

# *Analysis on the pre-molt and post-molt carapace size of Dungeness crabs*

## **Issue :**

The Dungeness crab, which is a big crustacean commonly found along the Pacific coast, is known for being one of the largest and most plentiful crab species. For the purpose of analyzing adult female Dungeness crabs, a database was compiled that includes information on pre-molt and post-molt carapace sizes. The crabs in the database underwent molting in either a laboratory or ocean environment.

Our objective is to investigate the correlation between the carapace size of Dungeness crabs before and after molting, and then provide a summary of the findings.

## **Findings:**

Our analysis of pre-molt and post-molt carapace sizes in Dungeness crabs revealed a remarkable correlation between the two variables. Specifically, we found a strong linear relationship between pre-molt size and post-molt size, as indicated by a remarkable correlation coefficient of 0.99 and a very low p-value of less than 0.001. These impressive statistical results provide robust evidence against the null hypothesis and demonstrate the high degree of statistical significance between pre-molt size and post-molt size in Dungeness crabs. This finding sheds new light on our understanding of the growth patterns and biology of this fascinating species.

## **Discussion :**

Using the data we have gathered, we conducted a simple linear regression analysis with post-molt size as the predictor variable and pre-molt size as the predicted variable. The results were impressive, with Pearson's  $r^2$  coefficient yielding a value of 0.9915901. This indicates a strong association between the two variables, highlighting the close relationship between pre-molt and post-molt size in Dungeness crabs.

To further validate our findings, we performed a Shapiro-Wilk test, which generated a value of 0.94589 for  $w$  and a  $p$ -value of less than 0.001. This strong evidence against the null hypothesis provides further support for the statistical significance of the relationship between pre-molt size and post-molt size in Dungeness crabs. These exciting findings contribute to our understanding of this fascinating species and its growth patterns.

## **Appendix A : Method**

"We imported the data on post-molt and pre-molt carapace sizes of Dungeness crabs, downloaded as a .csv file, into R-Studio. Pre-molt size, which represents the size of the crab's shell before molting, was analyzed as a function of post-molt size, the size of the shell after molting.

To explore the relationship between these variables, we employed various statistical tools including histograms, scatter plots, and quantile plots. We used Pearson's method to calculate the correlation coefficient and performed a Shapiro-Wilk test to determine the p-value.

Overall, these methods allowed us to gain valuable insights into the correlation between pre-molt and post-molt size in Dungeness crabs, shedding light on the growth patterns of this fascinating species."

## Appendix B : Results

Our data-base, which we imported into R-Studio, comprised a total of 487 data points. To visualize the distribution of pre-molt and post-molt carapace sizes in Dungeness crabs, we constructed histograms and smooth histograms, which provided useful insights into the growth patterns of this species.

Interestingly, when we compared the histograms of pre-molt size (represented by a red-colored histogram) and post-molt size (represented by a green-colored histogram), we observed a significant shift to the right for post-molt size. This finding suggests that Dungeness crabs tend to have larger carapace sizes after molting, which may reflect their growth and development over time.

These findings are important for our understanding of this fascinating species and may have implications for their management and conservation in the future.

