Morphometric Analysis of G. cruentata.

Nicholas Eteobong & Faith Oyewale OLABISI

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Location: Unilag Front

Introduction

This analysis was carried out to intreprete the morphometric analysis data taken from two selected location at Unilag front and National Theater.

Data Importation and Loading of the Libraries in R programming for Analysis.

Packages used for the analysis include the following packages: Tidyverse, dplyr, car, knitr, ggpubr, readxl and gridextra.

```
## Load the packages for Analysis
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.2.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.0.4
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(car)
```

```
Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:dplyr':

    recode

The following object is masked from 'package:purrr':

    some
```

```
library(readxl)
library(ggpubr)
library(janitor)
```

```
Attaching package: 'janitor'

The following objects are masked from 'package:stats':

    chisq.test, fisher.test
```

```
library(knitr)
```

Data Cleaning and Manipulation for Analysis

Data Structure and a glimpse into the Morphometric data.

```
Warning: There were 2 warnings in `mutate()`.
The first warning was:
i In argument: `log_cl = as.numeric(log_cl)`.
Caused by warning:
! NAs introduced by coercion
i Run `dplyr::last_dplyr_warnings()` to see the 1 remaining warning.
```

```
# A tibble: 6 x 20
  month cw_cm cl_cm l_c1_cm lc2_cm rc1_cm r_c2_cm th_cm abd_cm  tw_g  lw_g  rw_g
  <dbl> <dbl> <dbl>   <dbl>  <dbl>  <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl>
1     1   4.6   5.2     7.1    3.6    7.5     3.8   5.6    3.3  36.2   5     5.1
2     2   4.4   4       4.6    2.7    4.1     2.8   4.8    3.4  22.9   2     1.8
3     3   4.2   3.8     4.4    2.4    4.4     2.5   4.3    3.1  18     1     1.1
4     4   4.1   3.7     4      2.5    4.2     2.5   4.4    3.1  17.9   1     1.1
5     5   4.8   4.4     5      3      5       3     5.2    3.5  30.8   1.8   2
6     6   4     3.5     4.1    2.4    4       2.5   4.3    3.1  15.2   0.9   0.8
# i 8 more variables: s_e_x <fct>, st <chr>, sc <chr>, log_tw <dbl>,
#   log_cw <dbl>, log_cl <dbl>, station <fct>, season_2023_2024 <fct>
```

Test for Normality/Distribution of Data(Morphometric Data) across all sampling stations and sexes

The normality of the water quality parameters were tested across the sampling stations and seasons using Shapiro-Wilk test and K.S Test. Parameters with P>0.05 indicate a normal distribution of the data while parameters with a p value less than 0.05 indicate a non- normal distribution of the data set.

Shapiro-Wilk normality test

data: tw_g[station == "A"]
W = 0.93624, p-value = 0.03886

Shapiro-Wilk normality test

data: tw_g[station == "B"]
W = 0.87361, p-value = 0.0006993

Shapiro-Wilk normality test

data: tw_g[station == "C"]
W = 0.92075, p-value = 0.01324

Shapiro-Wilk normality test

data: tw_g[station == "D"]
W = 0.96641, p-value = 0.3358

Shapiro-Wilk normality test

data: tw_g[station == "E"]
W = 0.97655, p-value = 0.6282

Warning in ks.test.default(cruen_data$tw_g, "pnorm"): ties should not be present for the one-sample Kolmogorov-Smirnov test

Asymptotic one-sample Kolmogorov-Smirnov test

data: cruen_data$tw_g
D = 0.99984, p-value < 2.2e-16
alternative hypothesis: two-sided

Warning in ks.test.default(cruen_data$cw_cm, "pnorm"): ties should not be present for the one-sample Kolmogorov-Smirnov test

Asymptotic one-sample Kolmogorov-Smirnov test

data: cruen_data$cw_cm
D = 0.99653, p-value < 2.2e-16
alternative hypothesis: two-sided

Warning in ks.test.default(cruen_data$cl_cm, "pnorm"): ties should not be present for the one-sample Kolmogorov-Smirnov test

Asymptotic one-sample Kolmogorov-Smirnov test

data: cruen_data$cl_cm
D = 0.9861, p-value < 2.2e-16
alternative hypothesis: two-sided

Table showing the Summary Data of G. cruentata by Station, Sex and Season.

