

## Appendix C1. Technical Documentation and User’s Guide for UMaine Northern Shrimp Size-Structured Assessment Model (UME SSAM) version 01

### Introduction

Northern Shrimp Size-Structured Assessment Model (NS SSAM) is a size/stage-structured assessment model developed for the northern shrimp stock assessment. It contains a number of options that are described in this User’s Guide. The technical documentation provides the basic equations used in the program along with the statistical methods used to develop fit different objective function to fit the model to data. The assessment program has two independent options for the modeling time step, annual and seasonal (season 1= January -March; season 2 = April-June; season 3 = July –September; and season 4 = October – December).

### Basic Equations

The description of the model is for the seasonal time step. Models for the annual time step are similar (but simpler for many models). The calculation of the objective functions is described in the next section.

#### Natural mortality $M$

##### Weighted $M$

The weighted and seasonal  $M$  for shrimp of size bin  $k$ , in year  $t$ , season  $m$  is calculated as:

$$M_{k,t,m} = w_t w_k M_m \quad (1)$$

where  $w_t$  is pre-specified annual weighting factor,  $w_k$  is pre-specified size weighting factor; and  $M_m$  is seasonal natural mortality which could be either pre-specified or estimated.

##### Lorenzen $M$

The natural mortality for shrimp of size bin  $k$ , in year  $t$ , season  $m$  is calculated:

$$M_{k,t,m} = M_{u,m} W_{k,t}^{b_m} \quad (2)$$

where  $M_{u,m}$  is the natural mortality at unit weight in season  $m$ ;  $W_{k,t}$  is the weight at size bin  $k$ , in year  $t$ ; and  $b_m$  is allometric scaling factor.  $M_{u,m}$  and  $b_m$  are treated as parameters.

##### Fishing mortality

Fishing mortality is assumed to be separable, meaning it is the product of a year effect ( $Fmult$ ) and selectivity at size ( $S$ ). The fishing mortality for a fleet  $f$ , year  $t$ , season  $m$ , and size bin  $k$  is calculated as:

$$F_{f,m,t,k} = Fmult_{f,m,t} S_{f,b,k} \quad (3)$$

The  $Fmult$  for a fleet  $f$ , year  $t$  and season  $m$  is determined by two sets of parameters,  $Fmult_{f,m,1}$ , the parameter for first year and each season for that fleet, and  $FDev_{f,m,t}$ , the deviation of the parameter from the value in the first year for that fleet. Both sets of parameters are estimated in log space:

$$\log(Fmult_{f,m,t}) = \log(Fmult_{f,m-1,t}) + \log(FDev_{f,m,t}) \quad (4)$$

For a given fleet, multiple time blocks could be specified to allow for time dependence. Within each selectivity block, there are four options/functions for estimating selectivity ( $S_{f,b,k}$ ):

1. estimate parameters for each size bin (one parameter for each size bin)
2. logistic function (2 parameters: a, b)

$$S_{f,b,k} = \frac{1}{1 + \exp(b_{f,b}(a_{f,b} - L_k))} \quad (5)$$

3. double logistic (4 parameters: a, b, c, d)

$$S_{f,b,k} = \frac{1}{1 + \exp(b_{f,b}(a_{f,b} - L_k))} \left(1 - \frac{1}{1 + \exp(d_{f,b}(c_{f,b} - L_k))}\right) \quad (6)$$

4. double normal (4 or 6 parameters, details could be found in Methot Jr, Richard D., and Chantell R. Wetzel. "Stock synthesis: A biological and statistical framework for fish stock assessment and fishery management." *Fisheries Research* (2012).)

Note for option 2, 3 and 4, the selectivity at size is divided by the maximum value over all size bins for scaling, making the re-scaled selectivity vector having a maximum value of 1.0 for the defined time block.

### **Recruitment**

Recruitment is modeled as the product of annual recruitment and the proportion of the annual recruitment ( $R_t$ ) that recruits to each season ( $\lambda_m$ ) and each size-class ( $\lambda_k$ ):

$$R_{m,t,k} = R_t \lambda_k \lambda_m \quad (7)$$

The proportion of the recruitment in each pre-defined size-class can either be pre-specified or estimated along with the other parameters of the model. The proportion of the recruitment in each season is pre-specified.

### **Annual recruitment**

There are three options to estimate annual recruitment:

1. estimated as free parameters and modeled as:

$$R_t = \bar{R} e^{RDev_t} \quad (8)$$

where  $RDev_t$  is the recruitment deviation of year  $t$  from the expected  $R$  ( $R\_bar$ ) and treated as bounded parameters, meaning their sum is zero, so that they are centered on the expected  $R$ .

2. assumed to be temporally auto-correlated

$$RDev_t = \sqrt{R_h} RDev_{t-1} + \sqrt{1 - R_h} eps_t \quad (9)$$

where  $R_h$  is the degree of autocorrelation between recruitments of the neighboring years, and  $eps_t$  is  $RDev_t$  assuming there is no autocorrelation.  $R_h$  and  $eps_t$  are parameters.

3. related to spawning stock biomass according to a stock-recruitment relationship (B-H or Ricker)

$$\bar{R}_t = \frac{\alpha SSB_t}{\beta + SSB_t} \quad (10)$$

or

$$\bar{R}_t = \alpha SSB_t e^{-\beta SSB_t} \quad (11)$$

where  $\alpha$  and  $\beta$  are parameters and  $SSB_t$  is the spawning stock biomass of year  $t$ .

### **Initial conditions**

The numbers-at-size at the start of the first year which specifies the state of population when model starts could be specified by eight options:

0. estimate parameters for each size-class
1. pre-specified proportions-at-size ( $Pia_k$ ) and estimate the total numbers ( $N$ ) for the first year, the numbers-at-size is calculated as:

$$N_k = Pia_k N \quad (12)$$

2. pre-specified proportions-at-size ( $Pia_k$ ) and estimate the total numbers ( $N$ ) for the first year, the numbers-at-size is calculated as:

$$N_k = \frac{e^{Pia_k}}{1 + e^{Pia_k}} N \quad (13)$$

3. assume proportions-at-size ( $Pia_k$ ) follows a log-normal distribution with mean  $\mu$  and standard deviation  $\sigma$  and calculated as:

$$Pia_k = \frac{1}{\sqrt{2\pi}\sigma L_k} \exp\left(-\frac{(\ln(L_k) - \mu)^2}{2(\sigma)^2}\right) \quad (14)$$

The numbers-at-size is calculated as option 1.  $N$ ,  $\mu$ , and  $\sigma$  are the parameters to be estimated.

4. assume proportions-at-size ( $Pia_k$ ) follows a log-normal distribution as option 3 and the numbers-at-size is calculated as option 2 (3 parameters:  $N$ ,  $\mu$ , and  $\sigma$ ).
5. assume proportions-at-size ( $Pia_k$ ) follows a normal distribution with mean  $\mu$  and standard deviation  $\sigma$  and calculated as:

$$Pia_k = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{(L_k - \mu)^2}{2(\sigma)^2}\right) \quad (15)$$

The numbers-at-size is calculated as option 1.  $N$ ,  $\mu$ , and  $\sigma$  are the parameters to be estimated.

6. assume proportions-at-size ( $Pia_k$ ) follows a normal distribution as option 5 and the numbers-at-size is calculated as option 2 (3 parameters:  $N$ ,  $\mu$ , and  $\sigma$ ).
7. assume proportions-at-size ( $Pia_k$ ) follows a mixture normal distribution consists of three normal distributions to account for multiple peaks:

$$Pia_k = \pi_1 f_1(L_k) + \pi_2 f_2(L_k) + \pi_3 f_3(L_k) \quad (16)$$

where  $\pi_1 + \pi_2 + \pi_3 = 1$ ,  $f_1(L)$ ,  $f_2(L)$  and  $f_3(L)$  have a normal form but have different means and variances. The numbers-at-size is calculated as option 1. There are nine parameters in this case,  $N$ ,  $\mu_1$ ,  $\sigma_1$ ,  $\mu_2$ ,  $\sigma_2$ ,  $\mu_3$ ,  $\sigma_3$ ,  $\pi_1$ , and  $\pi_2$ .

Note for options 3-7, the proportion at size is divided by the summation value over all size bins, resulting in the final proportion vector having the summation of 1.

### **Growth**

Growth transition matrix, determining the probability of an average shrimp growing from a size class into other size-classes, is required in size-based models. NSLSAP allows time dependence in growth transition matrix by setting time blocks (maximum number of time blocks could be the number of time-steps, meaning that time-step specific growth transition matrix could be specified). There are two options for growth transition matrix:

1. estimated externally and pre-specified as inputs
2. derived from VBGF model, estimate VBGF parameters (5 parameters) along with other model parameters

The expected growth increment during a time-step (season) is assumed to follow a normal distribution with mean and variance calculated as:

$$E(\Delta L_m) = (L_{\infty, b} - L_k)(1.0 - e^{-\alpha_m K_b}) \quad (17)$$

$$Var(\Delta L_m) = Var(L_{\infty, b})(1 - e^{-\alpha_m K_b})^2 + \alpha_m^2 (L_{\infty, b} - L_k)^2 Var(K_b) e^{-2\alpha_m K_b} + 2\rho_b \alpha_m SD(L_{\infty, b}) SD(K_b)(1 - e^{-\alpha_m K_b})(L_{\infty, b} - L_k) e^{-\alpha_m K_b} \quad (18)$$

where  $L_{inf, b}$ ,  $K_b$ , standard deviation of  $L_{inf, b}$ ,  $K_b$ , and correlation between  $L_{inf, b}$ ,  $K_b$  ( $\rho$ ) are the five parameters could be estimated for a given time block ( $b$ ).  $\alpha_m$  is a input proportion used for partitioning the growth within a year. If  $\alpha_m = 1$ , the five parameters are seasonal

specific, otherwise, they are annual specific and the annual growth is partitioned according to the pre-specified proportion vector ( $\alpha_m$ ).

