Assessing growth dynamics and connectivity of blacklip abalone (Haliotis rubra) populations

Size-at-maturity (SAM)

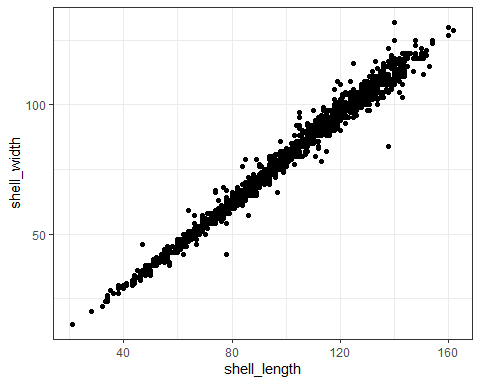
Jaime McAllister

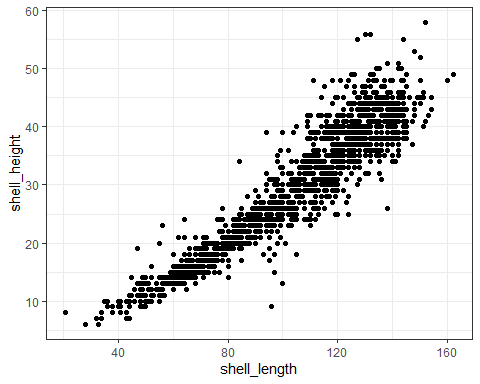
Last Updated on 01 April, 2025

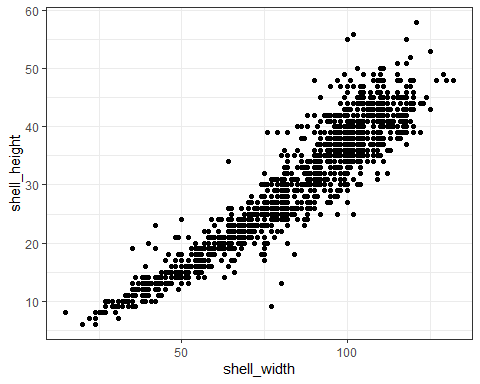
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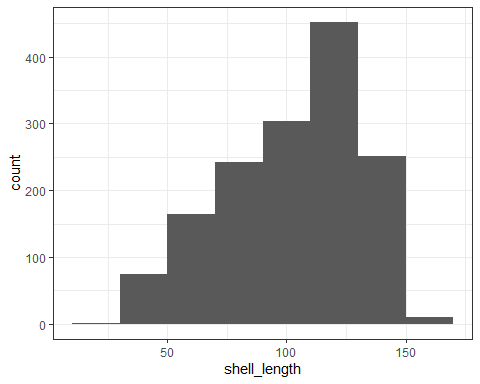
# Data checks and summaries

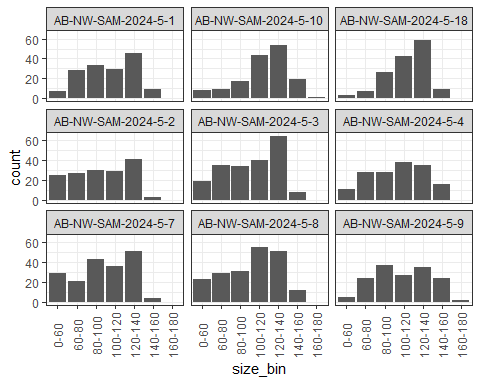
Quick summary plots to look for outliers in length data. Summary counts for each of the target size classes from dive collections.











# Size-at-maturity estimation

Size at maturity (SAM) estimation using ‘biology’ package developed by Malcom Haddon.

Maturity status was determined following Jones et al. 2009:

* Stage 0, has no apparent development of gonad (immature).
* Stage 1, gonad development has started, such that it is possible to determine sex of animal, although the gonad at this stage is very slight, at its most developed form it is translucent so that the digestive gland is still visible underneath (immature).
* Stage 2, gonad is obvious at the extremities of the digestive gland, it is opaque but not yet fully formed. The eggs in females are visible at low magnification while males are viscous creamy yellow (mature).
* Stage 3, fully formed gonad (mature). Stages 1 to 3 can be grouped by sex but only stages 2 and 3 are considered mature as although in stage 1 sex may be determined, that individual is unlikely to be reproductive and so is categorised as immature male or female (mature).

A dataframe has been created to run the ‘fitmaturity’ function where maturity has been classified as:

* I = stages 0-1
* M = stages 2-3.

## Size-at-maturity by site

library(biology)  
library(hplot)  
library(codeutils)  
  
# Convert lowercase to uppercase sex.  
sam\_dat <- sam\_dat %>%   
 mutate(sex = toupper(sex))  
  
# Classify gonad stage 1 abalone as immature.  
sam\_dat <- sam\_dat %>%   
 mutate(sex\_adj = case\_when(gonad\_score %in% c(0, 1) ~ 'I',  
 gonad\_score >= 2 ~ sex),  
 mature = case\_when(gonad\_score >= 2 ~ 1,  
 gonad\_score <= 1 ~ 0))  
  
# Create dataframe for fitmaturity function (site, sex, length, maturity)  
tas\_ab <- sam\_dat %>%  
 select(site, sex\_adj, shell\_length, mature) %>%  
 dplyr::rename(sex = 'sex\_adj',  
 length = 'shell\_length') %>%  
 filter(sex != 'T') #filter any trematodes  
  