`summarise()` has grouped output by 'station'. You can override using the `.groups` argument.

station	season_2023_2024	n	mean_cw	mean_cl	mean_tw	sd_cw	sd_cl	sd_tw
A	DRY	15	3.926667	3.593333	19.21333	0.7506822	0.7372407	10.954182
A	WET	21	3.880952	3.590476	18.61905	0.7487450	0.8172544	10.164773
B	DRY	15	4.126667	3.760000	17.93333	0.4527167	0.5039841	7.033153
B	WET	21	4.152381	3.752381	24.16190	0.4445436	0.4567483	11.086680
C	DRY	15	3.826667	3.546667	17.41333	0.6295879	0.6057659	13.817580
C	WET	21	3.990476	3.628571	20.98571	0.7224298	0.7721029	10.943139

station	season_2023_2024	n	mean_cw	mean_cl	mean_tw	sd_cw	sd_cl	sd_tw
D	DRY	15	4.280000	4.006667	24.54000	0.5185144	0.6452759	10.796878
D	WET	21	3.938095	3.628571	19.69524	0.6492120	0.6205988	8.943516
E	DRY	15	4.206667	3.880000	24.27333	0.4682287	0.5129745	8.773456
E	WET	21	4.400000	4.038095	23.28571	0.2983287	0.3247710	8.704096

s_e_x	n	mean_cw	mean_cl	mean_tw	sd_cw	sd_cl	sd_tw
F	94	4.111702	3.720213	19.27979	0.5285111	0.5369327	7.017116
M	86	4.030233	3.761628	23.02326	0.6733708	0.7137587	12.735007

Table showing the Number of Males and Female of G. cruentata

Var1	Freq
F	94
M	86

Regression Analysis of the Length-Weight Relationship of G. cruentata

The regression analysis was conducted to check the relationship between the length and weight relationship of the sampled species. $p<0.05$ indicate there is a sign difference between the length and weight of the sampled species. $p>0.05$ indicate that there is no sign difference between the length and weight of the sampled species.

Linear Regression for Combined Sexes

```
## Linear Regression Model for combined sex
lw_model <- lm(cruen_data$log_tw ~ cruen_data$log_cl)

print(coef(lw_model))
```

```
(Intercept) cruen_data$log_cl
 -0.4725812        3.0653411
```

```r
lw_summary <- lw_model |>
  summary()
## Check p value
lw_summary
```

```
Call:
lm(formula = cruen_data$log_tw ~ cruen_data$log_cl)

Residuals:
     Min       1Q   Median       3Q      Max
-0.16220 -0.04490 -0.00291  0.03415  0.31985

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      -0.47258    0.03532  -13.38   <2e-16 ***
cruen_data$log_cl  3.06534    0.06191   49.51   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.06847 on 177 degrees of freedom
  (1 observation deleted due to missingness)
Multiple R-squared:  0.9327,    Adjusted R-squared:  0.9323
F-statistic:  2452 on 1 and 177 DF,  p-value: < 2.2e-16
```

Check for either Isometric or Allometric Growth

When the b>3 we assume that there is a positive isometric growth among the sampled species indicating individuals gain weight faster. while when b <3: this indicate negative isometric (individuals gain weight slowly).

```r
## Check for Isometric or Allometric growth
b_value <- coef(lw_model)[2] ## Positive Isometric growth (b>3),
## Individual gain weight Faster
b_value |>
  kable()
```

