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	0.201	1	0.204	0.654
Season	8.029	3	2.712	0.057
Period:Season	7.575	3	2.558	0.068
Residuals	40.465	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the density ANOVA
density.anova.eta.squared <- eta_squared(
    Anova(density.anova, type = "II"),
    partial = TRUE
    )
```

Table 4: Table of the effect sizes in the density ANOVA.

Term	Eta-squared	CI	CI_Low	CI_High
Period	0.005	0.95	0	1
Season	0.166	0.95	0	1
Period:Season	0.158	0.95	0	1

Consumer & Predators ANOVAs

Biomass and density values were subset and summed for consumer and predator taxa. Biomass and density were then compared by sampling period, season, and the interaction using an ANOVA with Type II sums-of-squares [`Anova()`]. ANOVA assumptions were inspected graphically using `check_model()`, and effect sizes for the ANOVAs were calculated as η_P^2 using `eta_squared()`.

```
## Subset data to only include consumer taxa
# Biomass
consumer.biomass <- invertebrate.biomass.matrix[, 1:46] %>%
    rowSums()
consumer.biomass.data <- tibble(sampling.info, consumer.biomass)

# Density
consumer.density <- invertebrate.density.matrix[, 1:46] %>%
    rowSums()
consumer.density.data <- tibble(sampling.info, consumer.density)

## Subset data to only include predator taxa
# Biomass
predator.biomass <- invertebrate.biomass.matrix[, 47:72] %>%
    rowSums()
predator.biomass.data <- tibble(sampling.info, predator.biomass)

# Density
predator.density <- invertebrate.density.matrix[, 47:72] %>%
    rowSums()
predator.density.data <- tibble(sampling.info, predator.density)
```

Consumer ANOVAs

Biomass ANOVA

```
consumer.biomass.anova <- lm(
    consumer.biomass ~ Period * Season, data = consumer.biomass.data
    )
```

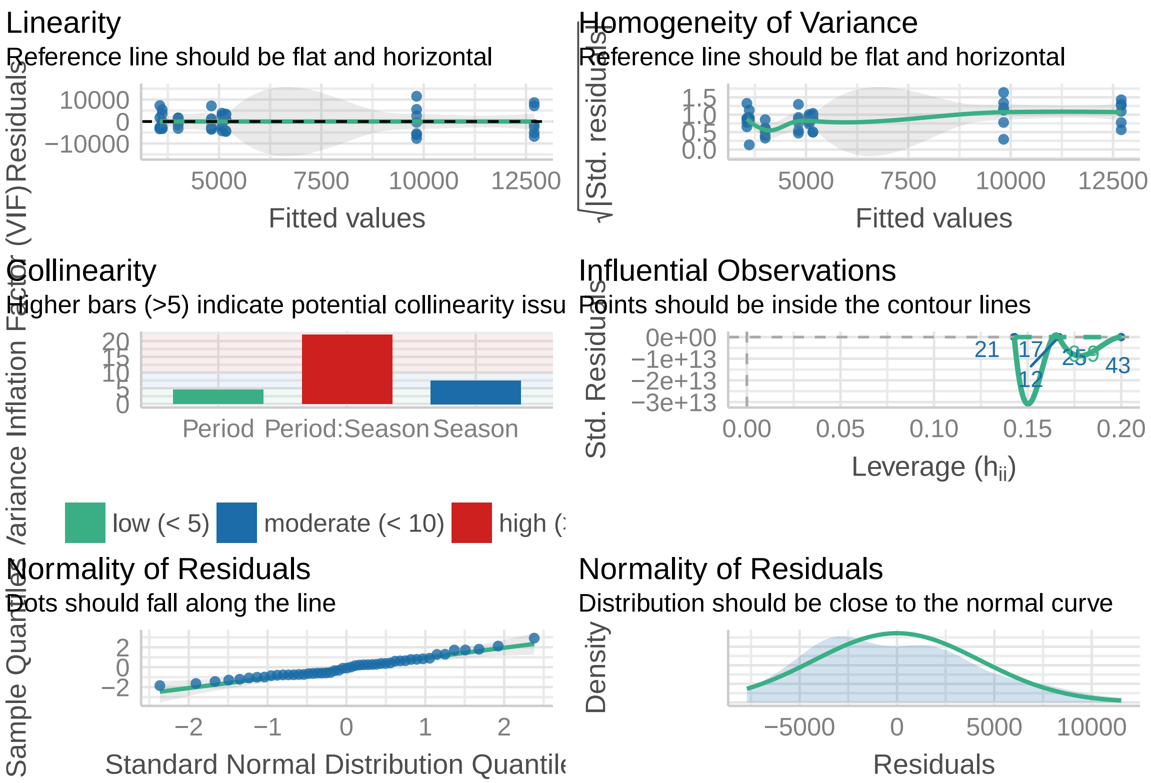


Figure 3: Diagnostic plots of the consumer biomass ANOVA.

Table 5: ANOVA results for consumer biomass by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	214935664	1	10.005	0.003
Season	113765041	3	1.765	0.169
Period:Season	158830701	3	2.465	0.076
Residuals	880756410	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the biomass ANOVA
consumer.biomass.anova.eta.squared <- eta_squared(
    Anova(consumer.biomass.anova, type = "II"),
    partial = TRUE
    )
```

Table 6: Table of the effect sizes in the consumer biomass ANOVA.

Term	Eta-squared	CI	CI_Low	CI_High
Period	0.196	0.95	0.046	1
Season	0.114	0.95	0.000	1
Period:Season	0.153	0.95	0.000	1

Density ANOVA

```
consumer.density.anova <- lm(
    log(consumer.density) ~ Period * Season, data = consumer.density.data
    )
```

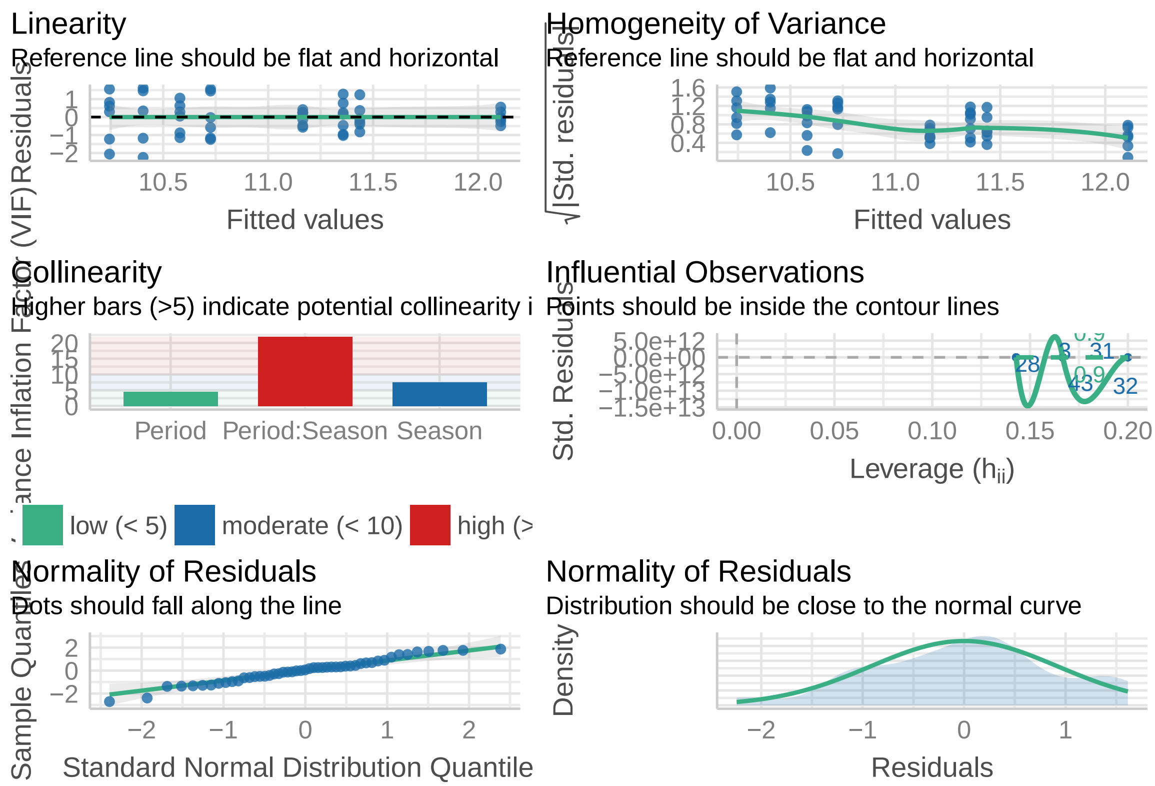


Figure 4: Diagnostic plots of the consumer density ANOVA.