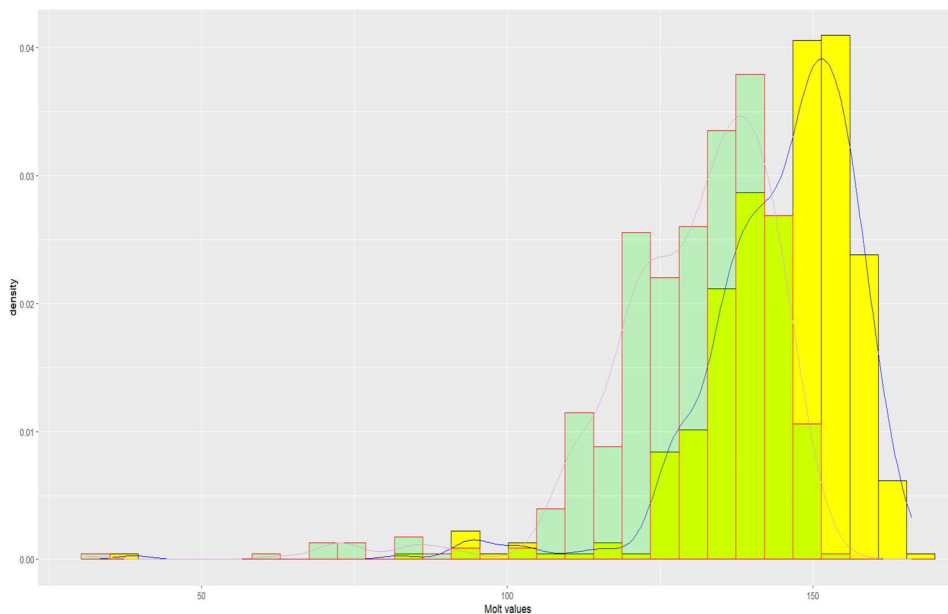


Figure 1: Distribution of post-molt size and pre-molt size

Our analysis of the relationship between pre-molt and post-molt carapace sizes in Dungeness crabs involved creating several informative figures. In Figure 2, we plotted pre-molt size as a function of post-molt size, which allowed us to visualize the relationship between these variables in a clear and intuitive way.

To gain a deeper understanding of this relationship, we performed a simple linear regression analysis using post-molt size as the predictor variable and pre-molt size as the predicted variable. Our findings, which we presented in Figure 3, revealed a strong association between these variables, providing valuable insights into the growth patterns of Dungeness crabs.

These figures, along with our statistical analysis, help us to better understand the complex interplay between pre-molt and post-molt carapace sizes in this fascinating species, and may have important implications for their conservation and management in the future