	x
cruen_data$log_cl	3.065341

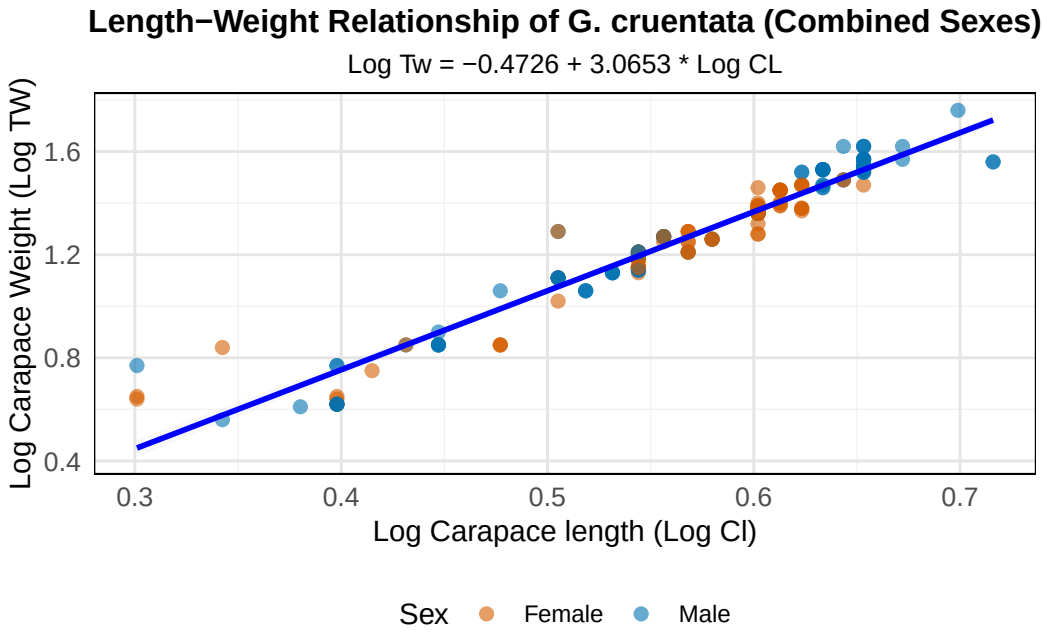
Regression Plot showing the Length and Weight Relationship of the Combined Sexes

`geom_smooth()` using formula = 'y ~ x'

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

Warning: Removed 1 row containing missing values or values outside the scale range (`geom_point()`).

Warning: Removed 1 row containing missing values or values outside the scale range (`geom_text()`).



Linear Regression of the Length-Weight for Male G. cruentata

Call:
lm(formula = male_lw$log_tw ~ male_lw$log_cl)

Residuals:
Min 1Q Median 3Q Max

```
-0.18305 -0.02981 -0.00343  0.03224  0.33858

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   -0.52001    0.04607  -11.29   <2e-16 ***
male_lw$log_cl  3.16071    0.08008   39.47   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.07004 on 84 degrees of freedom
Multiple R-squared:  0.9488,    Adjusted R-squared:  0.9482
F-statistic:  1558 on 1 and 84 DF,  p-value: < 2.2e-16
```

Check for either Isometric or Allometric Growth

```
## Check for Isometric or Allometric Growth
b_male <- coef(male_model)[2]
print(b_male) ## Positive Isometric Growth (b>3),
```

```
male_lw$log_cl
     3.160708
```

```
## Individual gain weight Faster
```

Linear Regression of the Length-Weight for Female G. cruentata

Check for either Isometric or Allometric Growth

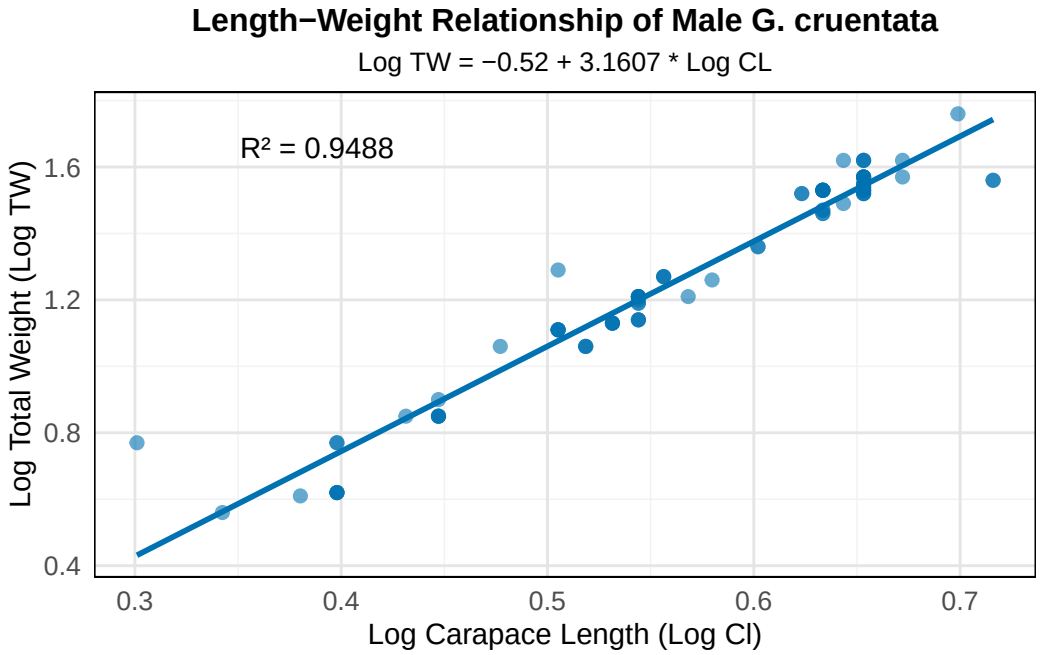
```
## Check for Isometric or Allometric Growth
b_female <- coef(female_model)[2]
print(b_female) ## Negative Isometric Growth (b<3)
```

```
female_lw$log_cl
      2.898028
```

```
## Individual gain weight Slower
```