Table 7: ANOVA results for consumer density by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	0.269	1	0.271	0.605
Season	8.236	3	2.768	0.054
Period:Season	7.867	3	2.644	0.062
Residuals	40.666	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the density ANOVA
consumer.density.anova.eta.squared <- eta_squared(
    Anova(consumer.density.anova, type = "II"),
    partial = TRUE
    )
```

Table 8: Table of the effect sizes in the consumer density ANOVA.

Term	Eta-squared	CI	CI_Low	CI_High
Period	0.007	0.95	0	1
Season	0.168	0.95	0	1
Period:Season	0.162	0.95	0	1

Predator ANOVAs

Biomass ANOVA

```
predator.biomass.anova <- lm(
    log(predator.biomass) ~ Period * Season, data = predator.biomass.data
    )
```

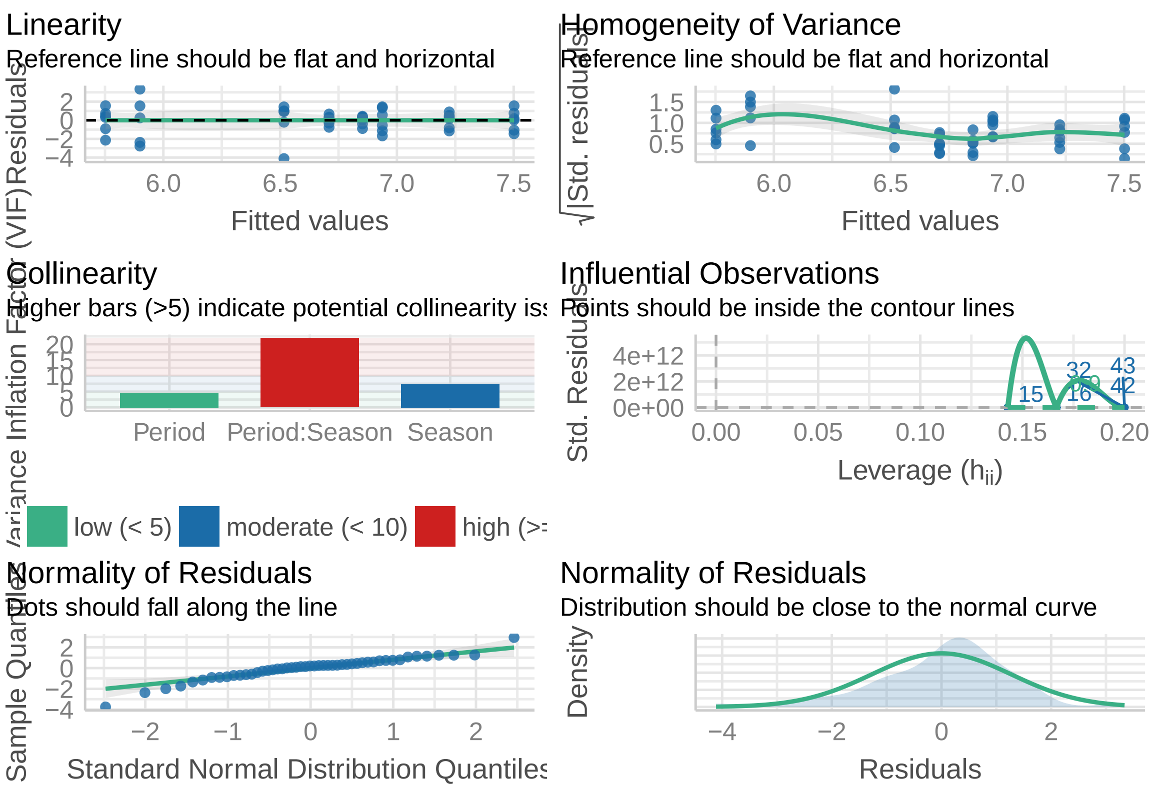


Figure 5: Diagnostic plots of the predator biomass ANOVA.

Table 9: ANOVA results for predator biomass by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	0.145	1	0.076	0.784
Season	12.100	3	2.121	0.112
Period:Season	2.442	3	0.428	0.734
Residuals	77.975	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the biomass ANOVA
predator.biomass.anova.eta.squared <- eta_squared(
    Anova(predator.biomass.anova, type = "II"),
    partial = TRUE
    )
```

Table 10: Table of the effect sizes in the predator biomass ANOVA.

Term	Eta-squared	CI	CI_Low	CI_High
Period	0.002	0.95	0	1
Season	0.134	0.95	0	1
Period:Season	0.030	0.95	0	1

Density ANOVA

```
predator.density.anova <- lm(
    log(predator.density) ~ Period * Season, data = predator.density.data
    )
```

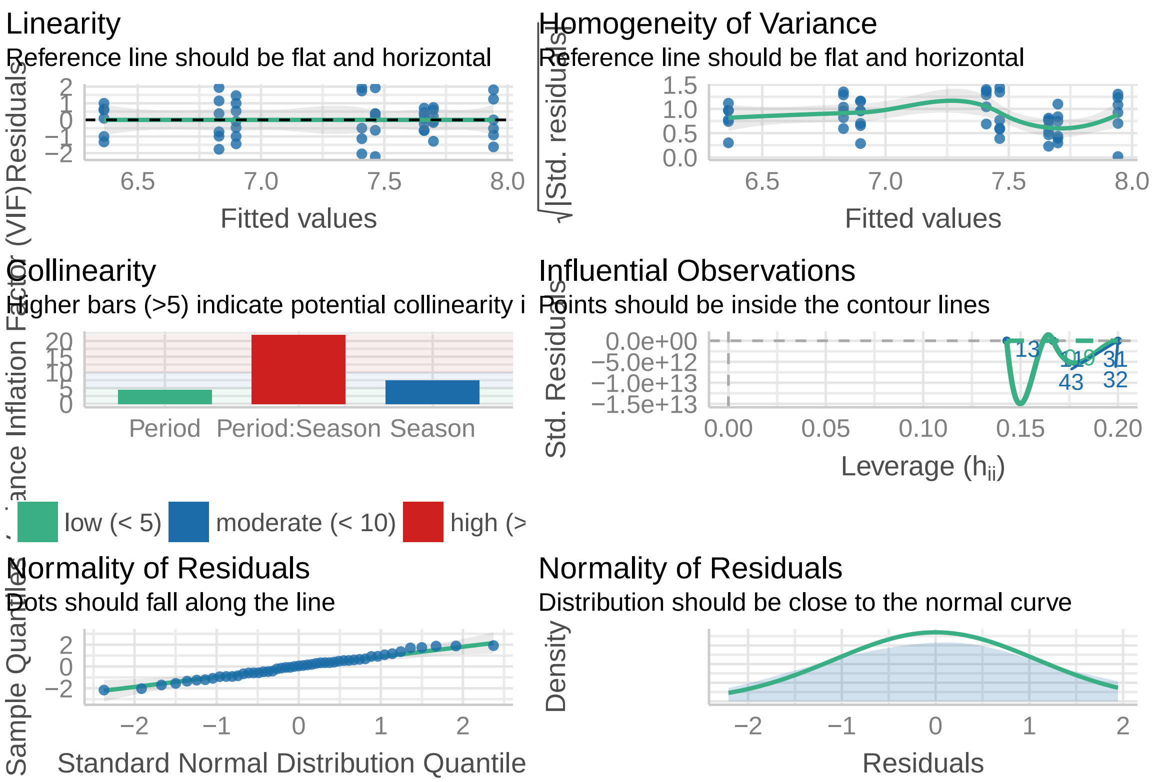


Figure 6: Diagnostic plots of the predator density ANOVA.

Table 11: ANOVA results for predator density by period, season, and the interaction.

	Sums-of-Squares	df	F	P-value
Period	7.688	1	5.651	0.022
Season	3.138	3	0.769	0.518
Period:Season	1.308	3	0.320	0.811
Residuals	55.780	41	NA	NA

```r
## Calculating partial eta-squared for each factor in the density ANOVA
predator.density.anova.eta.squared <- eta_squared(
    Anova(predator.density.anova, type = "II"),
    partial = TRUE
    )
```

Table 12: Table of the effect sizes in the predator density ANOVA.

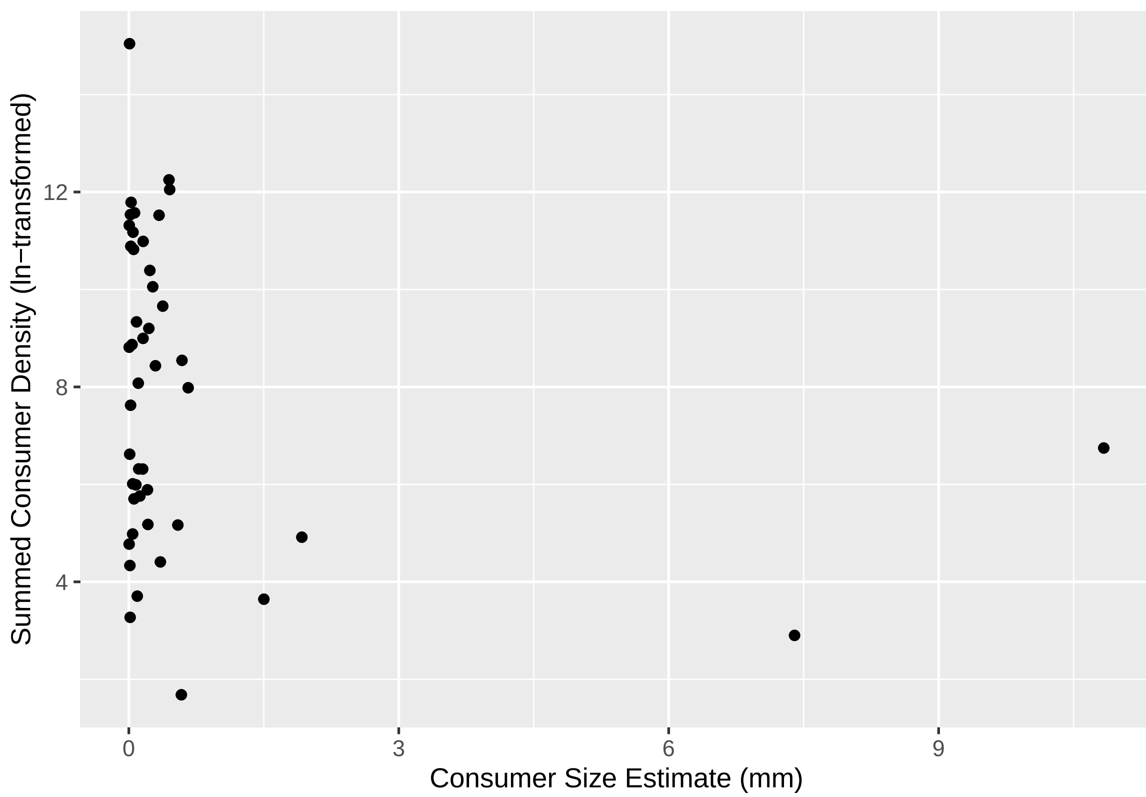
Term	Eta-squared	CI	CI_Low	CI_High
Period	0.121	0.95	0.01	1
Season	0.053	0.95	0.00	1
Period:Season	0.023	0.95	0.00	1