If  $d_{low}$  and  $d_{up}$  are the lower and upper ends of size class  $d$ , the probabilities of a shrimp growing from size class  $k$  to size class  $d$  can be computed as:

$$P_{k \rightarrow d} = \int_{d_{low}}^{d_{up}} f(x | E(\Delta L), Var(\Delta L)) dx \quad (19)$$

More detailed description could be found in Chen et al.2003.

### **Population dynamics**

The number of shrimp in size bin  $k$  at the beginning of year  $t$  and season  $m$  is calculated as:

$$N_{k,t,m} = N_{k,t,m-1} SV_{k,t,m-1} G_{k,m-1} + R_{k,t,m} \quad (20)$$

$G_{k,m-1}$  is the growth transition matrix in the previous season;  $R_{k,t,m}$  is the recruitment of year  $t$  that recruits to season  $m$  and size-class  $k$ ; and  $SV_{k,t,m-1}$  is the survival rate for shrimp in size bin  $k$  in previous season year  $t$ , and calculated as:

$$SV_{k,t,m} = \exp\left(-\left(\sum_f (F_{f,m,t,k}) + M_{m,t,k}\right)\right) \quad (21)$$

where  $F_{f,m,t,k}$  and  $M_{m,t,k}$  could be found in the sections of **Fishing mortality** and **Natural mortality**, respectively.

### **Stock biomass**

#### **Weight-at-size**

The weight of a shrimp in size-class  $k$ , year  $t$  is calculated as:

$$\log(W_{t,k}) = a_t + b_t \log(L_k) \quad (22)$$

where  $a_t$  and  $b_t$  are inputs.

#### **Maturity-at-size**

The proportion of matured shrimp for a size-class  $k$ , year  $t$  is calculated by a logistic function as:

$$Pm_{t,k} = \frac{G}{1 + \exp(-K_t(L_k - L_{50\%,t}))} \quad (23)$$

where  $G_t$ ,  $K_t$  and  $L_{50\%,t}$  are inputs.

#### **Sex change**

Sex change is assumed to be length-dependent and the proportion of shrimps that change sex to female in a given year is modeled by a logistic function:

$$PS_{t,k} = \frac{1}{1 + \exp\left(-\frac{2\log(3)}{R_{sex}}(L_k - L_{50\%,t})\right)} \quad (24)$$

where  $L_{50\%,t}$  and  $R_{sex}$  are two sets of parameters to be estimated.

The female biomass for year  $t$  could be calculated as:

$$B_t^f = \sum_k N_{t,k} W_{t,k} PS_{t,k} \quad (25)$$

The non-female biomass for year  $t$  could be calculated as:

$$B_t^{nf} = \sum_k N_{t,k} W_{t,k} (1 - PS_{t,k}) \quad (26)$$

### Spawning stock biomass

The spawning stock biomass is calculated based on the population abundance at size ( $N$ ), the weight at size ( $W$ ), proportion of maturity at size ( $Pm$ ), proportion of female at size ( $Ps$ ), and the proportion of the total mortality during the year prior to spawning ( $p_{SSB}$ ) as:

$$SSB_t = \sum_k N_{t,k} e^{-p_{SSB} Z_{t,k}} W_{t,k} Pm_{t,k} Ps_{t,k} \quad (27)$$

### Predicted catch

Predicted landings in units of numbers of shrimp for each fleet, year, season and size-class are derived from the Baranov catch equation:

$$C_{f,m,t,k}^{pred,n} = \frac{F_{f,m,t,k}}{F_{f,m,t,k} + M_{m,t,k}} (1 - \exp(-(F_{f,m,t,k} + M_{m,t,k}))) N_{t,k,m} \quad (28)$$

Predicted landings in weight for each fleet, year, season and size-class are calculated:

$$C_{f,m,t,k}^{pred,n} = \frac{F_{f,m,t,k}}{F_{f,m,t,k} + M_{m,t,k}} (1 - \exp(-(F_{f,m,t,k} + M_{m,t,k}))) N_{t,k,m} W_{t,k} \quad (29)$$

### Catchability

#### Fishery catchability

Time blocks could be set up for fishery catchability, within a block ( $b$ ), the fishery catchability for fleet  $f$  and season  $m$  is calculated internally as:

$$\ln(q_{f,m,b}) = \frac{1}{n_b} \sum_b \ln\left(\frac{CPUE_{f,m,t}^{Obs}}{(B_{f,m,t}^{exploit})^{E_{f,m,b}}}\right) \quad (30)$$

or

$$\ln(q_{f,m,b}) = \ln\left(\frac{1}{n_b} \sum_b \left(\frac{CPUE_{f,m,t}^{Obs}}{(B_{f,m,t}^{exploit})^{E_{f,m,b}}}\right)\right) \quad (31)$$

where  $CPUE_{f,m,t}^{Obs}$  is the observed CPUE for fleet  $f$ , year  $t$ , and season  $m$ ;  $n_b$  is the number of time block for a given fleet;  $E_{f,m,b}$  is the power parameter accounting for the nonlinearity;  $B_{f,m,t}^{exploit}$  is calculated as:

$$B_{f,m,t}^{exploit} = \sum_k \bar{N}_{m,t,k} S_{b,k} W_{t,k} \quad (32)$$

$$\bar{N}_{m,t,k} = N_{m,t,k} \frac{1 - e^{-(\sum_f F_{f,m,t,k} + M_{m,t,k})}}{\sum_f F_{f,m,t,k} + M_{m,t,k}} \quad (33)$$

#### Survey catchability

Survey catchability which is modeled similar as fleet catchability and calculated internally as:

$$\ln(q_{ind,b}) = \frac{1}{n_b} \sum_b \ln\left(\frac{I_{ind,t}^{Obs}}{B_{ind,t}^{Survey}}\right) \quad (34)$$

or

$$\ln(q_{ind,b}) = \ln\left(\frac{1}{n_b} \sum_b \frac{I_{ind,t}^{Obs}}{B_{ind,t}^{Survey}}\right) \quad (35)$$

where  $I_{ind,t}^{Obs}$  is the observed index for survey  $ind$ , and year  $t$ ;  $n_b$  is the number of time block for a given survey.  $B_{ind,t}^{Survey}$  is calculated as:

$$B_{ind,t}^{Survey} = \sum_k N_{ind,t,k}^{Survey} W_{t,k} \quad (36)$$

$$N_{ind,t,k}^{Survey} = N_{ind,t,k} S_{ind,t,k} \quad (37)$$

where  $S_{ind,t,k}$  is the selectivity of survey  $ind$ , year  $t$  and size-class  $k$ ,  $N_{ind}$  could be found in the the section of **Predicted indices** below.

### **Predicted indices**

The observed indices have two characteristics that are matched when predicted values are computed, the time of year of the index and the units (numbers or biomass). The estimated population numbers at size are modified to the time of the index according to:

$$N_{ind,t,k} = N_{t,k} \left( 1 - \exp\left(-(\text{indmonth}/12)Z_{t,k}\right) \right) \quad (38)$$

where  $\text{indmonth}$  refers to the end of the month, so  $\text{indmonth}=0$  is January 1 and  $\text{indmonth}=12$  is December 31. If the units for an index are biomass, then the  $N_{ind}$  values are multiplied by user defined weights at size matrix. The selectivity associated with each index is either matched to a fleet or modeled independently using the same way as the fleet selectivity (4 options: size based, logistic, double logistic or double normal). The final predicted index ( $I_{pred}$ ) is formed by summing the product of  $N_{ind}$  and selectivity values ( $S$ ) over the size classes and multiplying by the catchability ( $q$ ) for the index:

$$I_{pred,ind,t} = q_{ind,t} \sum_k N_{ind,t,k} S_{ind,t,k} \quad (39)$$

### **Predicted CPUE**

The predicted CPUE for fleet  $f$ , year  $t$ , and season  $m$  is calculated as:

$$CPUE_{f,m,t}^{pred} = q_{f,m,b} \left( B_{f,m,t}^{exploit} \right)^{E_{f,m,b}} \quad (40)$$

where  $q_{f,m,b}$  is the catchability for fleet  $f$ , time block  $b$ , and season  $m$ ;  $E_{f,m,b}$  is the power parameter;  $B_{f,m,t}^{exploit}$  is calculated as section **Fishery catchability**.

### **Predicted length composition**

The predicted catch length composition is calculated as:

$$P_{f,m,t,k}^{pred} = \frac{C_{f,m,t,k}^{pred}}{\sum_k C_{f,m,t,k}^{pred}} \quad (41)$$

where  $P_{f,m,t,k}^{pred}$  is the proportion of predicted catch for fleet  $f$ , year  $t$ , season  $m$  and size-class  $k$ ;  $C_{f,m,t,k}^{pred}$  is the predicted catch for fleet  $f$ , year  $t$ , season  $m$  and size-class  $k$ .

The predicted survey length composition is calculated as:

$$P_{ind,t,k}^{pred} = \frac{N_{ind,t,k}^{Survey}}{\sum_k N_{ind,t,k}^{Survey}} \quad (42)$$

where  $P_{ind,t,k}^{pred}$  is the proportion of abundance at the survey time of survey  $ind$ , year  $t$ , and size-class  $k$ .

### **Reference Points**

The program computes a number of common reference points based on estimated or pre-specified selectivity and biological characteristics. The reference points are computed through a bisection algorithm which produces an accuracy of approximately 1E-05. The reference points

computed are  $F_{0.1}$ ,  $F_{MAX}$ ,  $F_{30\%SPR}$ ,  $F_{40\%SPR}$ , and  $F_{MSY}$ . The associated maximum sustainable yield (MSY) and spawning stock biomass at  $F_{MSY}$  are also provided.

