

## Appendix C: Male maturity

Male maturity:

We used the 1991 EAG pot survey collected 2457 carapace length and chela height measurements (carapace length (CL) in mm and chela height (CH) up to one-tenth of a mm) for male maturity curve fitting and 50% maturity length determination. We determined the 50% maturity length and maturity proportion by size outside the assessment model using the ‘segmented regression’ package available in R (R Core Team 2016). We used the estimated maturity proportion by size in the assessment model to re-evaluate the 50% maturity length and fit a smooth maturity curve.

First we fitted a linear regression model to the data pair using the R package as follows:

$$\ln(CH) = \beta_0 + \beta_1 \ln(CL) \quad (C.1)$$

where  $\beta_0$  and  $\beta_1$  are regression parameters

The procedure of ‘segmented regression’ uses maximum likelihood to fit a somewhat different parameterization of the linear model. It can be approximated as

$$\ln(CH) = \beta_0 + \beta_1 \ln(CL) + \beta_2 [\ln(CL) - c] + \gamma I[\ln(CL) > c] \quad (C.2)$$

where  $\beta_2$  is a regression parameter and  $c$  is the break point.  $\gamma I[\ln(CL) > c]$  is a dummy variable. When  $\ln(CL) < c$ , the model reduces to,

$$\ln(CH) = \beta_0 + \beta_1 \ln(CL) + \beta_2 [\ln(CL) - c] \quad (C.3)$$

The  $\gamma$  term is a measure of the distance between the end of the first segment and the beginning of the next. The model converges when  $\gamma$  is minimized, thus this method constrains the segments to be (nearly) continuous.

Breakpoint analysis results:

Estimated breakpoint, ln(CL)	Standard error
4.687	0.012

Coefficients of the linear terms:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-1.74836	0.08487	-20.60	<2e-16 ***
logCL	1.04673	0.01899	55.13	<2e-16 ***
U1.logCL	0.61540	0.02727	22.57	NA

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Adjusted R-squared: 0.908, AIC: 2358.9

Thus, the break point estimate of male CL (i.e., 50% maturity length) =  $\exp(4.687) = 108.53$  mm CL.

Figure C.1 provides the segment regression fit to the log (CL) and log (CH) data pair:

