

Abalone Reproductive Data

Craig Mundy

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```
[1] "channel" "db.oocyte" "g3.g" "g3.h" "g3.oocyte" "g3.sf" "sb.g"
[8] "sb.h" "sb.sf" "sql" "sr.g" "sr.h" "sr.sf"
```

1 The project

Between 1988 and early 1992, Warwick Nash and team took monthly samples (~ 12 females) of abalone from George III Rock as part of a study on spawning periodicity. During the last year of sampling (1991), monthly samples were also taken at Shag Rock bay and Stinking Bay on the Tasman Peninsular. Morphometric data were collected from each animal, prior to the gonad being fixed. Routine histology was then done on the gonads. The section was taken approximately 1/3 of the way along the conical appendage on the basis that the gonad state was uniform throughout.

Warwick Nash and team processed the histology slides, mapping out the gonad state within the section into 8 categories. That work was never published. In 2002, I (CM) had Leigh Gurney review the 8 state- gonad classification system and re-classify the 8 states into a more typical 5 state system. Leigh also conducted detailed measurements of oocyte diameter for the 1991 Georges III Rock samples. Thi identified a transition from pre-vitellegenci to vitellegenic stages at around 95 microns. On the results of that exercise between 2004 and 2010 I had various people process the histology slides for stage- frequency analysis. The last person I employed casually was so efficient that I ended up getting her to do the entire 4-year George III slides and the slides from Shag Rock Bay and Stinking Bay, so that we had a consistent dataset.

1.1 The data

The stage frequency data were collected from 4 transects across the section oriented north, south, east, west. Within each transect the area of the gonad sampled (outer membrane to boundary with the digestive gland) was measured using imageJ, and a count done of the number of pre-vitellegenic and vitellegenic oocytes in each transect.

Several data frames are loaded from this .R Data file. Sites are designated as follows;

- g3.X = George III Rock
- sr.X = Shag Rock Bay
- sb.X = Stinking Bay

Different atatasets are designated as follows;

- g3.g = basic morphometric information
- g3.h = histology and gonad state information
- g3.sf = stage frequency information

Examples are given below on joining the data frames to make a useable dataset.

1.2 Gonad data

```
kable(g3.g[1:10,])
```

week_no	abalone_id	sample_date	shell_length_mm	shell_width_mm	whole_wt_g	meat_wt_g	viscera_wt_g
1	7402	1988-02-11	132	101	334.4	158.8	
1	7403	1988-02-11	140	NA	442.0	219.8	
1	7404	1988-02-11	142	111	404.7	188.4	
1	7405	1988-02-11	134	NA	363.6	179.7	
1	7406	1988-02-11	117	92	195.2	93.0	
1	7407	1988-02-11	136	115	390.4	170.7	
1	7408	1988-02-11	97	79	136.1	61.0	
1	7409	1988-02-11	132	107	380.5	189.5	
1	7410	1988-02-11	126	99	293.9	146.7	
1	7411	1988-02-11	123	93	190.5	80.7	

```
str(g3.g, digits.d = 2, vec.len = 3)
```

```
'data.frame':  3142 obs. of  16 variables:
 $ week_no      : num  1 1 1 1 1 1 1 1 ...
 $ abalone_id   : num  7402 7403 7404 7405 ...
 $ sample_date  : POSIXct, format: "1988-02-11" "1988-02-11" ...
 $ shell_length_mm: num  132 140 142 134 ...
 $ shell_width_mm: num  101 NA 111 NA ...
 $ whole_wt_g   : num  334 442 405 364 ...
 $ meat_wt_g    : num  159 220 188 180 ...
 $ viscera_wt_g : num  83 85 96 86 ...
 $ sex          : Factor w/ 4 levels "F","I","M","T": 1 3 1 3 2 1 2 1 ...
 $ shell_ht_mm  : num  42 NA 47 NA 30 41 25 33 ...
 $ shell_wt_g   : num  80 NA 93 NA ...
 $ no_major_rings: num  13 NA 13 NA 13 14 6 14 ...
 $ no_minor_rings: num  NA NA NA NA NA NA NA NA ...
 $ total_no_rings: num  13 NA 13 NA 13 14 6 14 ...
 $ samp_year    : num  1988 1988 1988 1988 ...
 $ samp_month   : num  2 2 2 2 2 2 2 2 ...
```

1.3 Histology data

```
kable(g3.h[1:10,])
```

week_no	abalone_id	shell_length_mm	whole_wt_g	no_major_rings	stage_1_mm2	stage_2_mm2	stage_3_mm2
1	7402	132	334.4	13	0.00	0.00	
1	7404	142	404.7	13	0.00	0.00	
1	7407	136	390.4	14	0.00	0.00	
1	7409	132	380.5	14	0.00	30.37	
1	7410	126	293.9	10	0.00	0.00	
1	7414	147	504.1	12	0.00	0.00	
1	7415	138	348.2	12	17.04	0.00	
1	7416	125	278.8	9	0.00	0.00	
1	7417	158	649.6	14	0.00	0.00	
1	7418	134	384.7	14	0.00	0.00	