### Objection Function Calculation (Fitting the model)

The overall objective function in NSLSAP is the sum of log likelihood functions linking observed and predicted values of various life history and fishery processes. A penalty function is also included in the overall objective function to exclude biologically unrealistic estimates. There are multiple assumptions for error distributions provided in the calculation of the objective function. All are converted to negative log likelihoods for use in the minimization conducted by ADMB. All log likelihood functions contain constant terms that do not change for any value of the parameters. These constants can be either included or excluded from the objective function. All model fits contain a lambda value that allows emphasis of that particular part of the objective function along with an input coefficient of variation (CV) that is used to measure how strong a particular deviation is. The CV is converted to a variance ( $\sigma^2$ ) and associated standard deviation ( $\sigma$ ) using the equation

$$\sigma^2 = \ln(CV^2 + 1) \quad (43)$$

### Likelihood functions for length composition

For catch and survey proportion at size, two likelihood functions are available:

1. Multinomial distribution

$$\ln(P) = \ln(ESS!) - \sum_k \ln(x_k!) + ESS \sum_k p_k^{Obs} \ln p_k^{pred} \quad (44)$$

where  $ESS$  is the input effective sample size and is used to create the number of shrimp in each bin ( $x_k$ );  $p_k^{Obs}$  denotes an observed proportion and  $p_k^{pred}$  denotes the associated predicted proportion. Model estimated  $ESS$  is calculated as:

$$ESS^{pred} = \frac{\sum_k p_k^{pred} (1 - p_k^{pred})}{\sum_k (p_k^{pred} - p_k^{Obs})^2} \quad (45)$$

2. Robust normal for proportion (Fourier *et al.* 1990)

$$\ln(P) = \sum_k \left( -\ln\left(\frac{1}{ESS} \sqrt{2\pi(p_k^{pred}(1-p_k^{pred}) + \frac{0.1}{SN})}\right) + \ln\left(\exp\left(-\frac{(p_k^{Obs} - p_k^{pred})^2}{2(p_k^{pred}(1-p_k^{pred}) + \frac{0.1}{SN})\left(\frac{1}{ESS}\right)^2}\right) + 0.01\right) \right) \quad (46)$$

### Likelihood functions for others

For catch, CPUE, indices, recruitment deviation and priors, seven log likelihood functions are provided:

1. Robust

$$\ln(P) = -\ln(\sqrt{2\pi}\sigma_I^{Obs}) + \ln\left(\exp\left(-\frac{(\ln(I^{Obs}) - \ln(I^{pred}))^2}{2(\sigma_I^{Obs})^2}\right) + 0.01\right) \quad (47)$$

2. Student t

$$\ln(P) = -\ln\left(\frac{1.32934}{\sqrt{4\pi}}\right) - 2.5 \ln\left(\left(\frac{\ln(I^{Obs}) - \ln(I^{pred})}{2\sigma_I^{Obs}}\right)^2 + 1\right) \quad (48)$$

3. Normal distribution for the recruitment deviation

$$\ln(P) = -\frac{\sum (Dev)^2}{2(\sigma_{eps})^2} - \ln(\sqrt{2\pi}\sigma_{eps}) \quad (49)$$

4. Log normal

$$\ln(P) = -\ln(\sqrt{2\pi}\sigma_I^{obs}) - \ln(I^{obs}) - \frac{(\ln(I^{obs}) - \ln(I^{pred}))^2}{2(\sigma_I^{obs})^2} \quad (50)$$

5. Log normal without the term for observations

$$\ln(P) = -\ln(\sqrt{2\pi}\sigma_I^{obs}) - \frac{(\ln(I^{obs}) - \ln(I^{pred}))^2}{2(\sigma_I^{obs})^2} \quad (51)$$

6. Normal

$$\ln(P) = -\ln(\sqrt{2\pi}\sigma_I^{obs}) - \frac{(I^{obs} - I^{pred})^2}{2(\sigma_I^{obs})^2} \quad (52)$$

7. Cauchy distribution

$$\ln(P) = -\ln\left(0.675\sigma\pi\left(1 + \left(\frac{I^{obs} - I^{pred}}{0.675\sigma}\right)^2\right)\right) \quad (53)$$

### **Penalty**

One penalty function is included for the estimated fishing mortality. It's a penalty associated with any F greater than an input maximum value, calculated as  $1000*(F - \max F)^2$  for  $F > \max F$ , where max F should be a maximum fishing mortality level that the user believe possible for the fishery and will be defined by the user.

## Users' Guide

### *Input*

The assessment model could operate on either annual time-step or seasonal time-step depending on the user's choice. For each time-step, **9 input files are required** to run the model. Of the 9 input files 3 are common files and 6 are time-step specific files. The names of the files should not be changed.

Appendix C1. Table 1. File names for each time-step.

COMMON FILES		ANNUAL TIME-STEP FILES	SEASONAL TIME-STEP FILES
	Control.DAT	BPR_Data_Year.DAT	BPR_Data_Season.DAT
	Biology_Data.DAT	CatchDataYear.DAT	CatchDataSeason.DAT
	Survey_Data.DAT	GrowthMatrix.DAT	GrowthMatrix.DAT
		Parameters_Ini_Year.DAT	Parameters_Ini_Season.DAT
		Prior_Year.DAT	Prior_Season.DAT
		Porjection_Year.DAT	Projection_Season.DAT
<b>Sub Folder</b>		<b>Year</b>	<b>Season</b>
<b>Folder</b>	<b>InputFiles</b>	<b>InputFiles</b>	<b>InputFiles</b>

In all these input files, “#” precedes a comment line which will not affect the run.

### *Summary of data required*

- Weight-at-size matrix
- Maturity-at-size matrix
- Survey indices, CV, ESS, length composition
- Proportion of female at size for each year
- Annual catch, CV, ESS, length composition
- Growth matrix or VBGF parameters

### *Summary of other information for specifying the model*

- Time-step
- Number of size bins and lower and upper boundary for each size bin
- Natural mortality weighting factors by size and year
- Number of size bins to which recruitment recruits
- Spawning month
- Initial condition
- Survey selectivity
- Fleet selectivity

### *Control file (Control.dat)*

- Model time-step set-up (1-year; 4-season)
- Number of years
- Number of seasons in each year
- Number of months in each season
- First year of the input data (e.g., 1985)
- First year of the data used for a particular run (any subset of the input data)

- Last year of the data used for a particular run (facilitate retrospective analysis)
- Likelihood constants set-up (1-included in the objective function; 0-excluded)
- Tracking a particular cohort (e.g., 1990; the program will output the dynamic of year class 1990)

***Biology data file (Biology\_Data.dat)***

- Number of size bins
- Lower and upper boundary for each size bin (units of millimeter)
- Parameters of Length-weight relation for calculating weight-at-size matrix

*(number of years by 3, the first column is year, the second and third columns are the parameters  $a_t$  and  $b_t$  in Equation 22)*

- Parameters of maturity-length model for calculating maturity-at-size matrix

*(4 by the number of years, the first column is year, the second, third and fourth columns are the parameters  $G_b$ ,  $K_t$  and  $L_{50\%,t}$  in Equation 23)*

- Size weighting factor for natural mortality ( $w_k$  in Equation 1)
- Annual weighting factor for natural mortality ( $w_t$  in Equation 1)
- Number of size bins to which recruitment recruits (the length of vector  $\lambda_k$  in Equation 7)
- Proportions of the annual recruitment recruits to each season ( $\lambda_m$  in Equation 7, only be used when time-step is season)
- Spawning month (defined as the beginning of the month)
- Stock-recruitment relation set-up (1-no functional relation; 2-BH model; 3- Ricker model)
- Initial condition set-up (0-7; see section **Initial Conditions**)
- Proportions-at-size ( $Pia_k$  in Equations 12 and 13; this vector will only be used when the initial condition is set to 1 or 2)

***Survey data file (Survey\_Data.dat)***

- Number of available survey indices
- Unit of each survey index (1-biomass; 0-numbers)
- Start size bin of selectivity for each survey
- End size bin of selectivity for each survey
- Tuning set-up for each index for a particular run (1-include; 0-not include)
- Likelihood function set-up for length composition data for each survey (1-multinomial [Equation 44]; 2-robust normal for proportion [Equation 46])
- Likelihood function set-up for index for each survey (1-7; see section **Likelihood functions for others**)
- Lambda value of composition component in objective function for each survey
- Lambda value of index component in objective function for each survey
- Number of data points for survey indices (e.g., 44: 2 indices \* 22 years)
- Survey data matrix (number of rows=number of data points, number of columns=6 + number of size bins)

Year	Index number	Index month	Index value	CV	ESS	Size bin 1	Size bin 2	.....	End size bin
		<i>Indmonth</i> in Equation 38			Effective sample size	Survey length composition			

- Lambda value of sex change component in objective function
- Proportions of female at size matrix (number of size bins by number of years)
- Number of survey catchability
- Catchability calculation method set-up (1-**Equation 34**; 2-**Equation 35**)
- Survey catchability time blocks set-up (a matrix of number of years by number of survey catchability plus one)

An example showing two time blocks for each of the two indices (4 blocks total):

year	Index 1	Index 2
1985	1	3
1986	1	3
1987	2	3
1988	2	4

Each cell in the shaded area indicates the time block in which a particular index falls for a particular year. For index 1, there are two time blocks, q1 for 1985-1986 and q2 for 1987-1988. For index 2, there are two time blocks as well, q3 for 1985-1987 and q4 for 1988.