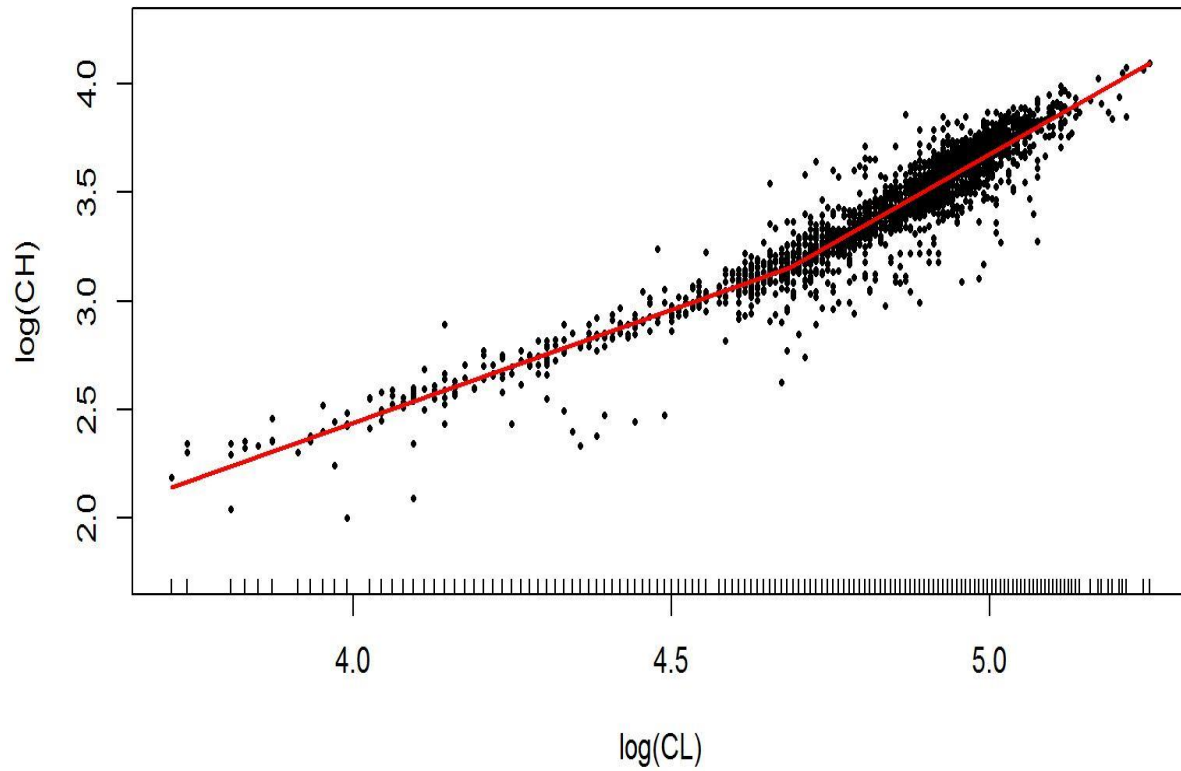


Figure C.1. Segmented linear regression fit to  $\ln(\text{CH})$  vs.  $\ln(\text{CL})$  data of male golden king crab in EAG.

Using the two segments of the estimated linear lines, we allocated each data point to be mature or immature, considering whether the vertical height of the data point [ $\ln(\text{CH})$ ] to the extended upper segment line is smaller or larger than the vertical height to the lower segment line (Figure C.2).