Regression Plot showing the Length and Weight Relationship of the Male G. cruentata

`geom_smooth()` using formula = 'y ~ x'



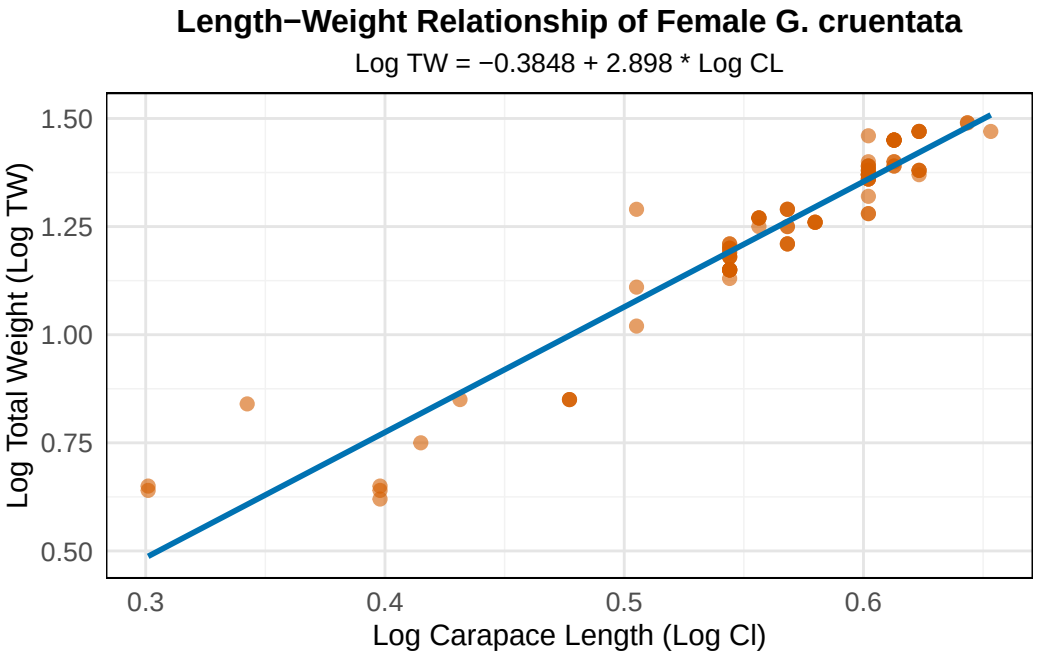
Regression Plot showing the Length and Weight Relationship of the Female G. cruentata

`geom_smooth()` using formula = 'y ~ x'

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

Warning: Removed 1 row containing missing values or values outside the scale range (`geom_point()`).

Warning: Removed 1 row containing missing values or values outside the scale range (`geom_text()`).



Test of Homogeneity of Variance for the Morphometric Data across the Sampling Stations.

When p>0.05 we assume the sampled data has equality of variance but when p<0.05 we assume equality of variance was not met.

For G. cruentata Length

	Df	F value	Pr(>F)
group	9	3.511044	0.0005196
	170	NA	NA

For G. cruentata Weight

	Df	F value	Pr(>F)
group	9	4.687414	1.45e-05
	170	NA	NA

Test of Significant differences in the mean of length and Weight of G. cruentata across the Stations.