```
str(g3.h, digits.d = 2, vec.len = 3)
```

```
'data.frame':  746 obs. of  30 variables:
 $ week_no      : num  1 1 1 1 1 1 1 1 ...
 $ abalone_id   : num  7402 7404 7407 7409 ...
 $ shell_length_mm: num  132 142 136 132 ...
```

```

$ whole_wt_g      : num  334 405 390 380 ...
$ no_major_rings  : num   13 13 14 14 10 12 12 9 ...
$ stage_1_mm2     : num    0 0 0 0 ...
$ stage_2_mm2     : num    0 0 0 30 ...
$ stage_3_mm2     : num   21 0 0 0 ...
$ stage_4_mm2     : num    1.4 103.6 86.3 0 ...
$ stage_5_mm2     : num    0 0 0 0 0 0 0 0 ...
$ stage_6_mm2     : num    0.84 2.27 6.92 0 ...
$ stage_7_mm2     : num   16.7 9.8 25.3 6.9 ...
$ stage_8_mm2     : num    0 0 0 2.7 ...
$ liver_area_mm2  : num   114 141 80 106 ...
$ gonad_area_mm2  : num    40 116 119 40 ...
$ gonad_index     : num    0.26 0.45 0.6 0.27 ...
$ tafi_index      : num    0 0 0 0 0 0 0 0 ...
$ pc_developing   : num    0 0 0 76 ...
$ pc_ripe         : num   56 90 73 0 ...
$ pc_spent        : num   44 10 27 24 ...
$ rec_dev         : int    0 0 0 33 0 0 17 0 ...
$ locules         : int   21 0 0 0 42 0 0 62 ...
$ mature          : int    1 104 86 0 0 215 0 0 ...
$ spawning        : int   17 10 25 7 7 0 0 6 ...
$ necrotic        : int    1 2 7 0 0 0 0 0 ...
$ pc_rec_dev      : int    0 0 0 83 0 0 100 0 ...
$ pc_locules      : int   53 0 0 0 86 0 0 91 ...
$ pc_mature       : int    3 90 73 0 0 100 0 0 ...
$ pc_spawning     : int   43 9 21 18 14 0 0 9 ...
$ pc_necrotic     : int    3 2 6 0 0 0 0 0 ...

```

1.4 Stage Frequency data

```
kable(g3.sf[1:10,])
```

site	sample_date	samp_year	samp_month	abalone_id	quadrant	previt	vit	qarea
G3R	1988-09-09	1988	9	36022	E	102	1	0.359
G3R	1988-09-09	1988	9	36022	N	0	0	0.000
G3R	1988-09-09	1988	9	36022	S	68	2	0.577
G3R	1988-09-09	1988	9	36022	W	72	4	0.324
G3R	1988-09-09	1988	9	36032	E	37	10	0.954
G3R	1988-09-09	1988	9	36032	N	13	4	1.287
G3R	1988-09-09	1988	9	36032	S	79	5	2.832
G3R	1988-09-09	1988	9	36032	W	141	17	3.498
G3R	1988-09-09	1988	9	36033	E	83	41	1.908
G3R	1988-09-09	1988	9	36033	N	35	33	2.280

```
str(g3.sf, digits.d = 2, vec.len = 3)
```

```

'data.frame':  2223 obs. of  9 variables:
 $ site      : Factor w/ 1 level "G3R": 1 1 1 1 1 1 1 1 ...
 $ sample_date: POSIXct, format: "1988-09-09" "1988-09-09" ...
 $ samp_year  : num  1988 1988 1988 1988 1988 ...
 $ samp_month : num   9 9 9 9 9 9 9 9 ...
 $ abalone_id : num  36022 36022 36022 36022 36022 ...
 $ quadrant   : Factor w/ 4 levels "E","N","S","W": 1 2 3 4 1 2 3 4 ...

```

```
$ previt      : num  102 0 68 72 ...
$ vit         : num   1 0 2 4 10 4 5 17 ...
$ qarea       : num   0.36 0 0.58 0.32 ...
```

2 Joining the tables

2.1 Morphometrics and Histology

```
## Add histology data to morphometric data
histodat <- left_join(g3.g, g3.h ) %>%
  filter(!is.na(tafi_index)) %>%
  ungroup()
```

Joining, by = c("week_no", "abalone_id", "shell_length_mm", "whole_wt_g", "no_major_rings")

```
histodat %>% filter(sex == "F" ) %>%
  group_by(samp_year, samp_month) %>%
  summarise(reps = n()) %>% kable()
```

samp_year	samp_month	reps
1988	2	15
1988	3	13
1988	4	9
1988	5	9
1988	7	13
1988	8	13
1988	9	13
1988	10	12
1988	11	13
1988	12	11
1989	1	14
1989	2	12
1989	5	7
1989	6	13
1989	7	14
1989	9	18
1989	10	4
1989	12	2
1990	1	1
1990	2	12
1990	3	6
1990	4	14
1990	5	11
1990	6	11
1990	7	15
1990	8	19
1990	9	15
1990	10	17
1990	11	16
1990	12	13
1991	1	15
1991	2	15
1991	3	16
1991	4	14
1991	5	14
1991	6	12
1991	7	12
1991	8	16
1991	9	13
1991	10	18
1991	11	17
1991	12	19
1992	1	16

2.2 Morphometrics and Histology

Not all histology slides were processed for stage frequency. Some sections were too fragmented or of poor quality, and were skipped.