# Re-classify sex as mature or immature  
tas\_ab <- tas\_ab %>%   
 mutate(sex = case\_when(sex %in% c('M', 'F') ~ 'M',  
 sex == 'I' ~ 'I'))  
  
# Quick summary of samples by site and maturity status(sex)  
table(tas\_ab$site, tas\_ab$sex)

I M  
 AB-NW-SAM-2024-5-1 77 75  
 AB-NW-SAM-2024-5-10 53 99  
 AB-NW-SAM-2024-5-18 80 66  
 AB-NW-SAM-2024-5-2 97 58  
 AB-NW-SAM-2024-5-3 141 61  
 AB-NW-SAM-2024-5-4 92 64  
 AB-NW-SAM-2024-5-7 121 63  
 AB-NW-SAM-2024-5-8 135 67  
 AB-NW-SAM-2024-5-9 79 75

# Create parameters for loop and plots  
sites <- sort(unique(tas\_ab$site))  
nsite <- length(sites)  
scenes <- c("AB-NW-SAM-2024-5-1", "AB-NW-SAM-2024-5-2", "AB-NW-SAM-2024-5-3", "AB-NW-SAM-2024-5-4",  
 "AB-NW-SAM-2024-5-7", "AB-NW-SAM-2024-5-8", "AB-NW-SAM-2024-5-9", "AB-NW-SAM-2024-5-10",  
 "AB-NW-SAM-2024-5-18")  
models <- makelist(scenes)  
count <- 0  
  
# Run model across each site for sexes combined  
for (i in 1:nsite) { # i = 1  
 count <- count + 1  
 picksite <- which(tas\_ab$site == sites[i])  
 models[[count]] <- fitmaturity(tas\_ab[picksite,],  
 length="length",mature="mature",lower=50,upper=160)  
 }  
  
str1(models)

List of 9  
 $ AB-NW-SAM-2024-5-1 :List of 4  
 $ AB-NW-SAM-2024-5-2 :List of 4  
 $ AB-NW-SAM-2024-5-3 :List of 4  
 $ AB-NW-SAM-2024-5-4 :List of 4  
 $ AB-NW-SAM-2024-5-7 :List of 4  
 $ AB-NW-SAM-2024-5-8 :List of 4  
 $ AB-NW-SAM-2024-5-9 :List of 4  
 $ AB-NW-SAM-2024-5-10:List of 4  
 $ AB-NW-SAM-2024-5-18:List of 4

str1(models[["Site1"]])

NULL

# Create maturity plots for each site  
plotprep(width=10, height=8)  
parset(plots=c(2,2))  
for (i in 1:length(models)) {  
 plotmaturity(models[[i]],label=scenes[i],col=2,xmin=0,xmax=0,CI=FALSE,  
 setpar=FALSE,lwd=2)   
}

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| Figure 1: Proportion mature at length for blacklip abalone maturity data at each surveyed site in Block 5 (NW Tasmania) in 2025. Length at 50% maturity is indicated by the green vertical line, and sample size is presented in the top-left corner of the plot. |

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| Figure 2: Proportion mature at length for blacklip abalone maturity data at each surveyed site in Block 5 (NW Tasmania) in 2025. Length at 50% maturity is indicated by the green vertical line, and sample size is presented in the top-left corner of the plot. |

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| Figure 3: Proportion mature at length for blacklip abalone maturity data at each surveyed site in Block 5 (NW Tasmania) in 2025. Length at 50% maturity is indicated by the green vertical line, and sample size is presented in the top-left corner of the plot. |

## Size-at-maturity across block

# Run model across block for sexes combined  
models <- fitmaturity(tas\_ab, length = "length", mature = "mature", lower = 50,upper = 160)  
  
# Create maturity plots for entire Block 5  
plotprep(width=10, height=8)  
# parset(plots=c(2,2))  
plotmaturity(models, label = 'AB-NW-SAM-2024-Block-5', col = 2, xmax = 0, CI = F, setpar = F, lwd = 2)

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| Figure 4: Proportion mature at length for blacklip abalone maturity data for Block 5 (NW Tasmania) in 2025. Length at 50% maturity is indicated by the green vertical line, and sample size is presented in the top-left corner of the plot. |

# Shellology maturity status

## Internal shell scaring vs maturity

A quick summary plot comparing Prince ‘shellology’ classification of internal shell scaring and maturity status determined from macroscopic examination of gonads. A summary of the Shell\_internal\_score:

1. No scar formation.
2. Some pitting.
3. Quite pitted.
4. Secondary deposition forming.
5. Secondary deposition covers most of muscle attachment site.
6. Secondary deposition covers all of muscle attachment site.

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| Figure 5: Total count of abalone for each internal shell classification from specimens sampled in Block 5 (NW Tasmania) in 2025. |

## External shell appearance vs maturity

A quick summary plot comparing Prince ‘shellology’ classification of external shell appearance and maturity status determined from external appearance and fouling of shell. A summary of the Shell\_external\_score:

1. Clean shell; no epiphytic growth.
2. Some epiphytic fouling but not advanced.
3. Hard fouling commenced around spire.
4. Fleshy fouling and coraline covering spire but ripple texture of shell apparent.
5. Fleshy fouling and coraline covering most of shell and ripple texture of shell non-apparent
6. Shell completely overgrown with hard fouling to growing edge.
7. Very thick fouling and shell completely overgrown.

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| Figure 6: Total count of abalone for each external shell classification from specimens sampled in Block 5 (NW Tasmania) in 2025. |