For Length

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
s_e_x	1	0.0770322	0.0770322	0.1975433	0.6572764
station	4	3.6671301	0.9167825	2.3510215	0.0561371
s_e_x:station	4	0.1562164	0.0390541	0.1001514	0.9822733
Residuals	170	66.2916214	0.3899507	NA	NA

For Weight

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
s_e_x	1	629.3644	629.3644	6.211524	0.0136499
station	4	628.5233	157.1308	1.550806	0.1897656
s_e_x:station	4	511.3720	127.8430	1.261749	0.2870280
Residuals	170	17224.7498	101.3221	NA	NA

Correlation analysis showing the relationship between the Length,Weight,Width of G.cruentata across all station.

	cw_cm	cl_cm	tw_g
cw_cm	1.0000000	0.9524871	0.5822703
cl_cm	0.9524871	1.0000000	0.6126576
tw_g	0.5822703	0.6126576	1.0000000

Correlation between Carapace Length and Total Weight

```
## Correlation between Cl and Tw
cl_tw_cor <- cor.test(cruen_data$cl_cm , cruen_data$tw_g,
       method = 'pearson')
print(cl_tw_cor)
```

```
    Pearson's product-moment correlation

data:  cruen_data$cl_cm and cruen_data$tw_g
t = 10.342, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5123013 0.6965074
sample estimates:
      cor
0.6126576
```

Correlation between Carapace width and Total Weight

```
## Correlation between cw and Tw
cw_tw_cor <- cor.test(cruen_data$cw_cm, cruen_data$tw_g)
print(cw_tw_cor)
```

```
    Pearson's product-moment correlation

data:  cruen_data$cw_cm and cruen_data$tw_g
t = 9.5553, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.4765962 0.6713576
sample estimates:
      cor
0.5822703
```

Correlation between Carapace Length and Width

```
## Correlation between cw and cl
cw_cl_cor <- cor.test(cruen_data$cw_cm, cruen_data$cl_cm)
print(cw_cl_cor)
```

```
    Pearson's product-moment correlation
```

```
data:  cruen_data$cw_cm and cruen_data$cl_cm
t = 41.722, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.9367223 0.9643966
sample estimates:
      cor
0.9524871
```

Location: NationalTheater

Introduction

This analysis was carried out to intreprete the morphometric analysis data taken from National Theater.

Data Importation and Loading of the Libraries in R programming for Analysis.

Packages used for the analysis include the following packages: Tidyverse, dplyr, car, knitr, ggpubr, readxl and gridextra.

```
data_cruen <- read_excel('Morphometric_data.xlsx', sheet = 2)
data_cruen |>
  head()
```

```
# A tibble: 6 x 20
  Month `cw (cm)` `CL (cm)` `L.C1 (cm)` `LC2 (cm)` `RC1 (cm)`       `R.C2 (cm)`
  <dbl>     <dbl>     <dbl>       <dbl>      <dbl> <chr>                  <dbl>
1     1       3.8       3.5         4.2        2.5 4.09999999999999~        2.5
2     2       3.4       3.3         3.5        2   3,7                      2.3
3     3       3         2.5         2.7        1.7 2.7                      1.7
4     4       3.3       3           3          1.6 3                        1.6
5     5       3         3.2         3.7        2.2 3.5                      2.3
6     6       4.1       3.6         4          2.5 4                        2.3
# i 13 more variables: `TH (cm)` <dbl>, `ABD (cm)` <dbl>, `TW (g)` <dbl>,
#   `LW (g)` <dbl>, `RW (g)` <dbl>, `S E X` <chr>, ST <chr>, SC <chr>,
#   `Log TW` <dbl>, `Log cw` <dbl>, `Log CL` <dbl>, STATION <chr>,
#   `SEASON(2023/2024)` <chr>
```

Data Cleaning and Manipulation for Analysis

Data Structure and a glimpse into the Morphometric data.

```
 [1] "month"          "cw_cm"          "cl_cm"          "l_c1_cm"
 [5] "lc2_cm"         "rc1_cm"         "r_c2_cm"         "th_cm"
 [9] "abd_cm"          "tw_g"           "lw_g"           "rw_g"
[13] "s_e_x"          "st"             "sc"             "log_tw"
[17] "log_cw"          "log_cl"         "station"        "season_2023_2024"
```

Table showing the Summary Data of G. cruentata by Station, Sex and Season.

```
`summarise()` has grouped output by 'station'. You can override using the
`.groups` argument.
```

station	season_2023_2024	n	mean_cw	mean_cl	mean_tw	sd_cw	sd_cl	sd_tw
V	DRY	15	3.880000	3.586667	21.52667	0.8486965	0.8887123	16.354574
V	WET	21	3.657143	3.371429	16.06667	0.6845228	0.6849400	9.183046
W	DRY	15	4.353333	4.080000	24.22667	0.2948769	0.4538722	7.915578
W	WET	21	4.290476	3.938095	25.44762	0.4592437	0.5103687	9.773823
X	DRY	15	4.113333	3.746667	21.05333	0.5054936	0.5974549	8.634389
X	WET	21	4.276191	3.904762	23.32857	0.4121951	0.3917604	7.460707
Y	DRY	15	4.146667	3.840000	22.49333	0.4733870	0.4579457	8.697821
Y	WET	21	3.638095	3.276190	14.80476	0.7546365	0.7725961	10.883128
Z	DRY	15	4.073333	3.766667	20.96667	0.5391351	0.5313953	11.705656
Z	WET	21	4.071429	3.719048	21.89524	0.6893061	0.7352680	12.802089