- Fleet selectivity reference (**negative value**-not use fleet selectivity as survey selectivity; **fleet number**-use that particular fleet selectivity as survey selectivity)
- Number of survey selectivity time blocks
- Survey selectivity option for each survey (1-4, same options as fleet selectivity, see section *Fishing Mortality*)
- Survey selectivity time blocks set-up

**Catch data file (CatchDataYear.dat)**

- Number of fleets
- Unit of catch for each fleet (0-number[million]; 1-biomass[1000mt])
- Start size bin of selectivity for each fleet
- End size bin of selectivity for each fleet
- Likelihood function set-up for length composition data for each survey (1-multinomial [**Equation 44**]; 2-robust normal for proportion [**Equation 46**])
- Likelihood function set-up for total catch for each fleet (1-7; see section *Likelihood functions for others*)
- Likelihood function set-up for CPUE for each fleet (1-7; see section *Likelihood functions for others*)
- Lambda value of composition component in objective function for each fleet
- Lambda value of total catch in objective function for each fleet
- Lambda value of CPUE in objective function for each fleet
- Number of data points for catch data
- Catch data matrix (number of rows=number of data points, number of columns=9 +

number of size bins)

•

Year	Time-step	Fleet number	Total catch	CV of catch	CPUE or effort value	CPUE or effort	CV of CPUE or effort	ESS	...
						1-CPUE 0-effort			Length comp

- Tuning set-up for each CPUE for a particular run (1-include; 0-not include)
- Number of CPUE catchability (time blocks)
- Catchability calculation method set-up (1-**Equation 34**; 2-**Equation 35**)
- CPUE catchability time blocks set-up (same as survey catchability)
- Number of fleet selectivity time blocks
- Fleet selectivity option for each fleet (1-4, see section **Fishing Mortality**)
- Fleet selectivity time blocks set-up

**Growth matrix data file (GrowthMatrix\_Year.dat)**

- Growth transition matrix set-up (1-use VBGF parameters to derive the growth transition matrix internally, see section of **Growth**, in this case the VBGF parameters could be estimated along with other model parameters; 0-input growth transition matrix directly)
- Number of growth transition matrices
- Growth proportion for each Season ( $\alpha_m$  in **Equation 17**, will not be used when time-step is year)

**Biology reference point data file (BPR\_Data\_Year.dat)**

- Maximum value of F in penalty term
- Selectivity set-up for calculating reference point (-1-input; 0-averaged fleet selectivity; **fleet number**-use that particular fleet selectivity)
- Selectivity input (only be used when above option is set to -1)
- Equilibrium period used for calculating reference point
- Reference year for natural mortality (e.g., 20: use the natural mortality of 20<sup>th</sup> year for calculating reference point)
- Proportions of F for each season (1 for annual time-step)
- Growth matrix set-up (specify which time block of growth matrix will be used for calculating reference point)

**Initial value of parameters input file (Parameters\_Ini\_Year.dat)**

- Fleet Selectivity Parameters
- Fishing mortality of the first year for each fleet
- Fishing mortality deviations for each year and fleet (fleet outer loop, year inner loop)
- CPUE catchability power parameter for each time block
- Survey index selectivity parameter for each time block
- Initial condition parameters
- R-S relationship parameters ( $\alpha$  and  $\beta$ )
- Recruitment deviations (log scale)
- Recruitment autocorrelation coefficient
- Standard deviation of recruitment deviation in log scale

- Natural mortality
- Lorenzen natural mortality ( $b_m$  in **Equation 2**)
- $L_{inf}$  for each time block ( $L_{inf, b}$  in **Equation 17**)
- $K$  for each time block ( $K_b$  in **Equation 17**)
- Standard deviation of  $L_{inf, b}$  (**Equation 18**)
- Standard deviation of  $K_b$  (**Equation 18**)
- Correlation between  $L_{inf, b}$  and  $K_b$  (**Equation 18**)
- Proportion of recruitment-at-size ( $\lambda_k$  in **Equation 7**)
- $L_{50}$  for each year ( $L_{50\%,t}$  in **Equation 24**)
- $R_{sex}$  ( $R_{sex}$  in **Equation 24**)

**Prior input file (Prior\_Year.dat)**

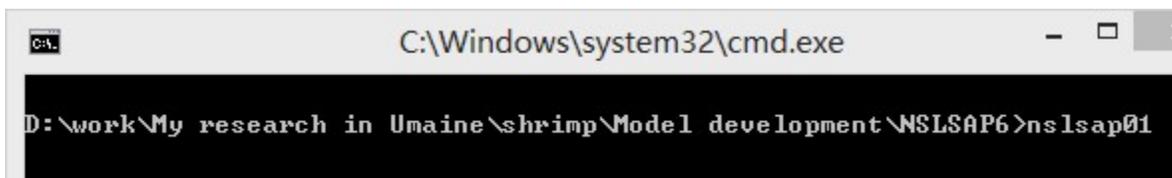
Prior file inputs the priors for each parameter for MCMC run. For each parameter, input the mean, lower bound, upper bound, phase (negative value turns off the parameter), standard deviation, lambda, and likelihood function.

**Running the model**

The NSLSAP01 model is written in ADMB (Automatic Differentiation Model Builder) and the source code could be found in NSLSAP01.tpl file. The process of creating the model with ADMB involves writing, compiling, and testing. An integrated development environment (IDE) allows the user to perform these tasks more efficiently than with a basic editor and a shell. ADMB-IDE is a great tool for modifying the code, compiling the code, and running the model. The manual for ADMB-IDE is available at:

<http://www.admb-project.org/tools/admb-ide/manual>

Once the code is compiled into an executable file (NSLSAP01.exe) the model could be run in a command window. Shift-Right-clicked on folder which contains the model files in windows explorer to open a command window and then type “nslsap01” into command window to run the model (see the example below). The results will be sent to a series of output files which are described in Output section.



**Output**

For each run the model produces a series of output files, most of them are standard ADMB output files. The independent variables of the optimization are in a file named NSLSAP01.par (NSLSAP01.bar is an equivalent binary file). A more user-friendly report is in the file NSLSAP01.rep. The estimated standard deviations and correlations are in files named NSLSAP01.std and NSLSAP01.cor. In addition, a report file named “NSLSAP01\_1985\_2001\_1.rep” which indicates the data range and time-step used for that particular run is also produced.

- 1 **NSLSAP01.rep:** Results for the run, including spawning biomass, numbers-at-length, recruitment, fits to the data, fishing mortality, MSY and related quantities, etc.

- 2 **NSLSAP01.par**: a standard ADMB output file, giving the objective function value, its gradient (this should be very small if the model has converged) and the parameters estimated/fixed for that run.
- 3 **NSLSAP01.std**: a standard ADMB output file, with the parameters estimated for that run and their estimated Hessian-based standard deviation.

R program is used to read and plot the ADMB output. Three r code files stored in the model folder were used. The file named “reptoRlist.r” reads the contents of the report file (NSLSAP01.rep) and stores the contents in R in the form of a list object. The file named “PlotFuncs.r” contains all the functions for producing different plots. The file named “OutputPlots.r” is used to call the functions and get the plots. The explanations of that file are as follows:

```
setwd("D:/work/My research in UMaine/shrimp/Model development/NSLSAP6")
# set working directory to the folder containing the model files (change to yours by typing
the directory in the “”)
```

```
source("reptoRlist.r")
# run the r code in reptoRlist.r
```

```
filename="NSLSAP01"
# specify the name of files outputted from ADMB
```

```
report<-read.admb(filename)
# read the contents of the report file (NSLSAP01.rep) and stores the contents in the list
object (report)
```

```
source("PlotFuncs.r")
# run the r code in PlotFuncs.r
```

```
PlotWL(2000,1)
# plot weighth-at-length
```

```
PlotML(2000)
# plot maturity-at-length
```

```
PlotGM(2000,20)
# plot growth transition matrix
```

```
PlotSelF(2000,1,1)
# plot fleet selectivity
```

```
PlotSelS(2000,1)
# plot survey selectivity
```

```
PlotF(1,1)
```

**# plot fishing mortality**

PlotM(2000)

**# plot natural mortality**

PlotR()

**# plot recruitment**

PlotSSB()

**# plot spawning stock biomass**

PlotAbun()

**# plot numbers-at-length**

PlotSLC(1)

**# plot survey length composition**

PlotSLCA()

**# plot aggregated survey length composition**

PlotSI(1)

**# plot survey index**

PlotTC()

**# plot total catch**

PlotC(2)

**# plot total catch by fleet**

PlotCC(2,1)

**# plot catch length composition**

PlotCCA(2)

**# plot aggregated catch length composition**

PlotRoSSB(1985,2002,2006,4)

**# plot retrospective error for SSB**

PlotSexComp()

**# plot sex composition**

PlotFfit()

**# plot the fit of sex change**

PlotLfifty()

**# plot the fit of L50**

```
PlotSpB()  
# plot the sex-specific biomass over time
```

R version 3.0.0 for windows is available at: <http://cran.r-project.org/bin/windows/base/>

Once you have R installed, open “OutputPlots.r” and run the code you will get the plots.

## Appendix C2. Predation Pressure Index

### Predation Pressure Index

A simple index of predation pressure on northern shrimp *Pandalus borealis* was developed using survey biomass indices of predators and frequency of occurrence of Pandalids in predator stomachs from food habits sampling conducted during NEFSC spring and autumn bottom trawl surveys. The motivation was to include information on predation on shrimp in the assessment models without having to develop absolute estimates of consumption, which require more detailed calculations and depend on several assumptions in order to scale to absolute estimates.

### Methods

Predators of Pandalids were identified based on food habits sampling in the northern shrimp assessment strata in the western Gulf of Maine (NEFSC bottom trawl strata 01240, 0126-1028, 0137-0140) during 1973-2011 spring and fall surveys. Predators were retained in the analysis if at least 100 stomachs containing Pandalids were sampled during all years and spring and fall seasons combined. I used ‘collection category’ prey taxonomic resolution and prey category ‘PANFAM’, which included *P. montagui*, *P. propinquus*, *Dichelopandalus leptocerus*, and unidentified Pandalids. *P. borealis* was identified to species in only about 3% of stomachs containing Pandalids. In survey catches in the shrimp assessment area, *P. borealis* accounted for 89-93% of the aggregate biomass of *P. montagui*, *D. leptocerus* and *P. borealis* on average (fall and summer surveys, respectively, Appendix C2. Figure 1). The Pandalid category excluded Euphausiids and Crangon shrimp.