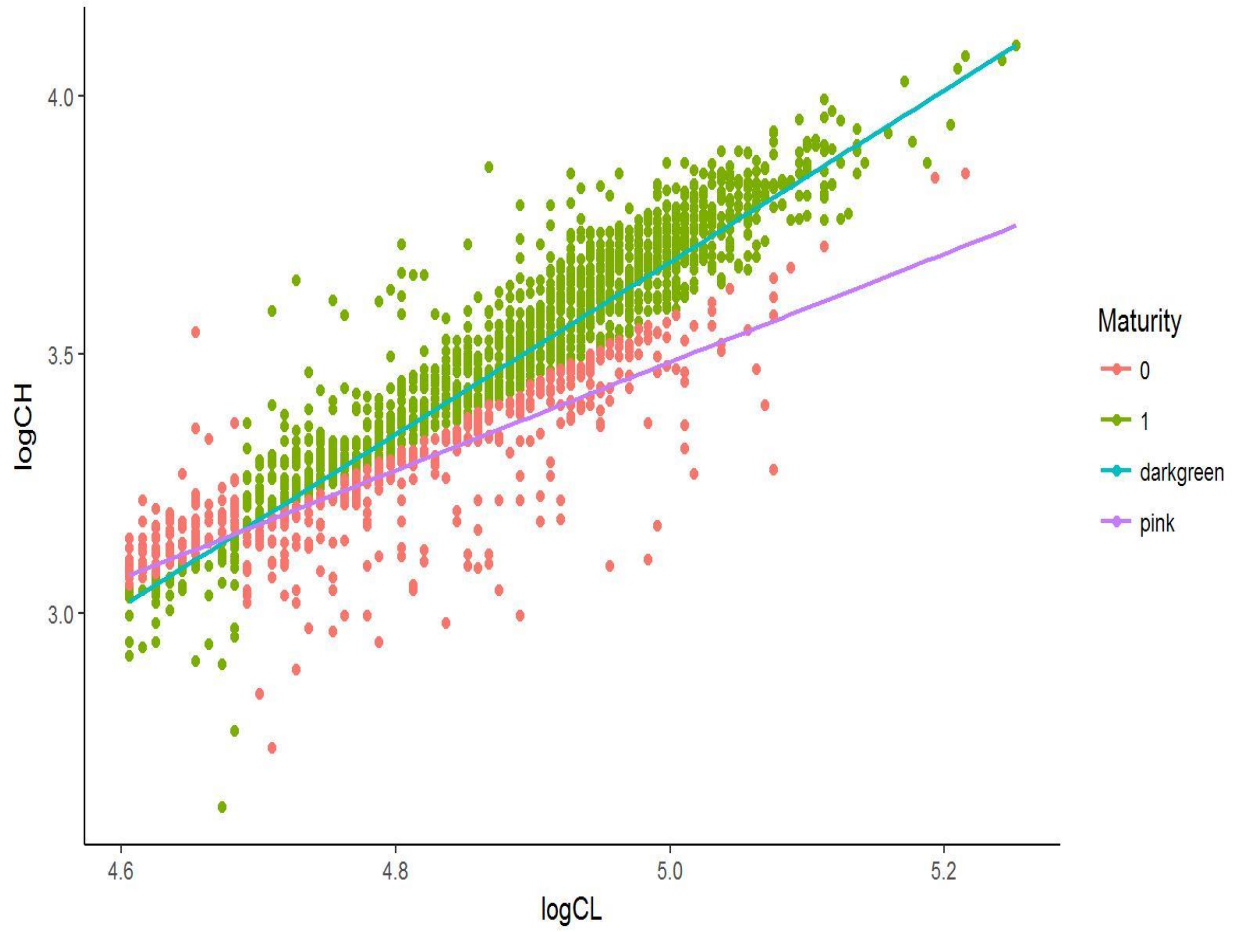


Figure C.2. Segmented linear regression fit to  $\ln(\text{CH})$  vs.  $\ln(\text{CL})$  data of male golden king crab in EAG with classification of mature (code 1, darkgreen) and immature (code 0, red) data points.

The estimated mature and immature proportions for each size bin are listed in Table C.1.

Table C.1. Mature and immature proportions by mid carapace length. This set of values is treated as observed maturity proportions for inputting to the population model.

Mid CL (mm)	Mature Frequency	Immature Frequency	Mature Proportion
	0	0	
103	56.0	314	0.1514
108	74.0	74	0.5000
113	124.0	59	0.6776
118	118.0	63	0.6519
123	139.0	43	0.7637
128	164.0	49	0.7700
133	197.0	47	0.8074
138	233.0	47	0.8321
143	188.0	29	0.8664
148	178.0	22	0.8900
153	105.0	8	0.9292
158	58.0	7	0.8923
163	26.0	1	0.9630
168	21.0	1	0.9545
173	2.0	0	1.0000
178	3.0	1	0.7500
183	5.0	1	0.8333

Then we fitted the proportion mature vs. mid CL by the logistic regression using GLM. The results are as follows:

Model: `glm(formula = Maturity State ~ CL, family = binomial(link = logit), data = Maturity)`

Deviance Residuals:

Min    1Q    Median    3Q    Max

-3.0188 -0.6310 0.4811 0.7320 2.6239

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-6.71466	0.36124	-18.59	<2e-16 ***
CL	0.06120	0.00294	20.82	<2e-16 ***

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1; AIC: 2358.9

The 50% maturity length (the carapace length at the predicted proportion of 0.5) was estimated as 109.72 mm CL.

When we used the mature proportions (Table C.1) in the population model, we obtained the 50% maturity length as 110.62 mm CL under base scenario (Sc1). Thus, for the knife-edge maturity selection scenario models (9 and 11), we considered all sizes above 111 mmCL to be fully mature (1) and below this size immature (0).

*Essential R steps:*

*# 1. Segmented regression:*

*# fit a single linear regression first then apply segmented*

```
library(segmented)
```

```
singleline.mod<- lm(logCH~logCL)
```

```
segmented.mod<- segmented(singleline.mod,seg.Z=~logCL)
```

*2. Logistic regression:*

```
library(MASS)
```

```
best.glm<- glm(MaturityState~CL,family=binomial(link=logit),data=Maturity)
```