s_e_x	n	mean_cw	mean_cl	mean_tw	sd_cw	sd_cl	sd_tw
F	92	4.036956	3.658696	19.08478	0.5352862	0.5287664	7.517378
M	88	4.042046	3.762500	23.07500	0.7191505	0.7668884	13.217128

Table showing the Number of Males and Female of G. cruentata

Var1	Freq
F	92
M	88

Regression Analysis of the Length-Weight Relationship of G. cruentata

The regression analysis was conducted to check the relationship between the length and weight relationship of the sampled species. $p<0.05$ indicate there is a sign difference between the length and weight of the sampled species. $p>0.05$ indicate that there is no sign difference between the length and weight of the sampled species.

Linear Regression for Combined Sexes

```
     (Intercept) data_cruen$log_cl
    1.250837e+00      1.980388e-06
```

```
Call:
lm(formula = data_cruen$log_tw ~ data_cruen$log_cl)

Residuals:
    Min      1Q  Median      3Q     Max
-0.69084 -0.11084  0.01916  0.21166  0.50916

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.251e+00  2.062e-02  60.650   <2e-16 ***
data_cruen$log_cl 1.980e-06  4.596e-06   0.431    0.667
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2759 on 178 degrees of freedom
Multiple R-squared:  0.001042,  Adjusted R-squared:  -0.00457
F-statistic: 0.1857 on 1 and 178 DF,  p-value: 0.6671
```

Check for either Isometric or Allometric Growth

When the $b>3$ we assume that there is a positive isometric growth among the sampled species indicating individuals gain weight faster. while when $b<3$: this indicate negative isometric (individuals gain weight slowly).

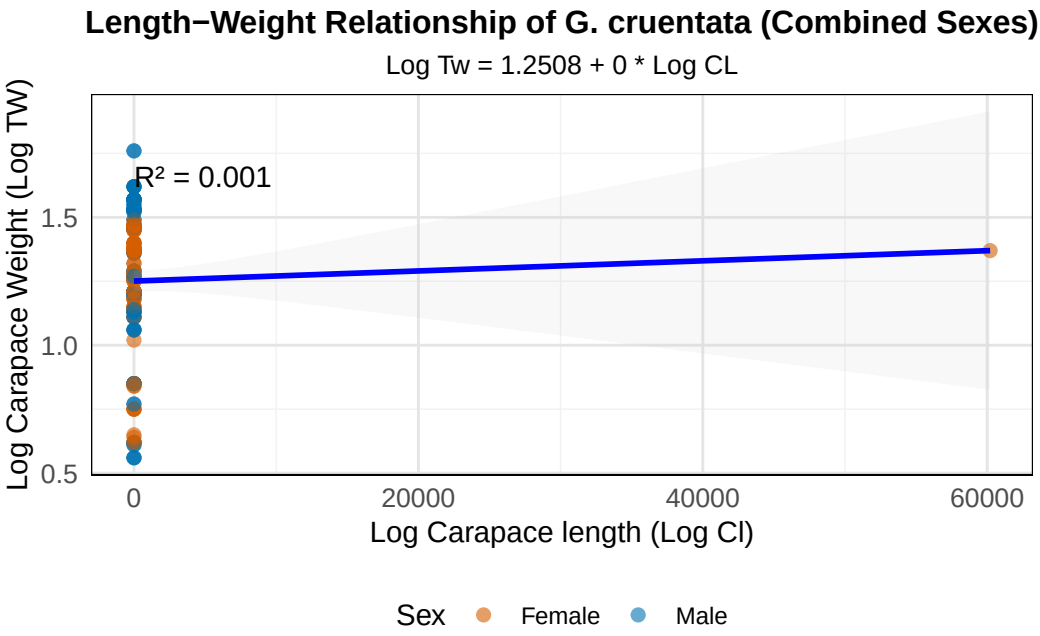
```
## Check for Isometric or Allometric growth
b_value_2 <- coef(lw_model_2)[2] ## Positive Isometric growth (b>3),
## Individual gain weight Faster
```

```
b_value_2 |>
  kable()
```

	x
data_cruen$log_cl	2e-06

Regression Plot showing the Length and Weight Relationship of the Combined Sexes

`geom_smooth()` using formula = 'y ~ x'