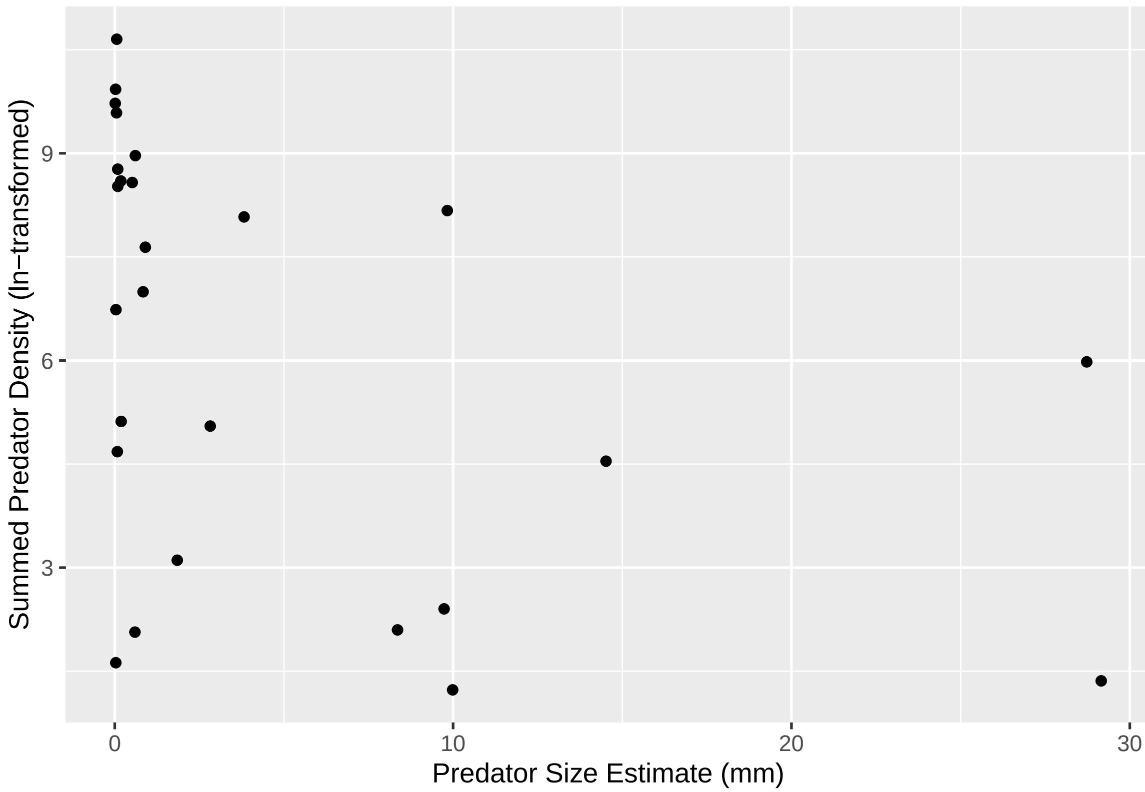
Size Groupings

Body sizes were plotted to estimate size groupings. For each taxon, we calculated mean body mass across time periods by dividing total biomass by total abundance. Primary consumers were classified as Small: 0 – 0.4 mg, Medium: 0.41 – 1.0 mg, and Large: 1.1 – 12.0 mg. Predators were classified as Small: 0 – 5.0 mg, Medium: 5.1 – 15.0 mg, and Large: 15.1 – 30.0 mg.

```
## Define size classes
# Consumers
consumer.summed.biomass <- colSums(invertebrate.biomass.matrix[, 1:46])
consumer.summed.density <- colSums(invertebrate.density.matrix[, 1:46])
consumer.size.estimates <- consumer.summed.biomass/consumer.summed.density
consumer.size.data      <- tibble(
    consumer.summed.biomass, consumer.summed.density, consumer.size.estimates
    )

# Predators
predator.summed.biomass <- colSums(invertebrate.biomass.matrix[, 47:72])
predator.summed.density <- colSums(invertebrate.density.matrix[, 47:72])
predator.size.estimates <- predator.summed.biomass/predator.summed.density
predator.size.data      <- tibble(
    predator.summed.biomass, predator.summed.density, predator.size.estimates
    )
```






```
## Divide groups up by size as per plot groupings
# Consumers
consumer.size.groups <- cut(
    consumer.size.data$consumer.size.estimates, c(0, 0.4, 1.0, 12.0, Inf),
    right = FALSE
    )
consumer.size.data$size.group <- as.numeric(consumer.size.groups)

# Predators
predator.size.groups <- cut(
    predator.size.data$predator.size.estimates, c(0, 5, 15, 30, Inf),
    right = FALSE
    )
predator.size.data$size.group <- as.numeric(predator.size.groups)
```

Percent Biomass Change

We quantified the percent biomass change in size groupings between sampling periods by illustrating numerical differences. We also compared differences in biomass of three dominant caddisfly taxa. We did not conduct any null hypothesis significance tests for this component of the study.

```
## Calculate percent change in overall biomass
full.summed.biomass.vector <- biomass.data$Summed_Biomass
summed.biomass.1980s       <- full.summed.biomass.vector[1:25]
summed.biomass.2010s       <- full.summed.biomass.vector[26:49]

## Divide mean 2010s biomass by mean 1980s biomass
percent.biomass.change <- (mean(summed.biomass.2010s)/mean(summed.biomass.1980s))*100
# 2010s biomass = 60.28% of 1980s biomass
```

Biomass Change & Contribution of Dominant Caddisflies

```
## Hydropsyche
Hydropsyche.biomass.1980s <- biomass.1980s$Hydropsyche
Hydropsyche.biomass.2010s <- biomass.2010s$Hydropsyche

## Chimarra
Chimarra.biomass.1980s <- biomass.1980s$Chimarra
Chimarra.biomass.2010s <- biomass.2010s$Chimarra

## Cheumatopsyche
Cheumatopsyche.biomass.1980s <- biomass.1980s$Cheumatopsyche
Cheumatopsyche.biomass.2010s <- biomass.2010s$Cheumatopsyche
```

Density Change

We numerically evaluated changes in density by size groupings for consumers and predators.

Consumers

Consumer taxa within each size grouping:

- Group 1: Amphinemura, Ancyronyx, Baetidae, Baetisca, Brachycentrus, Caenidae, Cheumatopsyche, Chironomidae, Crambidae, Cyrnellus, Dubiraphia,Elmidae, Ephemerellidae, Ephemeroptera, Heptageniidae, Hydropsychidae, Isonychia, Isopoda, Lepidoptera, Leptoceridae, Leptophlebiidae, Limnephilidae, Macronychus, Microcylloepus, Nectopsyche, Nemouridae, Neureclipsis, Polycentropodidae, Psephenus, Simuliidae, Stenelmis, Taeniopteryx, Tipulidae, Triaenodes, Trichoptera, Tricorythodes
- Group 2: Chimarra, Ectopria, Hydropsyche, Macrostemum, Paraponyx, Shipsa
- Group 3: Ironoquia, Neargyractis, Pteronarcys, Pycnopsyche

```
## Consumer data management
# 1980s
consumer.density.1980s <- density.data %>%
    filter(Period == "1980") %>%
    select(Amphinemura:Tricorythodes) %>%
    mutate(summed_density = rowSums(.))

# Sum all biomass for the 1980s consumers
consumer.density.1980s.total.density <- sum(consumer.density.1980s$summed_density)

# 2010s
consumer.density.2010s <- density.data %>%
    filter(Period == "2010") %>%
    select(Amphinemura:Tricorythodes) %>%
    mutate(summed_density = rowSums(.))

# Sum all biomass for the 2010s consumers
consumer.density.2010s.total.density <- sum(consumer.density.2010s$summed_density)
```

```r
## 1980s consumers group 1 taxa
group.1.consumer.density.1980s <- consumer.density.1980s %>%
    select(Amphinemura, Ancyronyx, Baetidae, Baetisca, Brachycentrus, Caenidae,
                 Cheumatopsyche, Chironomidae, Crambidae, Cyrnellus, Dubiraphia, Elmidae,
                 Ephemerellidae, Ephemeroptera, Heptageniidae, Hydropsychidae, Isonychia,
                 Isopoda, Lepidoptera, Leptoceridae, Leptophlebiidae, Limnephilidae,
                 Macronychus, Microcylloepus, Nectopsyche, Nemouridae, Neureclipsis,
                 Polycentropodidae, Psephenus, Simuliidae, Stenelmis, Taeniopteryx,
                 Tipulidae, Triaenodes, Trichoptera, Tricorythodes) %>%
    mutate(summed_density = rowSums(.))

## 1980s consumers group 1 total density
group.1.consumer.density.1980s.total.density <- sum(group.1.consumer.density.1980s$summed_density)
```

```r
## 1980s consumers group 2 taxa
group.2.consumer.density.1980s <- consumer.density.1980s %>%
    select(Chimarra, Ectopria, Hydropsyche, Macrostemum, Paraponyx, Shipsa) %>%
    mutate(summed_density = rowSums(.))

## 1980s consumers group 2 total density
group.2.consumer.density.1980s.total.density <- sum(group.2.consumer.density.1980s$summed_density)
```

```r
## 1980s consumers group 3 taxa
group.3.consumer.density.1980s <- consumer.density.1980s %>%
    select(Ironoquia, Neargyractis, Pteronarcys, Pycnopsyche) %>%
    mutate(summed_density = rowSums(.))

## 1980s consumers group 3 total density
group.3.consumer.density.1980s.total.density <- sum(group.3.consumer.density.1980s$summed_density)
```

```r
## 2010s consumers group 1 taxa
group.1.consumer.density.2010s <- consumer.density.2010s %>%
    select(Amphinemura, Ancyronyx, Baetidae, Baetisca, Brachycentrus, Caenidae,
                 Cheumatopsyche, Chironomidae, Crambidae, Cyrnellus, Dubiraphia, Elmidae,
                 Ephemerellidae, Ephemeroptera, Heptageniidae, Hydropsychidae, Isonychia,
                 Isopoda, Lepidoptera, Leptoceridae, Leptophlebiidae, Limnephilidae,
                 Macronychus, Microcylloepus, Nectopsyche, Nemouridae, Neureclipsis,
                 Polycentropodidae, Psephenus, Simuliidae, Stenelmis, Taeniopteryx,
                 Tipulidae, Triaenodes, Trichoptera, Tricorythodes) %>%
    mutate(summed_density = rowSums(.))

## 2010s consumers group 1 total density
group.1.consumer.density.2010s.total.density <- sum(group.1.consumer.density.2010s$summed_density)
```

```r
## 2010s consumers group 2 taxa
group.2.consumer.density.2010s <- consumer.density.2010s %>%
    select(Chimarra, Ectopria, Hydropsyche, Macrostemum, Paraponyx, Shipsa) %>%
    mutate(summed_density = rowSums(.))

## 2010s consumers group 2 total density
group.2.consumer.density.2010s.total.density <- sum(group.2.consumer.density.2010s$summed_density)
```

```r
## 2010s consumers group 3 taxa
group.3.consumer.density.2010s <- consumer.density.2010s %>%
    select(Ironoquia, Neargyractis, Pteronarcys, Pycnopsyche) %>%
    mutate(summed_density = rowSums(.))

## 2010s consumers group 3 total density
group.3.consumer.density.2010s.total.density <- sum(group.3.consumer.density.2010s$summed_density)
```