For each identified predator, I estimated relative frequency of occurrence of Pandalids in predator stomachs (% of stomachs containing Pandalids in fall and spring surveys during 1973-2011). Annual fall biomass indices (NEFSC surveys, stratified mean weight (kg) per tow) were estimated for each predator using only the northern shrimp assessment strata (listed above). The indices from 2009-2012 were converted to ‘Albatross units’ by applying conversion coefficients for biomass developed for each species (Miller 2010). For Atlantic halibut and pollock, data were insufficient for estimating conversion coefficients (Miller 2010). For halibut, I applied the value used in the most recent assessment, which was the average coefficient for all flatfish species (J. Blaylock, pers. comm.). For pollock, the coefficient was assumed equal to one (Miller 2013 CJFAS).

To calculate the predation pressure index, annual biomass indices for each predator were weighted by the % frequency of occurrence of shrimp (averaged over time for each predator) and then summed across predators to derive an annual index of predation pressure that took into account both the biomass of the predators and how heavily each appeared to prey on shrimp.

$$PPI_{is} = \sum_j^j B_{ijs} * P_j$$

Where

PPI = predation pressure index

i = year

s = season (fall)

j= predator species  
B = biomass index  
P = proportion of stomachs containing Pandalids

An alternative PPI was explored using annual estimates of percent frequency in each predator's diet (vs. the average over time for each predator) in order to reflect inter-annual variation in predator response to shrimp densities.

$$PPI(2)_{is} = \sum_{ij} B_{ijs} * P_{ij}$$

To reduce the number of predators for this more detailed analyses, we included only predators that contributed more than 1% to the PPI score for all years combined.

The PPI(2) approach required extrapolating to fill in years with missing data for some of the predators (Appendix C2. Table 1). This was done using relationships estimated for years when complete data were available for all 10 species (1999-2010). The relationships were between % frequency for each predator and (1) % freq for all predators with complete time series, (2) shrimp recruitment index or (3) mean shrimp carapace length (Appendix C2. Figure 2).

Complete data for 2011-2012 food habits became available after most of the work on the PPI had been completed, so only the annual PPI (PPI2) was updated for these years.

## Results

### *PPI*

Sixty species were recorded with Pandalidae in stomach contents during 1973-2011 NEFSC spring and fall surveys (Appendix C2. Table 1). Of these, 21 had at least 100 sampled stomachs over the time series and were retained for the PPI (Appendix C2. Table 2). Frequency of occurrence of Pandalids in stomachs of these 21 predators ranged 1.2% (American plaice) to 35.7% (barndoor skate) and averaged 8.9% (Appendix C2. Table 2, Appendix C2. Figure 3).

Trends in predator biomass are shown in Figure 4, and aggregate predator biomass for the 21 predator species and trends in the PPI are shown in Figure 5. The PPI index based on the top 10 predators accounted for 96% of the PPI overall (Appendix C2. Table 3) and closely followed trends in the PPI based on all 21 species (Appendix C2. Figure 6). In general, the PPI was lowest during the mid-1980s to mid-1990s, increased after 1999 and has remained relatively high since.

### *PPI(2)*

Filling in the gaps for missing data in the annual diet estimates did not have a strong effect on the annual averages over all predators (Appendix C2. Figure 7). Using annual % diet frequency (PPI(2)) resulted in the same broad trend of generally higher predation pressure after the mid-1990s, but there was a sharp divergence since 2010 (Appendix C2. Figure 8). PPI(2) was related to the annual shrimp recruitment index (Appendix C2. Figure 9). The relationship between %

frequency in the diet and % of diet (Appendix C2. Figure 10) suggests predators may take a higher proportion of the shrimp population when shrimp densities are higher.

## Discussion

The approach taken here is very different from the fine-grained approach of Link and Idoine (2009) (“L&I”) in which estimates of absolute consumption were developed. The L&I estimates were initially developed for SARC 45 (NEFSC 2007) for comparison with abundance estimates from the assessment models. The intent of the PPI is not to provide consumption estimates, but to give a broad indication of trends in predation pressure that may be factored into assessment models.

Appendix C2. Figure 11A shows a comparison of trends in the PPI and trends in the L&I consumption estimates (thousand mt) . The trends do not match, even when the PPI is based on the same 10 species included in Link and Idoine (2009). If only the 10 species identified by L&I are used to construct the PPI, the trends still do not match (Appendix C2. Figure 11B).

The L&I estimates were based on sampling in the entire Gulf of Maine including portions of the Scotian Shelf (NEFSC strata 01240-01400) to derive swept area estimates of predator abundance and to estimate per capita consumption of Pandalids. L&I noted that abundance changes would likely dominate the scaling of estimates of consumption. Divergent trends in biomass and abundance of the 10 predator species of L&I explains some of the divergence in trends in the PPI and L&I because trends in abundance and biomass do not track closely (Appendix C2. Figure 11). In addition, several influential species were not included in L&I (redfish, spiny dogfish, Atlantic herring, haddock) because of a large gap in sampling of these species early in the time series. Omitting these species from the PPI had a substantial effect on trends in the PPI (Appendix C2. Figure 12).

## References

- Link, J.S. & J. S. Idoine (2009). Estimates of predator consumption of the northern shrimp *Pandalus borealis* with implications for estimates of population biomass in the Gulf of Maine. *North American Journal of Fisheries Management* 29: 1567-1583.
- Miller T, Das C, Politis P, Long A, Lucey S, Legault C, Brown R, Rago P. 2010. Estimation of *Henry B. Bigelow*/ calibration factors. NEFSC Bottom Trawl Survey/ Calibration Peer Review Working Paper. NEFSC, Woods Hole, MA. 376 p.
- Miller, T.J. 2013. A comparison of hierarchical models for relative catch efficiency based on paired-gear data for US Northwest Atlantic fish stocks. *Can. J. Fish. Aquat. Sci.* 70: 1306–1316.

Appendix C2. Table 1. Complete list of species recorded as having Pandalids in stomach contents during NEFSC spring and fall surveys, 1973-2011.

<u>≥ 100 stomachs (included in PPI)</u>	<u>&lt; 100 stomachs (excluded from PPI)</u>
SILVER HAKE	SUMMER FLOUNDER
ATLANTIC COD	BLACKBELLY ROSEFISH
WHITE HAKE	SMOOTH DOGFISH
RED HAKE	ATLANTIC MACKEREL
LONGHORN SCULPIN	YELLOWTAIL FLOUNDER
LITTLE SKATE	WEAKFISH
FOURSPOT FLOUNDER	ROSETTE SKATE
SPINY DOGFISH	BLACK SEA BASS
WINDOWPANE	OFFSHORE HAKE
SPOTTED HAKE	CLEARNOSE SKATE
WINTER SKATE	AMERICAN SHAD
SMOOTH SKATE	WITCH FLOUNDER
POLLOCK	WINTER FLOUNDER
SEA RAVEN	BLUEBACK HERRING
THORNY SKATE	NORTHERN SEAROBIN
HADDOCK	CUSK
ACADIAN REDFISH	BLUEFISH
ATLANTIC HERRING	OCEAN POUT
BARNDOR SKATE	STRIPED SEAROBIN
GOOSEFISH	ATLANTIC WOLFFISH
AMERICAN PLAICE	SCUP
ATLANTIC HALIBUT	CUNNER
	FAWN CUSK-EEL
	CHAIN DOGFISH
	MOUSTACHE SCULPIN
	FOURBEARD ROCKLING
	ATLANTIC CROAKER
	GULF STREAM FLOUNDER
	NORTHERN SHORTFIN SQUID
	LONGFIN HAKE
	WRYMOUTH
	STRIPED BASS
	BULLNOSE RAY
	SPANISH MACKEREL
	ATLANTIC SHARPNOSE SHARK
	SPOT
	ALEWIFE
	BUTTERFISH

Appendix C2. Table 2. Overall frequency of occurrence of Pandalids in predator stomachs and percent by volume of Pandalids in stomachs containing Pandalids (unweighted estimate), 1973-2011 spring and fall NEFSC surveys combined.

Predator	Frequency of Occurrence	Avg % of prey that was Pandalids (by wt)	Number stomachs sampled
BARNDOOR SKATE	35.7	22.8	28
SMOOTH SKATE	20.8	15.8	751
WHITE HAKE*	15.5	12.4	6,924
RED HAKE*	13.1	10.5	5,111
ATLANTIC COD*	12.9	8.8	5,311
ATLANTIC HALIBUT	12.5	10.8	192
LITTLE SKATE	11.0	6.4	493
LONGHORN SCULPIN*	9.6	8.2	1,782
THORNY SKATE*	8.6	3.0	1,888
SILVER HAKE*	7.5	6.8	14,157
ACADIAN REDFISH	6.6	6.0	2,375
POLLOCK*	6.4	4.3	1,905
FOURSPOT FLDR*	5.0	4.6	337
WINTER SKATE	4.4	2.3	344
SEA RAVEN*	4.3	3.0	1,487
SPINY DOGFISH	3.5	2.2	6,825
GOOSEFISH	2.9	1.8	2,414
HADDOCK	2.8	1.7	1,985
ATLANTIC HERRING	1.9	1.7	4,527
WINDOWPANE*	1.4	1.2	213
AMERICAN PLAICE	1.2	1.1	5,284

\* species included in Link and Idoine (2009)