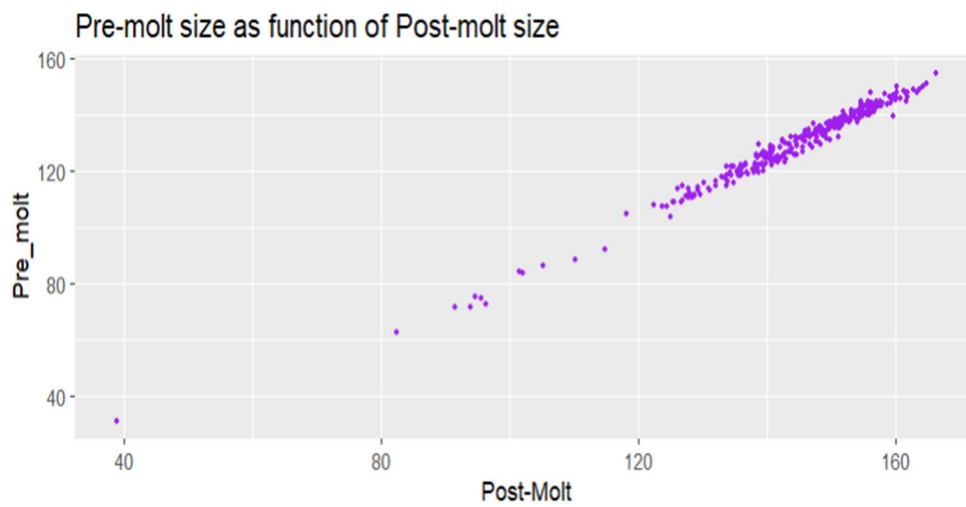


Figure 2: Scatter plot between pre-molt size and post-molt size

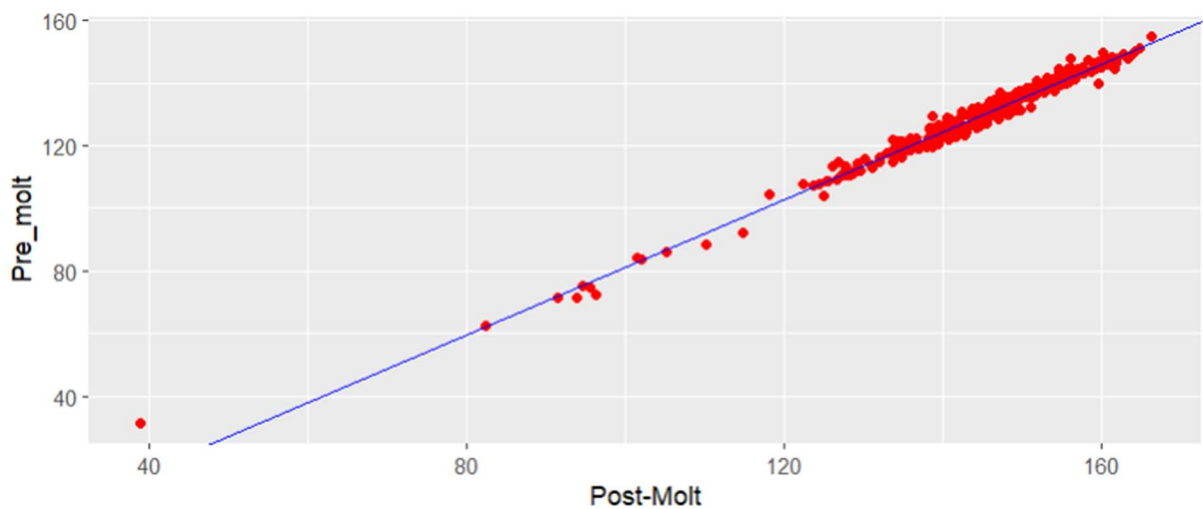


Figure 3: Linear regression relation between post-molt size and pre-molt size

Figure 3 provides a fascinating glimpse into the relationship between pre-molt and post-molt carapace sizes in Dungeness crabs. The scatter plot in this figure shows a cloud of points, which represent the individual observations in our data.

However, what is truly striking about this figure is the red line that passes through the scattered points. This line is the result of a simple linear regression analysis, which reveals that the relationship between pre-molt size and post-molt size is linear.

This finding is significant because it suggests that Dungeness crabs exhibit consistent growth patterns over time, which may be influenced by a range of environmental factors. By understanding the factors that shape these growth patterns