Predators

Predator taxa within each size grouping:

- Group 1: Acroneuria, Aeshnidae, Amphipoda, Anisoptera, Argia, Ceraclea, Ceratopogoninae, Cernotina, Coenagrionidae, Enallagma, Hemerodromia, Isoperla, Neoperla, Oecetis, Paragnetina, Perlesta, Perlidae, Perlodidae, Plecoptera
- Group 2: Aeshna, Boyeria, Corydalus, Hydroperla, Nasiaeschna
- Group 3: Helopicus, Neurocordulia

```
## Predator data management
# 1980s
predator.density.1980s <- density.data %>%
    filter(Period == "1980") %>%
    select(Acroneuria:Plecoptera) %>%
    mutate(summed_density = rowSums(.))

# Sum all biomass for the 1980s predators
predator.density.1980s.total.density <- sum(predator.density.1980s$summed_density)

# 2010s
predator.density.2010s <- density.data %>%
    filter(Period == "2010") %>%
    select(Acroneuria:Plecoptera) %>%
    mutate(summed_density = rowSums(.))

# Sum all biomass for the 2010s predators
predator.density.2010s.total.density <- sum(predator.density.2010s$summed_density)
```

```
## 1980s predators group 1 taxa
group.1.predator.density.1980s <- predator.density.1980s %>%
    select(Acroneuria, Aeshnidae, Amphipoda, Anisoptera, Argia, Ceraclea,
                 Ceratopogoninae, Cernotina, Coenagrionidae, Enallagma, Hemerodromia,
                 Isoperla, Neoperla, Oecetis, Paragnetina, Perlesta, Perlidae, Perlodidae, Plecoptera) %
    mutate(summed_density = rowSums(.))

## 1980s predators group 1 total density
group.1.predator.density.1980s.total.density <- sum(group.1.predator.density.1980s$summed_density)
```

```
## 1980s predators group 2 taxa
group.2.predator.density.1980s <- predator.density.1980s %>%
    select(Aeshna, Boyeria, Corydalus, Hydroperla, Nasiaeschna) %>%
    mutate(summed_density = rowSums(.))

## 1980s predators group 2 total density
group.2.predator.density.1980s.total.density <- sum(group.2.predator.density.1980s$summed_density)
```

```
## 1980s predators group 3 taxa
group.3.predator.density.1980s <- predator.density.1980s %>%
    select(Helopicus, Neurocordulia) %>%
    mutate(summed_density = rowSums(.))

## 1980s predators group 3 total density
group.3.predator.density.1980s.total.density <- sum(group.3.predator.density.1980s$summed_density)
```

```r
## 2010s predators group 1 taxa
group.1.predator.density.2010s <- predator.density.2010s %>%
    select(Acroneuria, Aeshnidae, Amphipoda, Anisoptera, Argia, Ceraclea,
                 Ceratopogoninae, Cernotina, Coenagrionidae, Enallagma, Hemerodromia,
                 Isoperla, Neoperla, Oecetis, Paragnetina, Perlesta, Perlidae, Perlodidae, Plecoptera) %
    mutate(summed_density = rowSums(.))

## 2010s predators group 1 total density
group.1.predator.density.2010s.total.density <- sum(group.1.predator.density.2010s$summed_density)
```

```r
## 2010s predators group 2 taxa
group.2.predator.density.2010s <- predator.density.2010s %>%
    select(Aeshna, Boyeria, Corydalus, Hydroperla, Nasiaeschna) %>%
    mutate(summed_density = rowSums(.))

## 2010s predators group 2 total density
group.2.predator.density.2010s.total.density <- sum(group.2.predator.density.2010s$summed_density)
```

```r
## 2010s predators group 3 taxa
group.3.predator.density.2010s <- predator.density.2010s %>%
    select(Helopicus, Neurocordulia) %>%
    mutate(summed_density = rowSums(.))

## 2010s predators group 3 total density
group.3.predator.density.2010s.total.density <- sum(group.3.predator.density.2010s$summed_density)
```

Biomass Chi-Squared Tests

We performed a chi-squared test to determine whether there were differences in density by size groupings between sampling period for consumers and predators. Chi-squared tests were performed using `chisq.test()`, with observed and expected frequencies examined to confirm test assumptions were met. Additionally, we assessed residuals to determine over- and under-represented size groupings by sampling period. Residuals were calculated as:

$$\frac{Observed - Expected}{\sqrt{Expected}}$$

Consumers

```
## Set consumer chi-square dataframe
consumer.chi.square.data <- as.data.frame(data.frame(matrix(0, nrow = 3, ncol = 2)))
colnames(consumer.chi.square.data) <- c("1980s", "2010s")
rownames(consumer.chi.square.data) <- c("Group_1", "Group_2", "Group_3")

## Add biomass values by groups for the 1980s and 2010s
# 1980s
consumer.chi.square.data$`1980s` <- c(
    group.1.consumer.density.1980s.total.density,
    group.2.consumer.density.1980s.total.density,
    group.3.consumer.density.1980s.total.density
    )

# 2010s
consumer.chi.square.data$`2010s` <- c(
    group.1.consumer.density.2010s.total.density,
    group.2.consumer.density.2010s.total.density,
    group.3.consumer.density.2010s.total.density
    )
```

```
consumer.chi.square.test <- chisq.test(consumer.chi.square.data)
# chi-squared = 46424, df = 2, P < 0.00001
```

Table 13: Observed densities by size groupings for the consumer chi-squared test.

	1980s	2010s
Group_1	2302319.190	1999622.789
Group_2	277220.761	111083.255
Group_3	913.892	130.078

Table 14: Expected densities by size groupings for the consumer chi-squared test.

	1980s	2010s
Group_1	2366292.170	1935649.809
Group_2	213587.435	174716.581
Group_3	574.238	469.732

Table 15: Residual densities by size groupings for the consumer chi-squared test.

	1980s	2010s
Group_1	-41.587	45.982
Group_2	137.688	-152.236
Group_3	14.174	-15.672

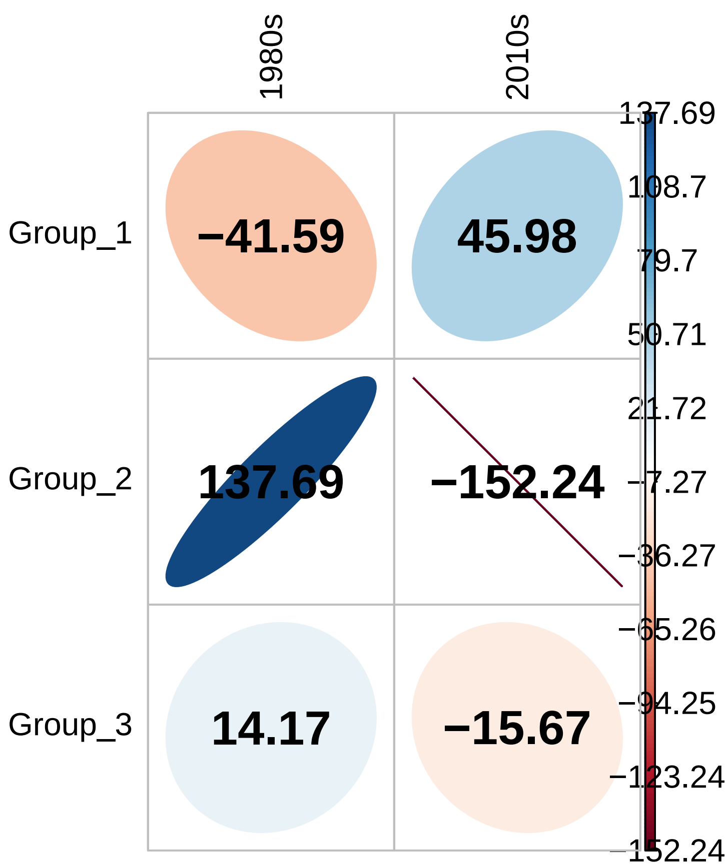


Figure 7: Plot of residuals from the consumer chi-squared test.