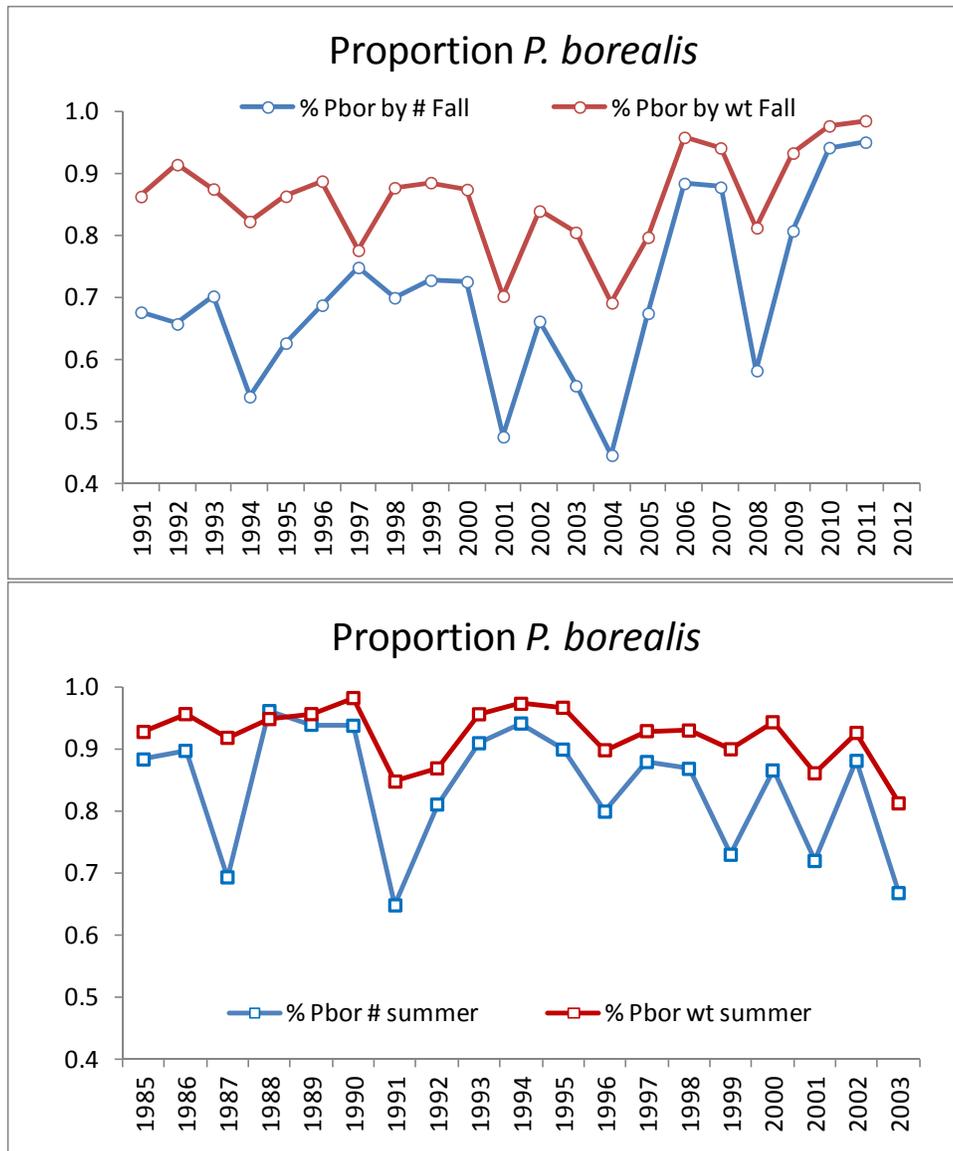
Appendix C2. Table 3. Relative importance of each predator ranked by % contribution to the PPI (A.) averaged over all years, (B.) during 1977-1993 and (C.) during 1994-2010.

A. Predator	% of PPI all years	B. Predator	% of PPI <=1993	C. Predator	% of PPI >1993
ACADIAN REDFISH	20.6%	WHITE HAKE*	23.8%	ACADIAN REDFISH	28.8%
WHITE HAKE*	17.3%	ATLANTIC COD*	19.8%	SPINY DOGFISH	26.3%
SPINY DOGFISH	15.2%	ACADIAN REDFISH	14.0%	WHITE HAKE*	9.2%
ATLANTIC COD*	15.1%	THORNY SKATE*	10.5%	ATLANTIC COD*	9.2%
SILVER HAKE*	7.5%	SILVER HAKE	7.0%	SILVER HAKE	8.2%
THORNY SKATE*	6.4%	SPINY DOGFISH	6.3%	RED HAKE*	5.7%
RED HAKE*	5.1%	POLLOCK*	5.2%	HADDOCK	2.7%
POLLOCK*	3.8%	RED HAKE*	4.7%	ATLANTIC HERRING	2.4%
HADDOCK	3.0%	HADDOCK	3.2%	POLLOCK*	2.1%
ATLANTIC HERRING	1.5%	GOOSEFISH	1.1%	THORNY SKATE*	1.3%
AMERICAN PLAICE	0.8%	AMERICAN PLAICE	1.1%	BARNDOR SKATE	0.9%
GOOSEFISH	0.8%	ATLANTIC HERRING	0.9%	LONGHORN SCULPIN*	0.8%
SMOOTH SKATE	0.7%	SMOOTH SKATE	0.7%	SMOOTH SKATE	0.6%
LONGHORN SCULPIN*	0.6%	LONGHORN SCULPIN*	0.4%	AMERICAN PLAICE	0.5%
BARNDOR SKATE	0.6%	WINTER SKATE	0.4%	GOOSEFISH	0.5%
WINTER SKATE	0.3%	BARNDOR SKATE	0.3%	WINTER SKATE	0.3%
ATLANTIC HALIBUT	0.3%	ATLANTIC HALIBUT	0.3%	ATLANTIC HALIBUT	0.2%
SEA RAVEN*	0.2%	SEA RAVEN*	0.2%	SEA RAVEN*	0.2%
LITTLE SKATE	0.1%	LITTLE SKATE	0.1%	LITTLE SKATE	0.2%
FOURSPOT FLOUNDER*	0.0%	FOURSPOT FLOUNDER*	0.0%	FOURSPOT FLOUNDER*	0.0%
WINDOWPANE*	0.0%	WINDOWPANE*	0.0%	WINDOWPANE*	0.0%

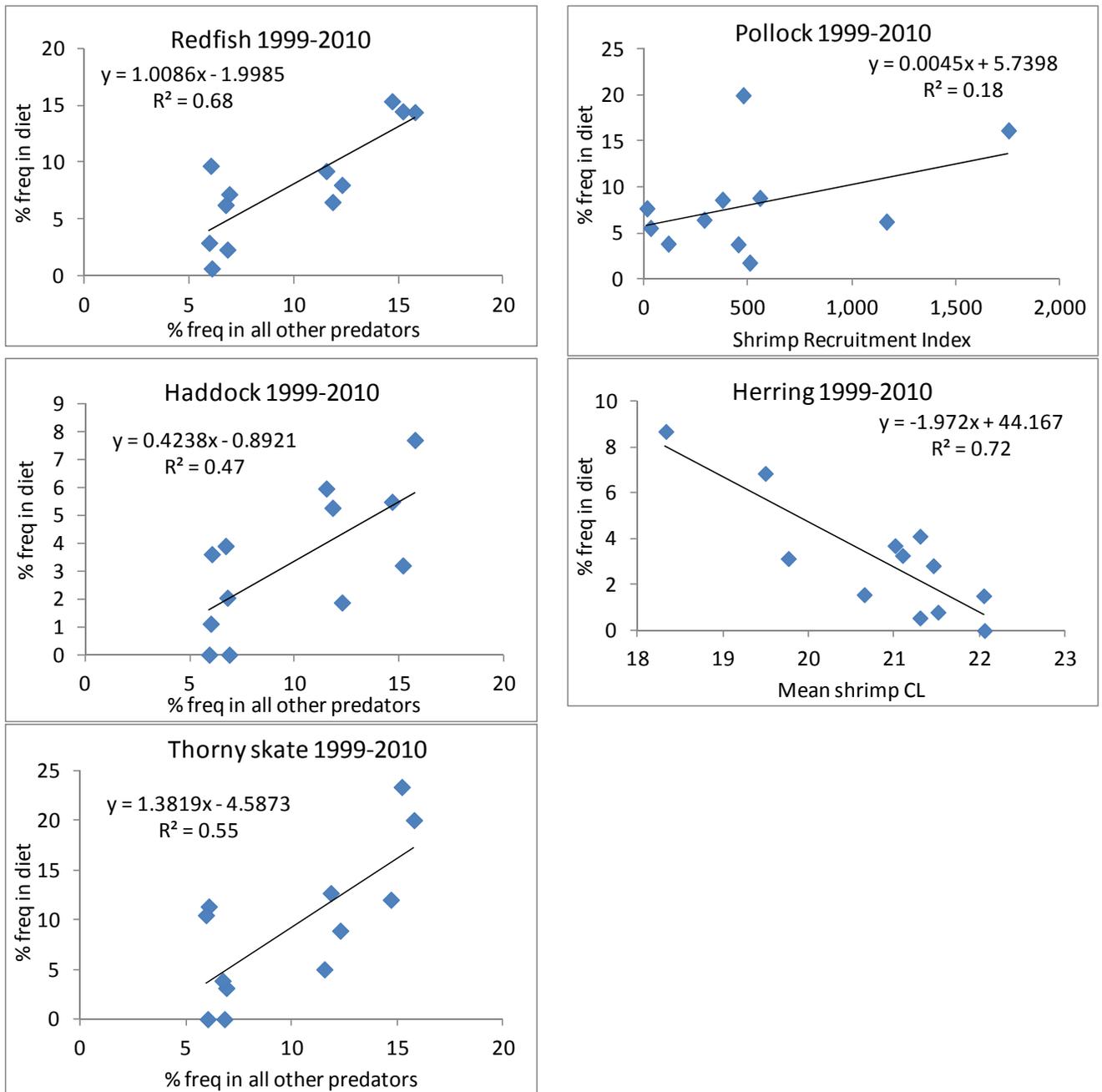
\* included in Link and Idoine (2009)

Appendix C2. Table 4. Percent frequency of occurrence of Pandalids in stomachs of predators with highest % contribution to the PPI. Shaded cells were estimated from relationships shown in Figure 2.