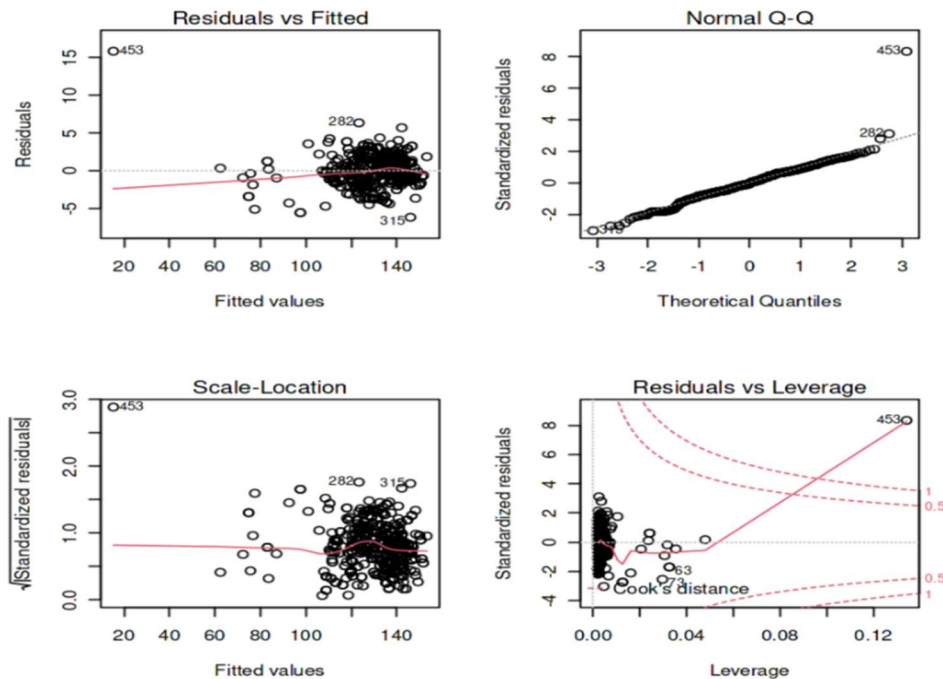


Figure 4: Heteroscedasticity with the help of Plots

### Appendix C : Code

```
install.packages("readxl") library(readxl) file <-
"C:\\Users\\sasik\\OneDrive\\Desktop\\crab_molt_data_mullapudi_sasi.xls" data1 <-
read_excel(file,sheet=1)
```

### Data summary

```
summary(data1)
```

### standard Deviation

```
sd(data1$`Post-Molt`) sd(data1$Pre_molt)
```

```
install.packages("moments") library(moments)
```

### Skewness

```
skewness(data1$`Post-Molt`) skewness(data1$Pre_molt)
```

```
#Kurtosis kurtosis(data1$`Post-Molt`) kurtosis(data1$Pre_molt)
install.packages('ggplot2') library(ggplot2) install.packages('dplyr') library(dplyr)
```

## Probability Density function of Each variable

```
data1 %>% ggplot(aes(x=Post-Molt)) + geom_histogram(aes(y=..density..),alpha =
0.5,col='blue') + geom_density(aes(y=..density..),col = 'red',lwd = 1) + ggtitle("Post-molt
histogram")
```

```
data1 %>% ggplot(aes(x= Pre_molt)) + geom_histogram(aes(y=..density..),alpha =
0.5,col='blue') + geom_density(aes(y=..density..),col = 'red',lwd = 1) + ggtitle("Post-molt
histogram")
```

## overlying of histograms for each variable

```
data1 %>% ggplot(aes(x= Post-Molt)) +
geom_histogram(aes(y=..density..),color='black',fill='yellow')+
geom_density(aes(y=..density..),color='blue', lwd=0.5)+ geom_histogram(aes(x=
Pre_molt,y=..density..),color='red' ,fill='green',alpha=0.2)+ geom_density(aes(x=
Pre_molt,y=..density..),color='plum', lty=1,lwd=0.5) + labs(x="Molt values")
ggtitle("Overlying of Smooth Histograms for Each Variable")
```

## Pre-molt size as function of Post-molt size

```
data1 %>% ggplot(aes(x = Post-Molt,y= Pre_molt)) + geom_point(col = 'purple', pch = 20) +
ggtitle("Pre-molt size as function of Post-molt size")
```

## Simple linear Regression

```
linear_regression <- lm(data1$Pre_molt ~ data1$Post-Molt) summary(linear_regression)
```

```
data1 %>% ggplot(aes(x= Post-Molt,y=Pre_molt)) + geom_point(col = 'red') +
geom_abline(intercept = -26.785511 ,slope = 1.083216 , col = 'blue' )
```

```
pearson_cor <- cor(data1$`Post-Molt`,data1$Pre_molt,method = "pearson")
print(pearson_cor)
```

## Stats of residuals and quantile plot

```
residuals <- resid(linear_regression) summary(residuals)
```

```
qqnorm(residuals) qqline(residuals)
```

## Shapiro-Walks test

```
shapiro.test(residuals)
```

## Plot the residuals against the dependent variable

```
plot(data1$Pre_molt, residuals, xlab="Pre-molt values" , ylab="residuals" , main = "Residual  
analysis") abline(0,0)
```

## about heteroscedasticity

```
par(mfrow=c(2,2))
```

```
plot(linear_regression)
```