Predators

```r
## Set predator chi-square dataframe
predator.chi.square.data <- as.data.frame(data.frame(matrix(0, nrow = 3, ncol = 2)))
colnames(predator.chi.square.data) <- c("1980s", "2010s")
rownames(predator.chi.square.data) <- c("Group_1", "Group_2", "Group_3")

## Add biomass values by groups for the 1980s and 2010s
# 1980s
predator.chi.square.data$`1980s` <- c(
    group.1.predator.density.1980s.total.density,
    group.2.predator.density.1980s.total.density,
    group.3.predator.density.1980s.total.density
    )

# 2010s
predator.chi.square.data$`2010s` <- c(
    group.1.predator.density.2010s.total.density,
    group.2.predator.density.2010s.total.density,
    group.3.predator.density.2010s.total.density
    )
```

```r
predator.chi.square.test <- chisq.test(predator.chi.square.data)
# chi-squared = 6.8918, df = 2, P = 0.03188
```

Table 16: Observed densities by size groupings for the predator chi-squared test.

	1980s	2010s
Group_1	46049.372	85669.746
Group_2	1225.790	2425.899
Group_3	158.157	241.046

Table 17: Expected densities by size groupings for the predator chi-squared test.

	1980s	2010s
Group_1	46018.078	85701.040
Group_2	1275.773	2375.916
Group_3	139.467	259.735

Table 18: Residual densities by size groupings for the predator chi-squared test.

	1980s	2010s
Group_1	0.146	-0.107
Group_2	-1.399	1.025
Group_3	1.583	-1.160

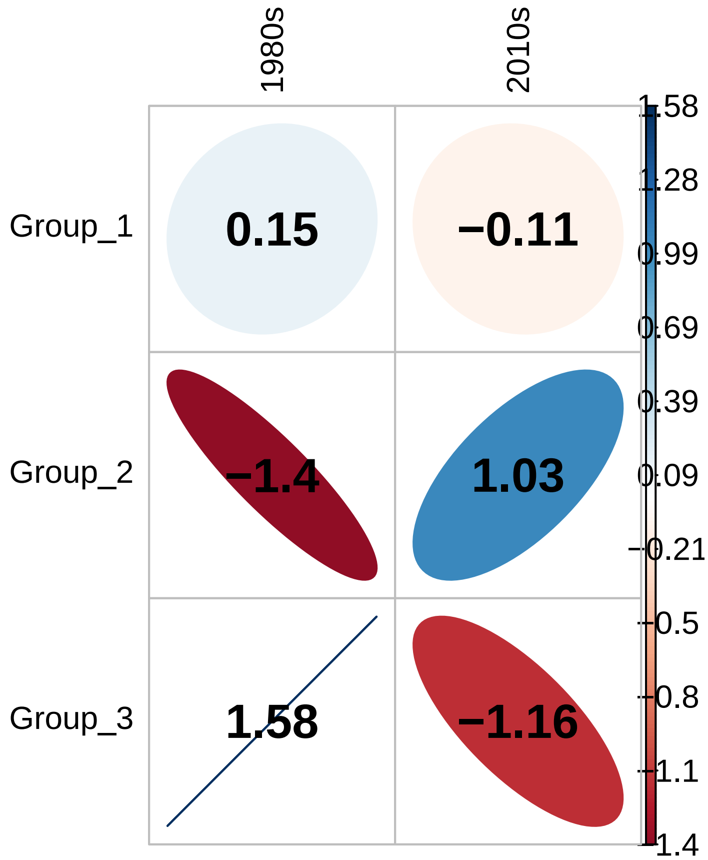


Figure 8: Plot of residuals from the predator chi-squared test.

Biomass Contributions

Biomass contributions were calculated for consumer and predator groups. We again illustrated numerical differences without conducting any null hypothesis significance tests.

```r
## Filter and format total biomass data by sampling period
# 1980s
total.1980s.biomass <- invertebrate.biomass.matrix[1:25, ]
total.1980s.mean.biomass <- t(colMeans(total.1980s.biomass))
total.1980s.percent.biomass.contribution <- (
    (total.1980s.mean.biomass/total.1980s.biomass)*100
)

# 2010s
total.2010s.biomass <- invertebrate.biomass.matrix[1:25, ]
total.2010s.mean.biomass <- t(colMeans(total.2010s.biomass))
total.2010s.percent.biomass.contribution <- (
    (total.2010s.mean.biomass/total.2010s.biomass)*100
)
```

Consumers

```r
## Separate consumer biomass data by sampling period
# 1980s
consumer.1980s.biomass <- invertebrate.biomass.matrix %>%
    select(Amphinemura:Tricorythodes) %>%
    slice(1:25)
consumer.1980s.mean.biomass <- t(colMeans(consumer.1980s.biomass))
consumer.1980s.biomass.contribution <- (
    (consumer.1980s.mean.biomass/consumer.1980s.biomass)*100
)

# 2010s
consumer.2010s.biomass <- invertebrate.biomass.matrix %>%
    select(Amphinemura:Tricorythodes) %>%
    slice(26:49)
consumer.2010s.mean.biomass <- t(colMeans(consumer.2010s.biomass))
consumer.2010s.biomass.contribution <- (
    (consumer.2010s.mean.biomass/consumer.2010s.biomass)*100
)
```

Predators

```r
## Separate predator biomass data by sampling period
# 1980s
predator.1980s.biomass <- invertebrate.biomass.matrix %>%
    select(Acroneuria:Plecoptera) %>%
    slice(1:25)
predator.1980s.mean.biomass <- t(colMeans(predator.1980s.biomass))
predator.1980s.biomass.contribution <- (
    (predator.1980s.mean.biomass/predator.1980s.biomass)*100
)

# 2010s
predator.2010s.biomass     <- invertebrate.biomass.matrix %>%
    select(Acroneuria:Plecoptera) %>%
    slice(26:49)
predator.2010s.mean.biomass <- t(colMeans(predator.2010s.biomass))
predator.2010s.biomass.contribution <- (
    (predator.2010s.mean.biomass/predator.2010s.biomass)*100
)
```

Individual Body Size Change

We tested whether mean body sizes of the most dominant primary consumers and predators were different between sampling periods. We calculated the average percent composition of biomass for each taxon within each sampling period and focused on the five most dominant consumers and the three most dominant predators. We calculated average individual mass for each sampling month by dividing biomass by abundance and performed two-sample Welch t-tests on average mass between the 1980s and the 2010s for each of the dominant taxa.

- Dominant consumers = Hydropsyche, Cheumatopsyche, Chimarra, Heptageniidae, Chironomidae
- Dominant predators = Corydalus, Paragnetina, Neurocordulia

Body Size t-Tests

```
## Data management for body size t-tests

## Hydropsyche
Hydropsyche.80.size <- ((biomass.1980s$Hydropsyche)/(density.1980s$Hydropsyche))
Hydropsyche.10.size <- ((biomass.2010s$Hydropsyche)/(density.2010s$Hydropsyche))

## Cheumatopsyche
Cheumatopsyche.80.size <- ((biomass.1980s$Cheumatopsyche)/(density.1980s$Cheumatopsyche))
Cheumatopsyche.10.size <- ((biomass.2010s$Cheumatopsyche)/(density.2010s$Cheumatopsyche))

## Chimarra
Chimarra.80.size <- ((biomass.1980s$Chimarra)/(density.1980s$Chimarra))
Chimarra.10.size <- ((biomass.2010s$Chimarra)/(density.2010s$Chimarra))

## Heptageniidae
Heptageniidae.80.size <- ((biomass.1980s$Heptageniidae)/(density.1980s$Heptageniidae))
Heptageniidae.10.size <- ((biomass.2010s$Heptageniidae)/(density.2010s$Heptageniidae))

## Chironomidae
Chironomidae.80.size <- ((biomass.1980s$Chironomidae)/(density.1980s$Chironomidae))
Chironomidae.10.size <- ((biomass.2010s$Chironomidae)/(density.2010s$Chironomidae))

## Corydalus
Corydalus.80.size <- ((biomass.1980s$Corydalus)/(density.1980s$Corydalus))
Corydalus.10.size <- ((biomass.2010s$Corydalus)/(density.2010s$Corydalus))

## Paragnetina
Paragnetina.80.size <- ((biomass.1980s$Paragnetina)/(density.1980s$Paragnetina))
Paragnetina.10.size <- ((biomass.2010s$Paragnetina)/(density.2010s$Paragnetina))

## Neurocordulia
Neurocordulia.80.size <- ((biomass.1980s$Neurocordulia)/(density.1980s$Neurocordulia))
Neurocordulia.10.size <- ((biomass.2010s$Neurocordulia)/(density.2010s$Neurocordulia))
```

```r
## Hydrospyche
t.test(log(Hydropsyche.80.size + 0.00001), log(Hydropsyche.10.size + 0.00001),
       paired = FALSE)
# t = 1.8613, df = 46.739, P-value = 0.069
```

```r
## Cheumatopsyche
t.test(log(Cheumatopsyche.80.size + 0.00001), log(Cheumatopsyche.10.size + 0.00001),
       paired = FALSE)
# t = 5.1915, df = 46.86, P-value < 0.001
```

```r
## Chimarra
t.test(log(Chimarra.80.size + 0.00001), log(Chimarra.10.size + 0.00001),
       paired = FALSE)
# t = 0.42278, df = 44.042, P-value = 0.675
```

```r
## Heptageniidae
t.test(log(Heptageniidae.80.size + 0.00001), log(Heptageniidae.10.size + 0.00001),
       paired = FALSE)
# t = -0.40634, df = 46.633, P-value = 0.686
```

```r
## Chironomidae
t.test(log(Chironomidae.80.size + 0.00001), log(Chironomidae.10.size + 0.00001),
       paired = FALSE)
# t = -0.17408, df = 46.334, P-value = 0.863
```

```r
## Corydalus
t.test(log(Corydalus.80.size + 0.00001), log(Corydalus.10.size + 0.00001),
       paired = FALSE)
# t = 1.2464, df = 31.152, P-value = 0.222
```

```r
## Paragnetina
t.test(Paragnetina.80.size + 0.00001, Paragnetina.10.size + 0.00001,
       paired = FALSE)
# t = 0.2442, df = 26.9, P-value = 0.809
```

```r
## Neurocordulia
t.test(Neurocordulia.80.size + 0.00001, Neurocordulia.10.size + 0.00001,
       paired = FALSE)
# t = 1.3378, df = 28.187, P-value = 0.192
```

Community Composition

Community composition was evaluated by calculating a Bray-Curtis distance matrix on a taxon-by-sample biomass matrix. We then conducted a PERMANOVA on this distance matrix to test for effects of sampling period, season, and the interaction on community structure.

```
## Data management for the PERMANOVA
# Sample information for the distance matrix
distance.matrix.info <- biomass.data %>%
    select(UID, Year, Season, Period)

# Taxa-by-abundance community matrix
community.matrix <- log(invertebrate.biomass.matrix + 1)
```

```
## Calculate Bray-Curtis Distance
BC.distance.biomass <- vegdist(community.matrix, method = "bray")
```

```
## NMDS Ordination
BC.NMDS.biomass <- monoMDS(BC.distance.biomass, k = 2, model = "global")
# Stress = 0.1819
```

```
## PERMANOVA by period, season, and the interaction
community.composition.PERMANOVA <- adonis(
    BC.distance.biomass ~ Period * Season,
    data = distance.matrix.info,
    permutations = 10000
    )
```

Table 19: Summary of the PERMANOVA comparing composition by period, season, and the interaction.