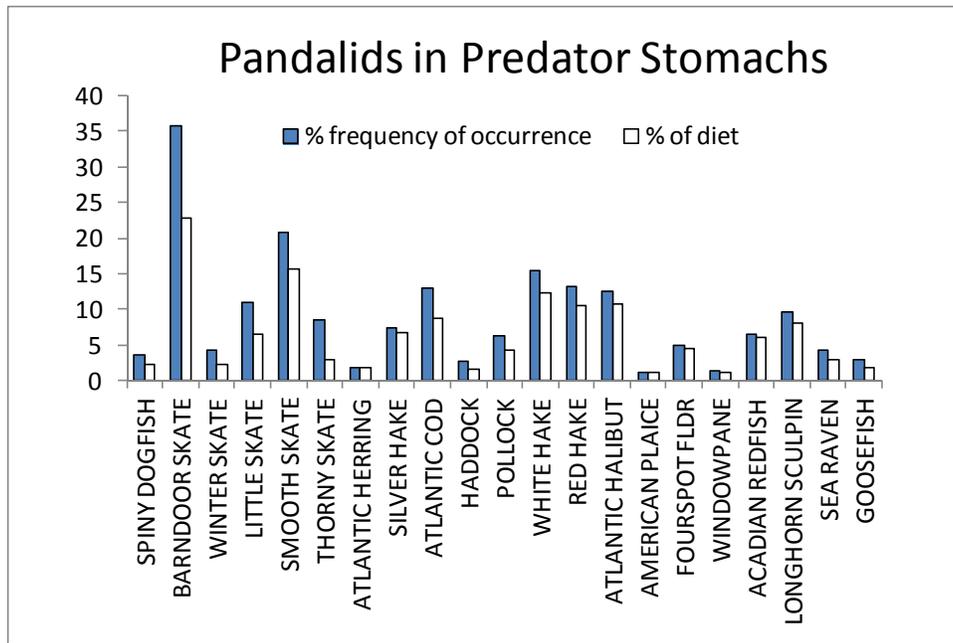
	WHITE HAKE*	RED HAKE*	SILVER HAKE*	ATLANTIC COD*	HADDOCK	POLLOCK*	ACADIAN REDFISH	ATLANTIC HERRING	THORNY SKATE*	SPINY DOGFISH
1984	8.8	4.2	0.0	9.7	0.0	5.8	0.0	1.3	0.9	0.9
1985	3.6	1.9	0.6	5.4	0.0	2.2	3.3	1.3	2.8	1.3
1986	9.0	4.4	2.2	5.6	1.7	7.4	0.0	0.0	1.1	1.6
1987	6.2	8.2	1.8	4.5	0.0	2.4	0.0	0.0	0.0	0.0
1988	13.6	12.7	5.2	2.5	2.1	2.0	0.0	1.3	4.1	1.1
1989	6.4	9.2	3.2	7.8	0.0	1.5	0.0	1.3	3.4	0.5
1990	9.6	17.2	4.3	11.3	2.9	2.6	0.0	0.0	4.5	2.5
1991	23.2	21.7	9.7	15.4	5.3	6.9	12.7	1.3	6.0	2.6
1992	14.4	19.3	5.9	14.4	3.8	2.5	9.1	1.6	8.0	1.2
1993	15.8	16.4	10.6	21.7	4.8	4.4	11.6	0.9	16.5	2.8
1994	22.4	25.0	10.7	24.4	6.6	8.3	15.9	1.0	24.1	6.1
1995	28.9	22.0	15.5	22.5	0.0	7.1	16.6	2.3	8.3	3.3
1996	19.9	12.3	6.1	19.1	4.5	6.8	10.9	3.1	2.7	6.4
1997	8.0	8.5	9.7	21.3	3.3	14.7	8.0	1.2	11.1	2.0
1998	23.0	14.4	11.6	13.3	4.1	13.8	11.6	0.7	15.4	5.1
1999	23.0	18.6	11.5	16.0	3.2	3.8	14.5	0.5	23.3	7.0
2000	18.1	12.3	9.9	16.2	1.9	3.8	8.0	3.1	8.9	5.0
2001	4.5	6.2	11.0	12.4	0.0	5.8	7.2	0.8	3.1	0.5
2002	7.1	5.8	6.6	7.7	1.1	6.3	9.7	8.7	0.0	3.0
2003	8.7	1.1	7.2	7.3	3.6	7.7	0.7	3.3	11.3	6.1
2004	21.3	10.9	9.9	10.6	6.0	6.5	9.2	2.8	5.0	5.1
2005	20.7	16.7	11.1	11.7	7.7	16.2	14.4	6.9	20.0	18.8
2006	27.2	12.6	7.0	17.2	5.5	8.6	15.3	3.7	12.0	9.5
2007	13.2	2.9	2.5	12.9	3.9	5.6	6.3	1.5	3.8	2.3
2008	11.8	7.3	5.1	5.8	2.0	1.8	2.3	0.0	0.0	4.1
2009	15.5	14.7	8.5	13.0	5.3	8.8	6.5	4.1	12.7	7.5
2010	5.5	6.1	5.7	5.5	0.0	20.0	2.9	1.6	10.4	7.0
2011	9.8	7.0	3.4	12.5	0.0	6.7	1.0	0.6	6.7	4.4
2012	5.6	5.3	4.2	3.6	0.7	4.3	1.3	0.5	3.6	3.2



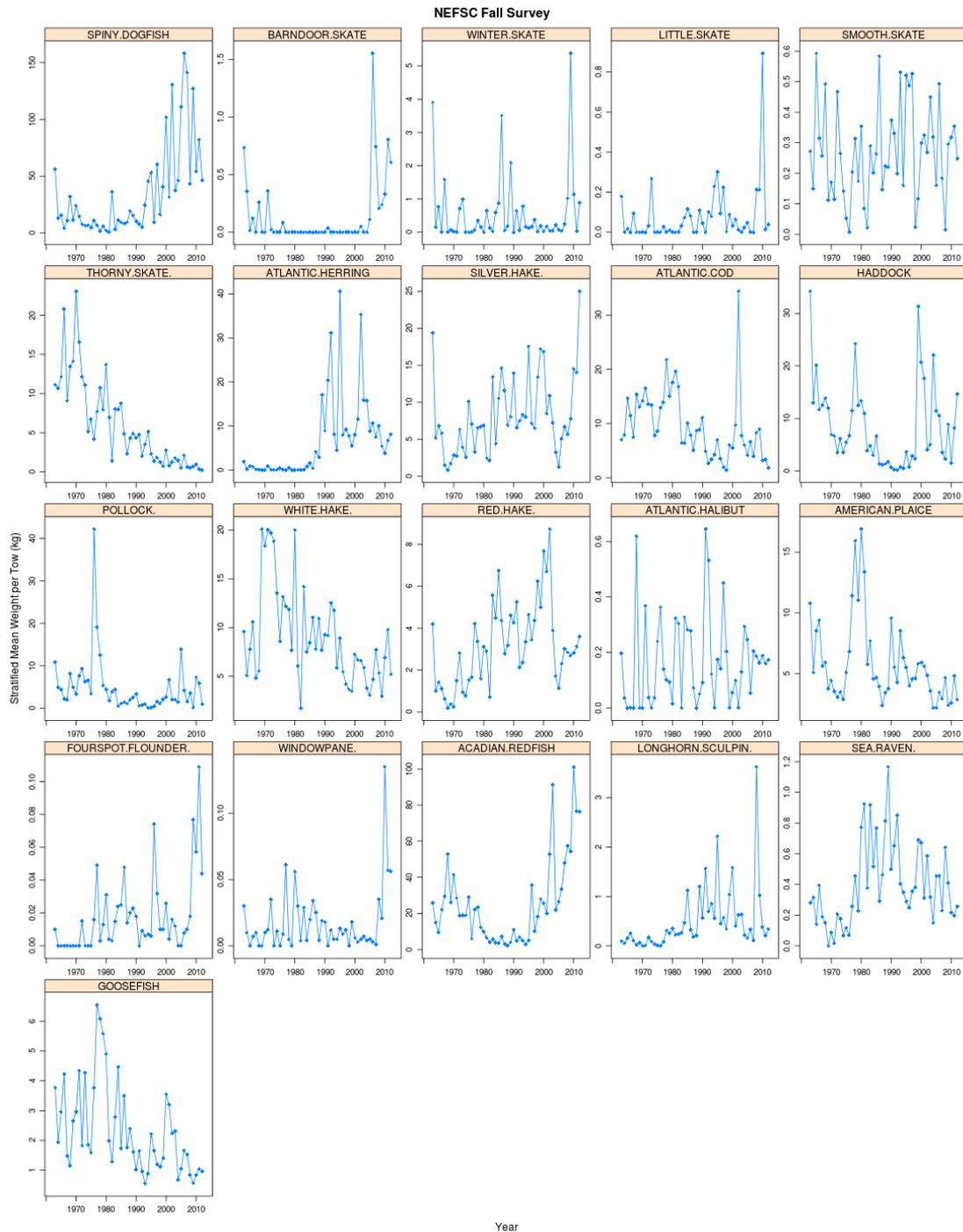
Appendix C2. Figure 1. Proportion of *P. borealis* in surveys (of total Pandalids not including *P. propinquus*), top panel fall survey; bottom panel summer shrimp survey.