Linear Regression of the Length-Weight for Male G. cruentata

Check for either Isometric or Allometric Growth

```
## Check for Isometric or Allometric Growth
b_male_2 <- coef(male_model_2)[2]
print(b_male_2) ## Positive Isometric Growth (b>3),
```

male_lw_2$log_cl
3.300717

```
## Individual gain weight Faster
```

Linear Regression of the Length-Weight for Male G. cruentata

Check for either Isometric or Allometric Growth

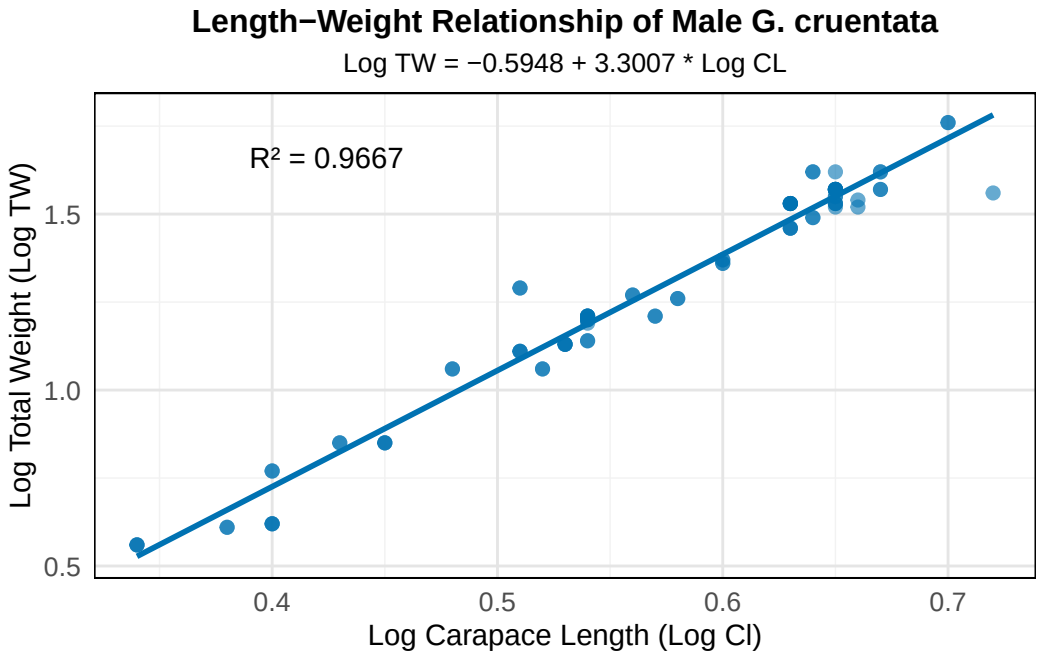
```
## Check for Isometric or Allometric Growth
b_female_2 <- coef(female_model_2)[2]
b_female_2 |>
  kable()## Negative Isometric Growth (b<3)
```