Term	df	Sums-of-Squares	Mean Square	F	R^2	P-value
Period	1	0.985	0.985	14.868	0.196	0.000
Season	3	1.046	0.349	5.265	0.209	0.000
Period:Season	3	0.267	0.089	1.341	0.053	0.133
Residuals	41	2.716	0.066	NA	0.542	NA
Total	48	5.013	NA	NA	1.000	NA

Indicator Taxa Analysis

We conducted an indicator species analysis to determine which taxa characterized specific sampling period and season groups.

```
## Create groups based on season: Group 1 = 1980s, Group 2 = 2010s
period.groups <- c(rep(1, 25), rep(2, 24))
```

```
## Run indicator analysis comparing by period
indicator.analysis <- multipatt(
    community.matrix,
    period.groups,
    control = how(nperm = 10000)
    )
```

Table 20: Summary table of the sign of the relationship from the indicator taxa analysis.

	1980s	2010s	Index	Test Statistic	P-value
Amphinemura	1	0	1	0.346	0.233
Ancyronyx	1	1	3	0.857	NA
Baetidae	1	1	3	1.000	NA
Baetisca	0	1	2	0.552	0.030
Brachycentrus	0	1	2	0.764	0.000
Caenidae	1	1	3	0.795	NA
Cheumatopsyche	1	1	3	1.000	NA
Chimarra	1	1	3	0.979	NA
Chironomidae	1	1	3	1.000	NA
Crambidae	0	1	2	0.281	0.354
Cyrnellus	0	1	2	0.645	0.000
Dubiraphia	1	1	3	0.319	NA
Ectopria	1	0	1	0.400	0.107
Elmidae	0	1	2	0.945	0.000
Ephemerellidae	1	1	3	0.795	NA
Ephemeroptera	0	1	2	0.996	0.000
Heptageniidae	1	1	3	1.000	NA
Hydropsyche	1	1	3	1.000	NA
Hydropsychidae	1	1	3	0.881	NA
Ironoquia	1	1	3	0.319	NA
Isonychia	1	1	3	0.904	NA
Isopoda	1	1	3	0.728	NA
Lepidoptera	0	1	2	0.568	0.004
Leptoceridae	0	1	2	0.886	0.000
Leptophlebiidae	0	1	2	0.599	0.002
Limnephilidae	0	1	2	0.284	0.359
Macronychus	1	1	3	0.958	NA
Macrostemum	0	1	2	0.839	0.000
Microcylloepus	0	1	2	0.704	0.000
Neargyractis	1	0	1	0.400	0.110
Nectopsyche	0	1	2	0.889	0.000

Table 20: Summary table of the sign of the relationship from the indicator taxa analysis. *(continued)*

	1980s	2010s	Index	Test Statistic	P-value
Nemouridae	1	0	1	0.200	1.000
Neureclipsis	1	1	3	0.589	NA
Paraponyx	1	1	3	0.429	NA
Polycentropodidae	0	1	2	0.661	0.003
Psephenus	1	0	1	0.200	1.000
Pteronarcys	1	0	1	0.937	0.000
Pycnopsyche	1	1	3	0.202	NA
Shipsa	1	0	1	0.200	1.000
Simuliidae	1	1	3	0.926	NA
Stenelmis	1	1	3	0.990	NA
Taeniopteryx	1	1	3	0.589	NA
Tipulidae	1	0	1	0.529	0.009
Triaenodes	0	1	2	0.733	0.000
Trichoptera	0	1	2	0.537	0.035
Tricorythodes	1	1	3	0.742	NA
Acroneuria	1	1	3	0.833	NA
Aeshna	1	0	1	0.200	1.000
Aeshnidae	0	1	2	0.289	0.227
Amphipoda	0	1	2	0.875	0.000
Anisoptera	0	1	2	0.289	0.236
Argia	0	1	2	0.745	0.000
Boyeria	0	1	2	0.507	0.039
Ceraclea	0	1	2	0.680	0.002
Ceratopogoninae	1	1	3	0.958	NA
Cernotina	0	1	2	0.577	0.001
Coenagrionidae	0	1	2	0.524	0.062
Corydalus	1	1	3	0.881	NA
Enallagma	0	1	2	0.537	0.006
Helopicus	1	0	1	0.200	1.000
Hemerodromia	1	1	3	0.881	NA
Hydroperla	0	1	2	0.289	0.234
Isoperla	0	1	2	0.426	0.105
Nasiaeschna	0	1	2	0.289	0.236
Neoperla	1	1	3	0.904	NA
Neurocordulia	1	1	3	0.821	NA
Oecetis	1	1	3	0.904	NA
Paragnetina	1	1	3	0.915	NA
Perlesta	1	1	3	0.795	NA
Perlidae	1	1	3	0.881	NA
Perlodidae	0	1	2	0.354	0.110
Plecoptera	1	1	3	0.728	NA

Climate Comparisons

We compared monthly averages of mean discharge, water temperature, precipitation, and air temperature values between sampling periods using two-sample Welch t-tests.

Discharge

```r
## Vectors of winter and spring discharge by period
# Winter discharge
winter.discharge.1980s <- biomass.data %>%
    filter(Season == "winter", Period == "1980") %>%
    select(Mean_Discharge)
winter.discharge.2010s <- biomass.data %>%
    filter(Season == "winter", Period == "2010") %>%
    select(Mean_Discharge)

# Spring discharge
spring.discharge.1980s <- biomass.data %>%
    filter(Season == "spring", Period == "1980") %>%
    select(Mean_Discharge)
spring.discharge.2010s <- biomass.data %>%
    filter(Season == "spring", Period == "2010") %>%
    select(Mean_Discharge)
```

```r
## Winter discharge
t.test(log(winter.discharge.1980s), log(winter.discharge.2010s),
       paired = FALSE)
# t = -0.552, df = 6.401, P-value = 0.600

## Spring discharge
t.test(log(spring.discharge.1980s), log(spring.discharge.2010s),
       paired = FALSE)
# t = 2.571, df = 9.434, P-value = 0.029
```

Water Temperature

```r
## Vectors of water temperature for each season by period
# Winter
winter.water.temperature.1980s <- biomass.data %>%
    filter(Season == "winter", Period == "1980") %>%
    select(Water_Temperature)
winter.water.temperature.2010s <- biomass.data %>%
    filter(Season == "winter", Period == "2010") %>%
    select(Water_Temperature)

# Spring
spring.water.temperature.1980s <- biomass.data %>%
    filter(Season == "spring", Period == "1980") %>%
    select(Water_Temperature)
spring.water.temperature.2010s <- biomass.data %>%
    filter(Season == "spring", Period == "2010") %>%
    select(Water_Temperature)

# Summer
summer.water.temperature.1980s <- biomass.data %>%
    filter(Season == "summer", Period == "1980") %>%
    select(Water_Temperature)
summer.water.temperature.2010s <- biomass.data %>%
    filter(Season == "summer", Period == "2010") %>%
```

```
    select(Water_Temperature)

# Fall
fall.water.temperature.1980s <- biomass.data %>%
    filter(Season == "fall", Period == "1980") %>%
    select(Water_Temperature)
fall.water.temperature.2010s <- biomass.data %>%
    filter(Season == "fall", Period == "2010") %>%
    select(Water_Temperature)
```

```r
## Winter water temperature
t.test(log(winter.water.temperature.1980s), log(winter.water.temperature.2010s),
       paired = FALSE)
# t = -3.397, df = 5.433, P-value = 0.017

## Spring water temperature
t.test(log(spring.water.temperature.1980s), log(spring.water.temperature.2010s),
       paired = FALSE)
# t = -0.666, df = 9.827, P-value = 0.521

## Summer water temperature
t.test(log(summer.water.temperature.1980s), log(summer.water.temperature.2010s),
       paired = FALSE)
# t = -2.217, df = 9.929, P-value = 0.051

## Fall water temperature
t.test(log(fall.water.temperature.1980s), log(fall.water.temperature.2010s),
       paired = FALSE)
# t = 0.530, df = 9.988, P-value = 0.608
```

Air Temperature

```r
## Vectors of winter and spring air temperature by period
# Winter
winter.air.temperature.1980s <- biomass.data %>%
    filter(Season == "winter", Period == "1980") %>%
    select(Air_Temperature)
winter.air.temperature.2010s <- biomass.data %>%
    filter(Season == "winter", Period == "2010") %>%
    select(Air_Temperature)

# Spring
spring.air.temperature.1980s <- biomass.data %>%
    filter(Season == "spring", Period == "1980") %>%
    select(Air_Temperature)
spring.air.temperature.2010s <- biomass.data %>%
    filter(Season == "spring", Period == "2010") %>%
    select(Air_Temperature)
```

```r
## Winter air temperature
t.test(log(winter.air.temperature.1980s), log(winter.air.temperature.2010s),
       paired = FALSE)
# t = -1.652, df = 8.364, P-value = 0.136

## Spring air temperature
t.test(log(spring.air.temperature.1980s), log(spring.air.temperature.2010s),
       paired = FALSE)
# t = -0.268, df = 9.832, P-value = 0.794
```

