

Leptograpsus crab morphology manuscript

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##Introduction

Leptograpsus variegatus is a species of small shore crab found throughout the Southern Pacific, including on the shores of western Australia where the crabs dataset was collected (Campbell and Mahon 1974). These crabs play an important role in the flow of nutrients through mangrove ecosystems, where they break down mangrove leaves and provide particulate organic matter to many species of detritivores (Camilleri 1992).

#Data and analysis

Data for this project was originally collected and published in Campbell and Mahon (1974). Take a look at the distribution of some of the variables show below in Figure 1. Based on visually examining the distributions, (and reading what the original authors did in their analysis), and since all variables are already in a common unit measure (mm) I decided not to transform the data.

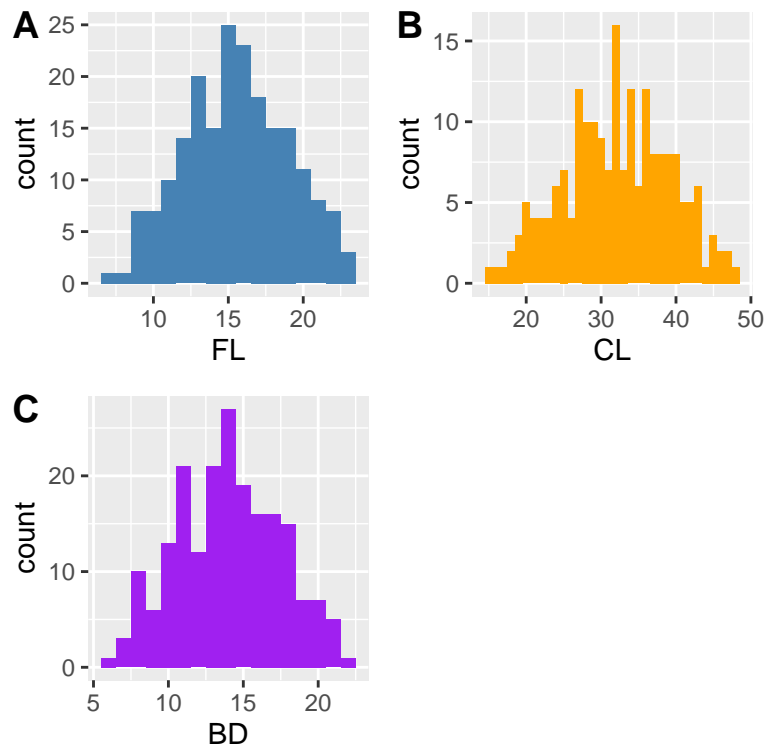


Figure 1: Histograms showing distributions of frontal lobe (FL), carapace length (CL), and body depth (BD).

Analysis and data visualizations were all performed in R.

We used R version 4.4.0 (R Core Team 2024) and the following R packages: ggordiplots v. 0.4.3 (Quensen et al. 2024), prereg v. 0.6.0 (Aust and Spitzer 2022), rmarkdown v. 2.28 (Xie et al. 2018, 2020; Allaire et al.

2024), tidyverse v. 2.0.0 (Wickham et al. 2019), vegan v. 2.6.8 (Oksanen et al. 2024).

##Results

Results of the PCA demonstrated some distinction between blue and orange morphs along the first principal component, and a larger distinction between males and females along the second axis of variation as seen in the following code chunk.

```
#we need the vegan stats package, ggplot, and
#gordiplots which allows us to create biplots using ggplot
library(vegan)

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.6-8

library(ggplot2)
library(ggordiplots)

## Loading required package: glue

#reading crabs data from the raw data folder
crabs <- read.csv('../00_rawdata/crabs_measurements.csv')
#perform pca using vegan's rda function
pca_crabs <- rda(crabs[5:9])
#creating a species+sex column for visualization in the plot
crabs$spsex <- paste0(crabs$sp, crabs$sex)
#using ggordiplot. Ellipses are 1 standard deviation about the centroid.
gg_ordiplot(pca_crabs, groups = crabs$spsex, pt.size = 1,
             kind = 'sd')
```

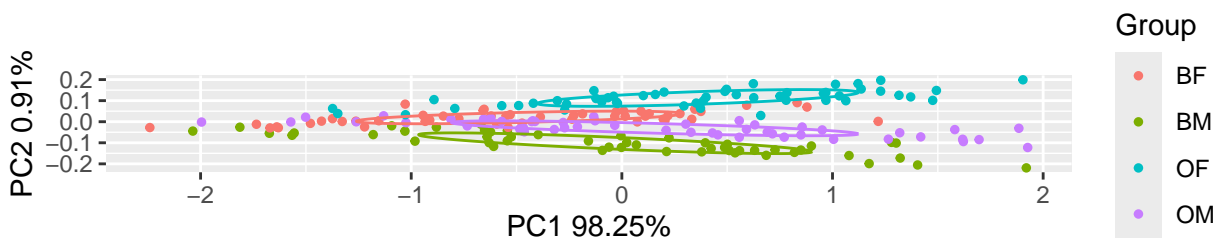


Figure 2: Biplot showing the first and second principal components from the PCA using the crabs morphological data. Point represent individual crabs and are coloured by sex and colour morph

##References

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