```
## first step is to summarise the data in each transect
g3sfdat <- g3.sf %>% filter(qarea > 0) %>%
```

```
group_by(abalone_id) %>%
  summarise(vits = sum(vit, na.rm=T),
            previts = sum(previt, na.rm=T),
            sum_area = sum(qarea, na.rm=T),
            ntrans = n())

## Add summarised stage frequency data to histo and morphometric data
stagedat <- left_join(histodat, g3sfdat ) %>%
  ungroup()
```

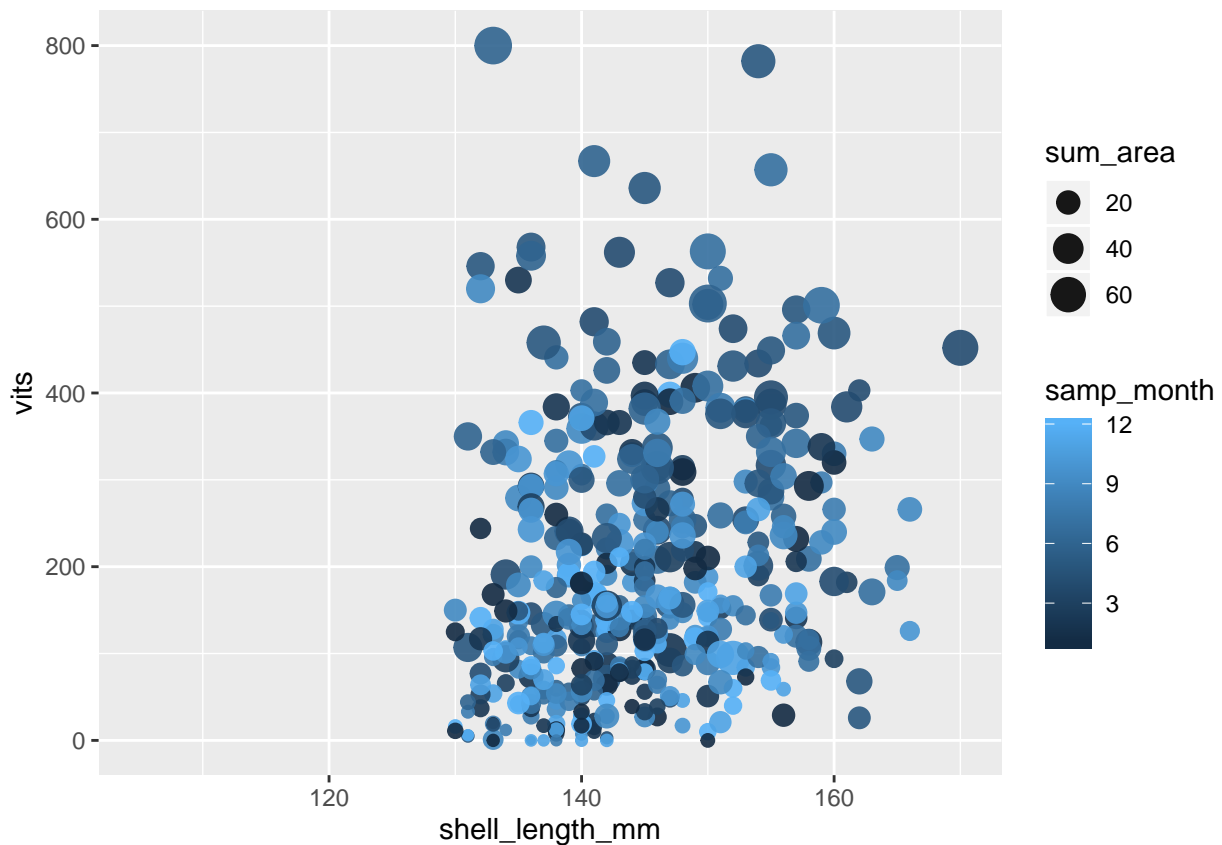
Joining, by = "abalone_id"

2.3 simple stage frequency plots

Some basic plots of the relationship between shell length and the number of vits and previts, colour coded by month, and with a bubble size set by the section area sampled.

```
stagedat %>% ggplot(aes(x=shell_length_mm, y=vits, colour=samp_month, size = sum_area)) +
  geom_point(alpha = 0.9)
```

Warning: Removed 138 rows containing missing values (geom_point).



```
stagedat %>% ggplot(aes(x=shell_length_mm, y=previts, colour=samp_month, size = sum_area)) +
  geom_point(alpha = 0.9)
```

Warning: Removed 138 rows containing missing values (geom_point).