Precipitation

```r
## Vectors of winter and spring precipitation
# Winter
winter.precipitation.1980s <- biomass.data %>%
    filter(Season == "winter", Period == "1980") %>%
    select(Precipitation)
winter.precipitation.2010s <- biomass.data %>%
    filter(Season == "winter", Period == "2010") %>%
    select(Precipitation)

# Spring
spring.precipitation.1980s <- biomass.data %>%
    filter(Season == "spring", Period == "1980") %>%
    select(Precipitation)
spring.precipitation.2010s <- biomass.data %>%
    filter(Season == "spring", Period == "2010") %>%
    select(Precipitation)
```

```r
## Winter precipitation
t.test(log(winter.precipitation.1980s), log(winter.precipitation.2010s),
       paired = FALSE)
# t = -0.029, df = 6.496, P-value = 0.978

## Spring precipitation
t.test(log(spring.precipitation.1980s), log(spring.precipitation.2010s),
       paired = FALSE)
# t = 0.448, df = 7.760, P-value = 0.666
```

Climate Time Series Analyses

We assessed temporal trends in discharge, precipitation, water temperature, and air temperature using autocorrelation function estimation and Mann-Kendall tests. We calculated monthly averages for each variable, and then assessed autocorrelation using `acf()` and a shift in the time series using `MannKendall()`.

```
## Load water time series data
climate.time.series.data <- read_csv("data/OGC_long_term_climate_data.csv", show_col_types = FALSE)

## Discharge
discharge.time.series <- climate.time.series.data$Mean_Discharge %>%
    na.omit()

## Precipitation
precipitation.time.series <- climate.time.series.data$Precipitation %>%
    na.omit

## Water temperature
water.temperature.time.series <- climate.time.series.data$Water_Temperature %>%
    na.omit()

## Air temperature
air.temperature.time.series <- climate.time.series.data$Air_Temperature %>%
    na.omit()
```

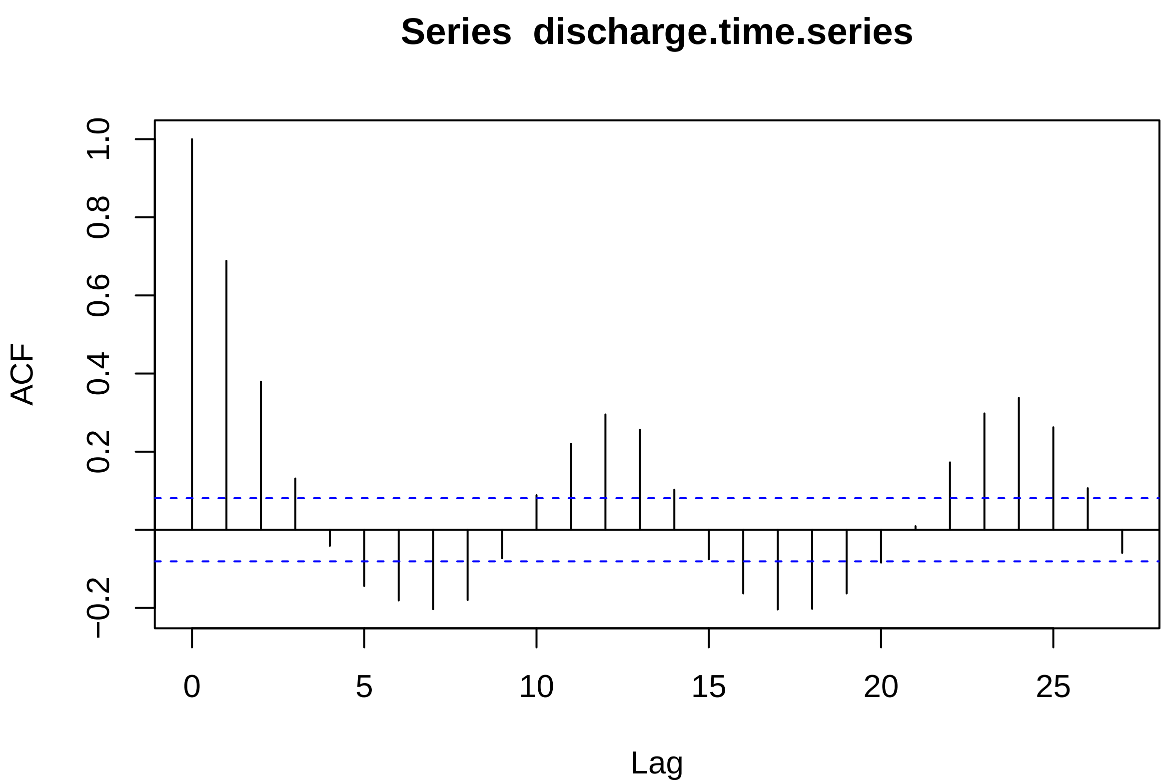


Figure 9: Plot of the autocorrelation function lag for the discharge time series.

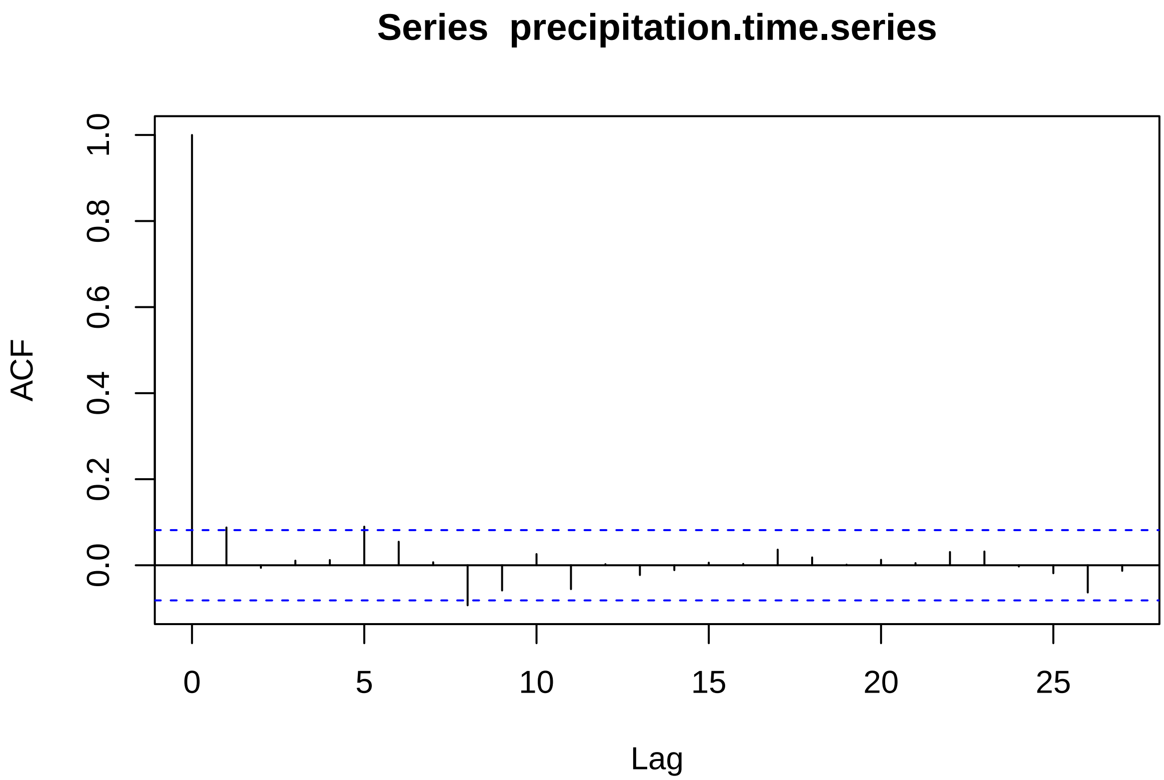


Figure 10: Plot of the autocorrelation function lag for the precipitation time series.

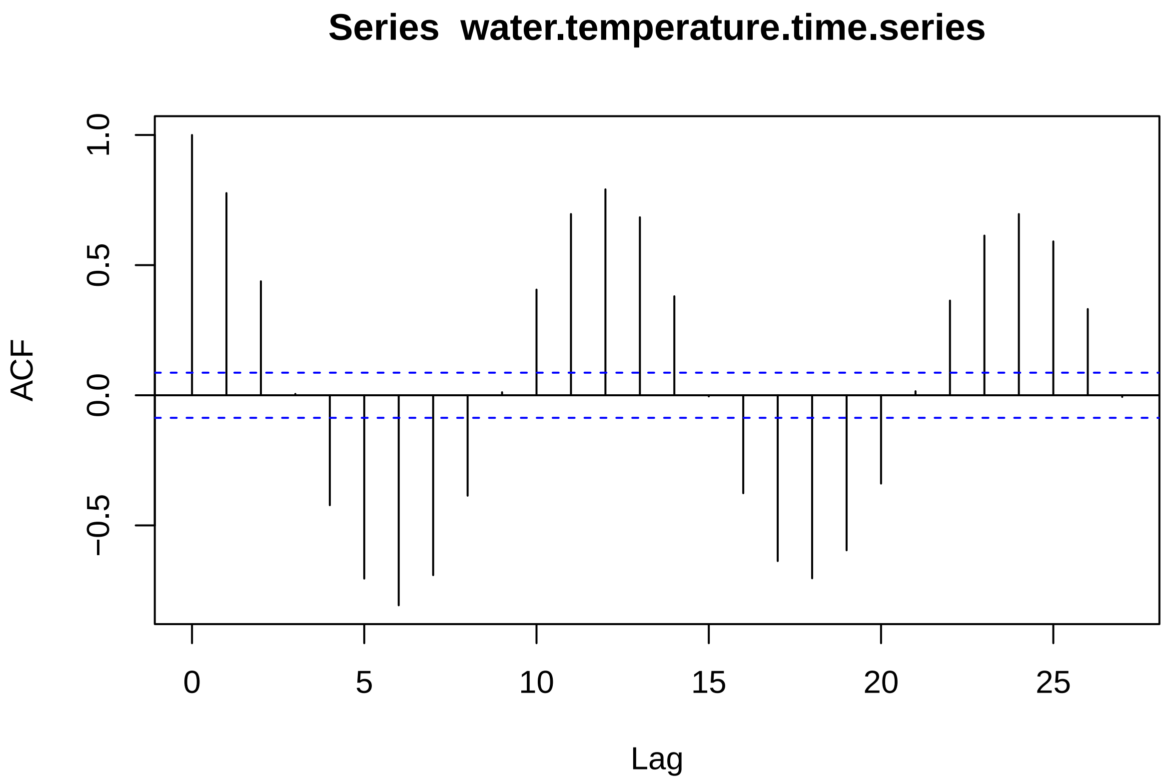


Figure 11: Plot of the autocorrelation function lag for the water temperature time series.