	x
female_lw_2$log_cl	2.3e-06

```
## Individual gain weight Slower
```

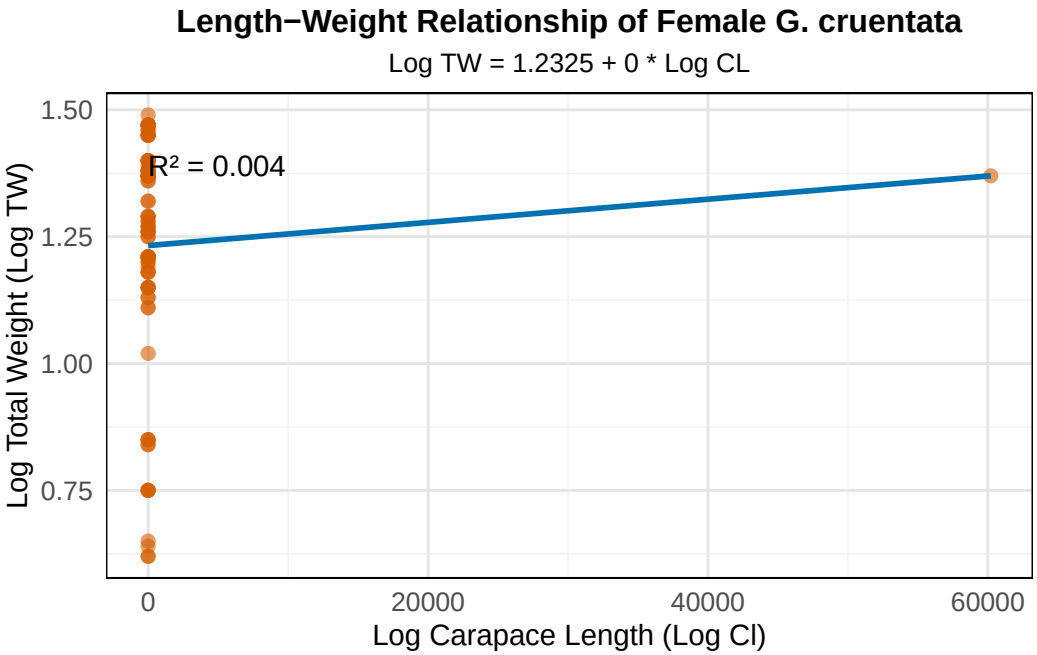
Regression Plot showing the Length and Weight Relationship of the Male G. cruentata

`geom_smooth()` using formula = 'y ~ x'



Regression Plot showing the Length and Weight Relationship of the Female G. cruentata

`geom_smooth()` using formula = 'y ~ x'



Test of Homogeneity of Variance for the Morphometric Data across the Sampling Stations.

When p>0.05 we assume the sampled data has equality of variance but when p<0.05 we assume equality of variance was not met.

For G. cruentata Length

	Df	F value	Pr(>F)
group	9	2.489116	0.0107171
	170	NA	NA

For G. cruentata Weight

```
tw_var_2 <- leveneTest(data_cruen$tw_g ~ data_cruen$s_e_x * data_cruen$station)

tw_var_2 |>
  kable()
```

	Df	F value	Pr(>F)
group	9	3.532572	0.0004869
	170	NA	NA

Test of Significant differences in the mean of length and Weight of G. cruentata across the Stations.

For Length

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
s_e_x	1	0.484651	0.4846510	1.238343	0.2673618
station	4	8.119358	2.0298395	5.186489	0.0005754
s_e_x:station	4	1.956923	0.4892308	1.250045	0.2917497
Residuals	170	66.533012	0.3913707	NA	NA

For Weight

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
s_e_x	1	716.1287	716.1287	6.680580	0.0105863
station	4	1554.5808	388.6452	3.625571	0.0073019
s_e_x:station	4	562.9126	140.7281	1.312817	0.2671871
Residuals	170	18223.2504	107.1956	NA	NA

Correlation analysis showing the relationship between the Length,Weight,Width of G.cruentata across all station.

	cw_cm	cl_cm	tw_g
cw_cm	1.0000000	0.9649052	0.9069646
cl_cm	0.9649052	1.0000000	0.9362372
tw_g	0.9069646	0.9362372	1.0000000

Correlation between Carapace width and Total Weight

```r
## Correlation between cw and Tw
cw_tw_cor_2 <- cor.test(data_cruen$cw_cm, data_cruen$tw_g)
print(cw_tw_cor_2)
```

```
    Pearson's product-moment correlation

data:  data_cruen$cw_cm and data_cruen$tw_g
t = 28.728, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.8770465 0.9298748
sample estimates:
      cor
0.9069646
```

Correlation between Carapace width and Length

```r
## Correlation between cw and cl
cw_cl_cor_2 <- cor.test(data_cruen$cw_cm, data_cruen$cl_cm)
print(cw_cl_cor_2)
```

```
    Pearson's product-moment correlation

data:  data_cruen$cw_cm and data_cruen$cl_cm
t = 49.023, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.9531618 0.9737438
sample estimates:
      cor
0.9649052
```

Correlation between Carapace Length and Total Weight

```r
## Correlation between Cl and Tw
cl_tw_cor_2 <- cor.test(data_cruen$cl_cm , data_cruen$tw_g,
                    method = 'pearson')
print(cl_tw_cor_2)
```

```
    Pearson's product-moment correlation

data:  data_cruen$cl_cm and data_cruen$tw_g
t = 35.549, df = 178, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.9153144 0.9521199
sample estimates:
      cor
0.9362372
```

```r
library(tidyverse)
```