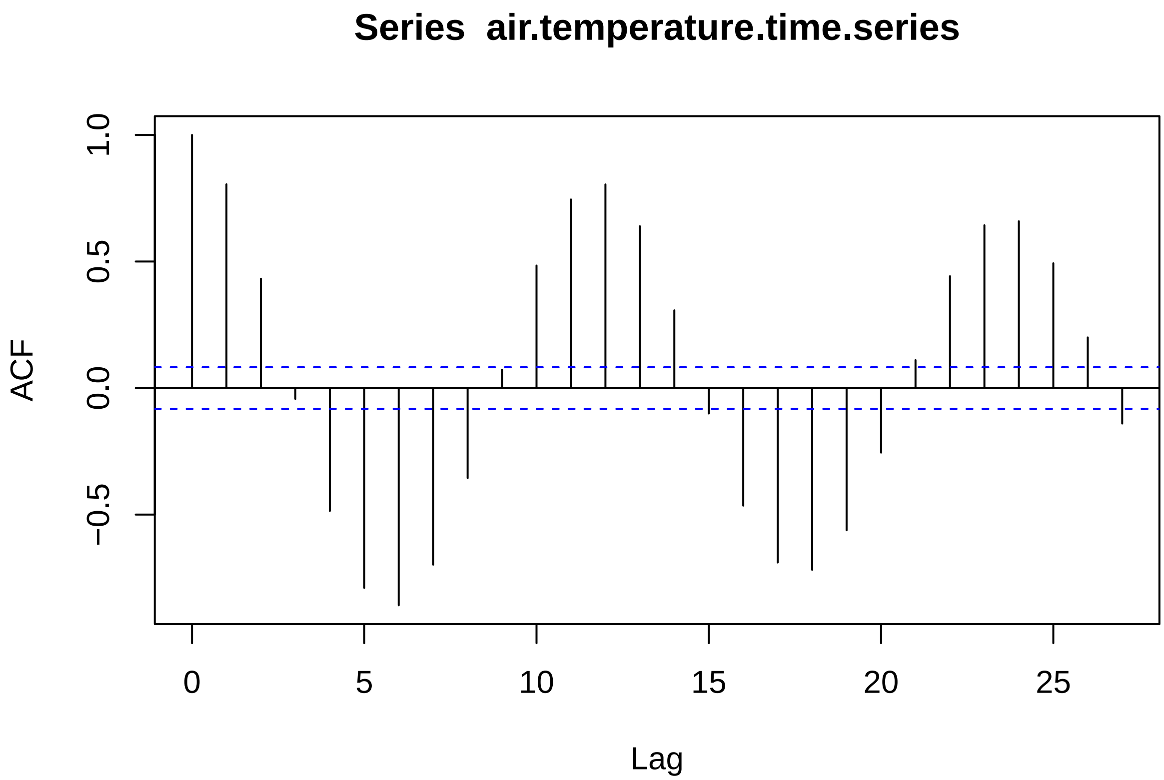


Figure 12: Plot of the autocorrelation function lag for the air temperature time series.

Carbon & Discharge Regression

We evaluated the relationship between dissolved organic carbon and discharge using linear regression. Monthly averages of carbon and discharge during our sampling periods (i.e., 1980s = December 1981-November 1983, 2010s = July 2015-August 2017). We fitted the regression using `lm()` and checked assumptions using `check_model()`.

```
carbon.discharge.regression <- lm(
    log(Carbon) ~ log(Mean_Discharge),
    data = biomass.data
    )
```

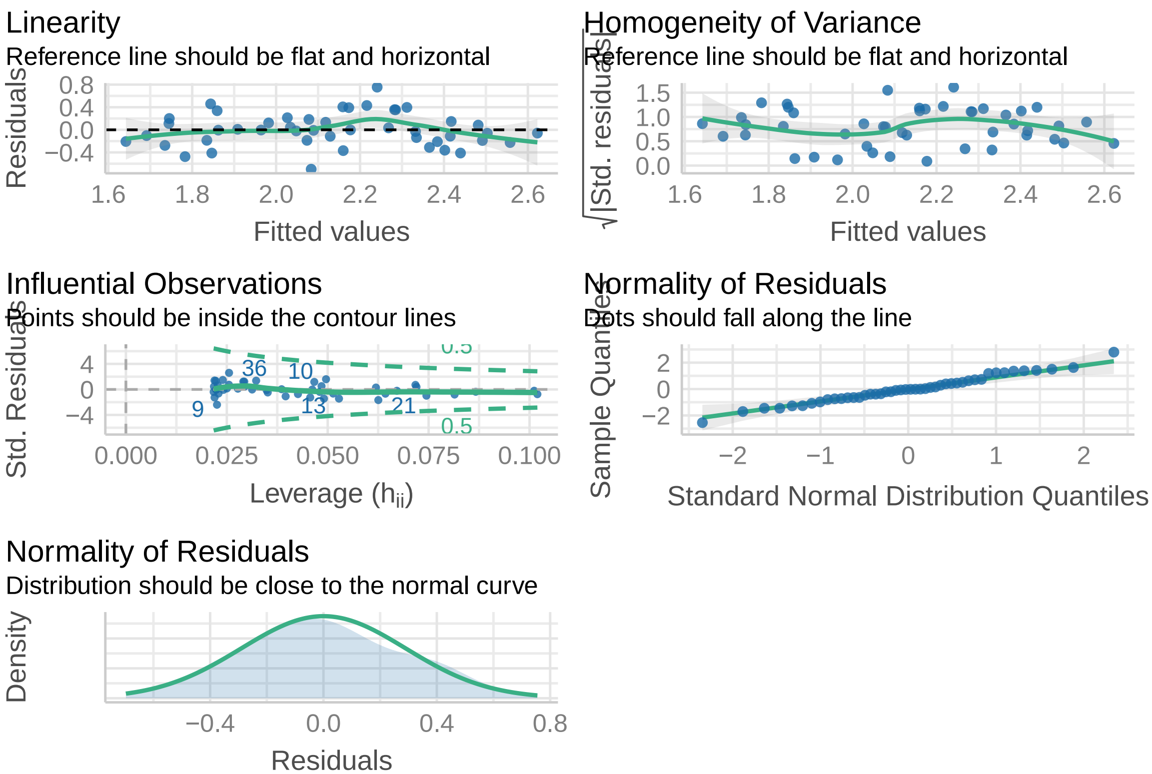


Figure 13: Diagnostic plots of the carbon and discharge regression.

Table 21: Summary of the carbon by discharge regression.

Term	Estimate	SE	t-statistic	P-value
(Intercept)	0.387	0.299	1.297	0.201
log(Mean_Discharge)	0.244	0.041	5.907	0.000

R Session Information

Table 22: R session information for transparency and reproducing results.

Setting	Value
version	R version 4.1.2 (2021-11-01)
os	macOS Big Sur 10.16
system	x86_64, darwin17.0
ui	X11
language	(EN)
collate	en_CA.UTF-8
ctype	en_CA.UTF-8
tz	America/New_York
date	2022-01-05
pandoc	2.14.0.3 @ /Applications/RStudio.app/Contents/MacOS/pandoc/ (via rmarkdown)

Table 23: Packages for data management and analysis.

Package	Loaded Version	Date
bayestestR	0.11.5	2021-10-30
broom	0.7.11	2022-01-03
car	3.0-12	2021-11-06
carData	3.0-4	2020-05-22
correlation	0.7.1	2021-10-06
datawizard	0.2.2	2022-01-04
dplyr	1.0.7	2021-06-18
easystats	0.4.3	2021-11-07
effectsize	0.5	2021-10-04
forcats	0.5.1	2021-01-27
ggplot2	3.3.5	2021-06-25
indicspecies	1.7.9	2020-02-04
insight	0.14.5	2021-10-16
kableExtra	1.3.4	2021-02-20
Kendall	2.2	2011-05-18
knitr	1.37	2021-12-16
lattice	0.20-45	2021-09-22
modelbased	0.7.0.1	2021-11-17
parameters	0.15.0	2021-10-18
performance	0.8.0	2021-10-01
permute	0.9-5	2019-03-12
purrr	0.3.4	2020-04-17
readr	2.1.1	2021-11-30
report	0.4.0	2021-09-30
reshape2	1.4.4	2020-04-09
see	0.6.8	2021-10-03
stringr	1.4.0	2019-02-10
tibble	3.1.6	2021-11-07
tidyr	1.1.4	2021-09-27
tidyverse	1.3.1	2021-04-15
vegan	2.5-7	2020-11-28
waterData	1.0.8	2017-04-28