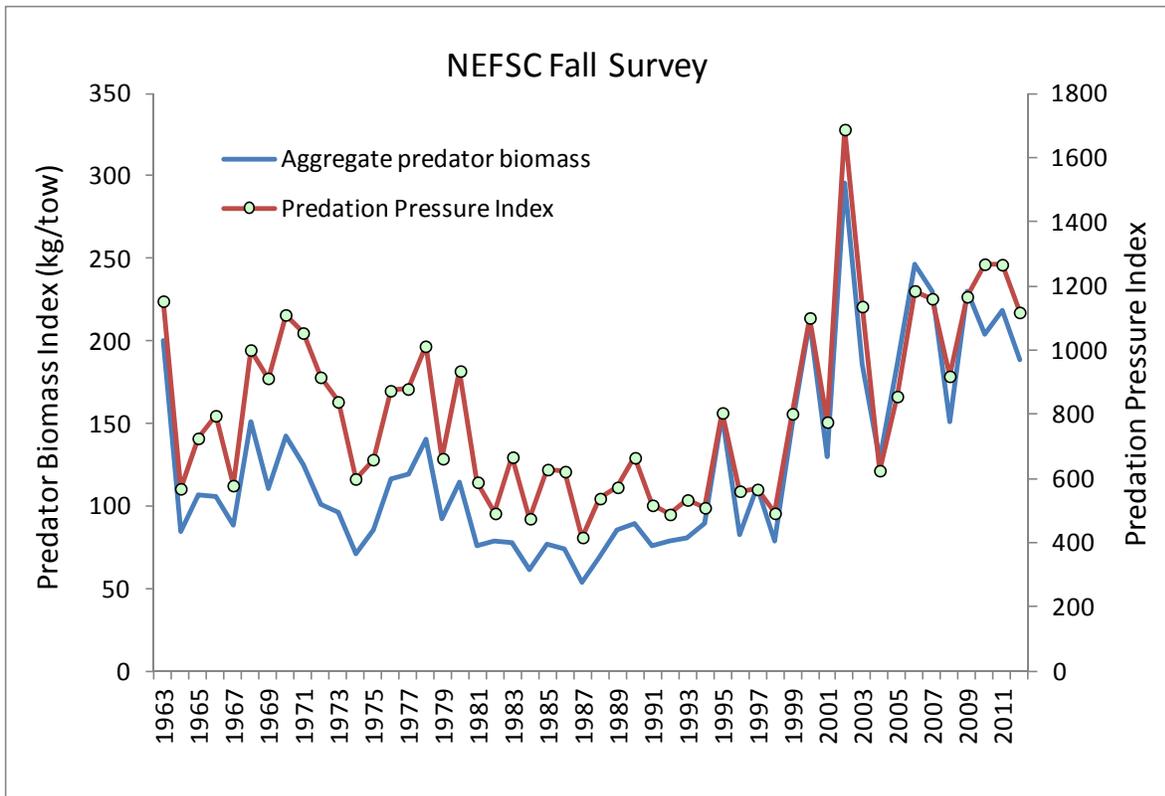
Appendix C2. Figure 2. Relationships used to fill gaps in annual % frequency in diet for predators with missing data during 1984-1998. X-axis labeled “% freq in all other predators” indicates predators with complete time series starting in 1984. CL carapace length.



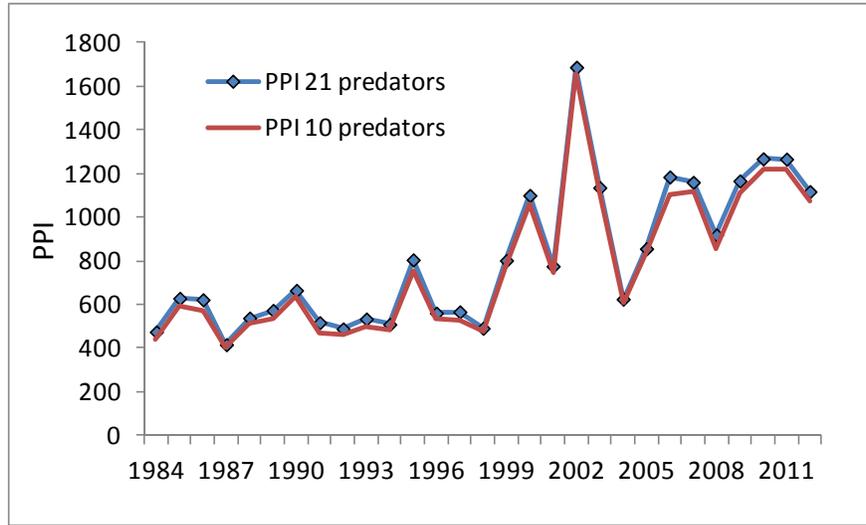
Appendix C2. Figure 3. Overall frequency of occurrence of Pandalids in predator stomachs and percent by volume of Pandalids in stomachs containing Pandalids (unweighted estimate), 1973-2011 spring and fall NEFSC surveys. 2011 data incomplete for some species.



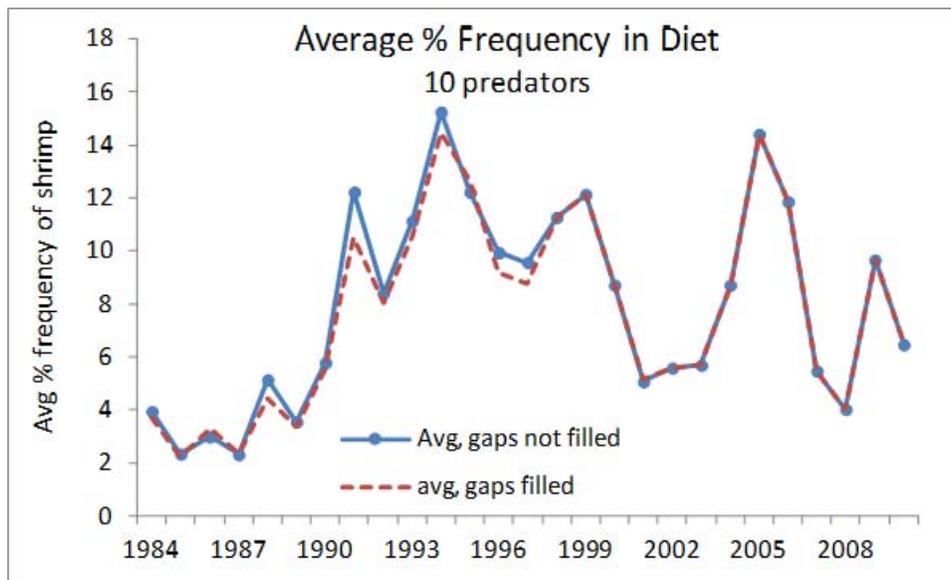
Appendix C2. Figure 4. Biomass indices (stratified mean kg per tow) for 21 predators of Pandalids in the western Gulf of Maine from NEFSC fall bottom trawl surveys. Indices for years after 2008 were adjusted for change in survey methods in 2009.



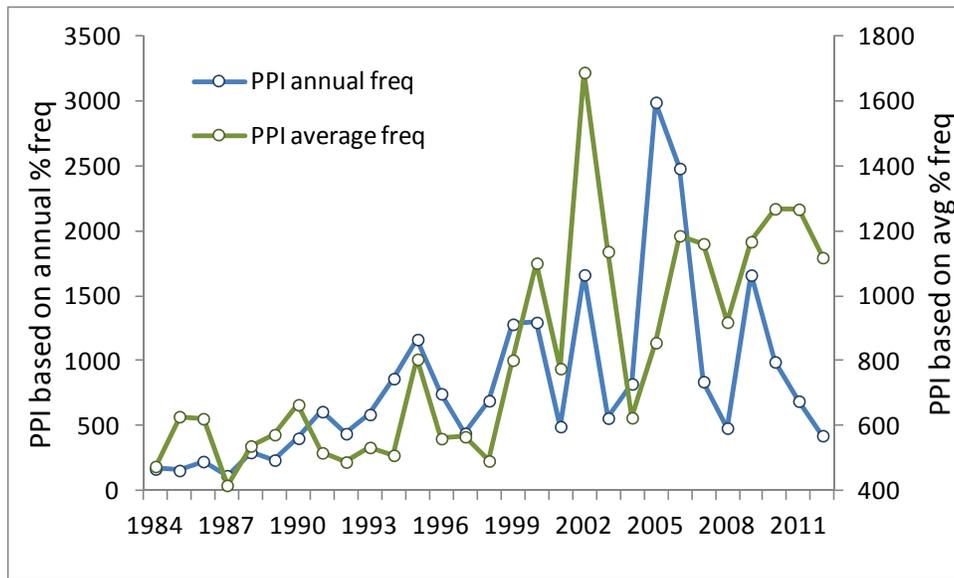
Appendix C2. Figure 5. Aggregate predator biomass indices from NEFSC fall survey (stratified mean kg per tow in shrimp assessment strata) and PPI, 1963-2012.



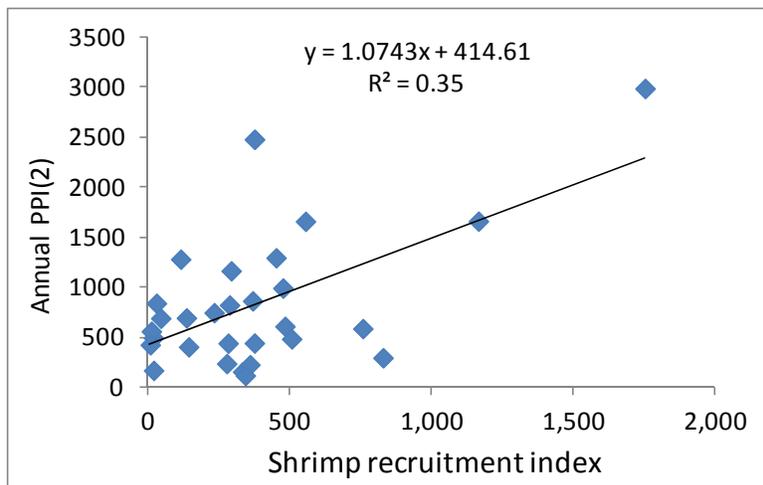
Appendix C2. Figure 6. PPI estimated from 21 species of predators vs. 10 predators that were most influential.



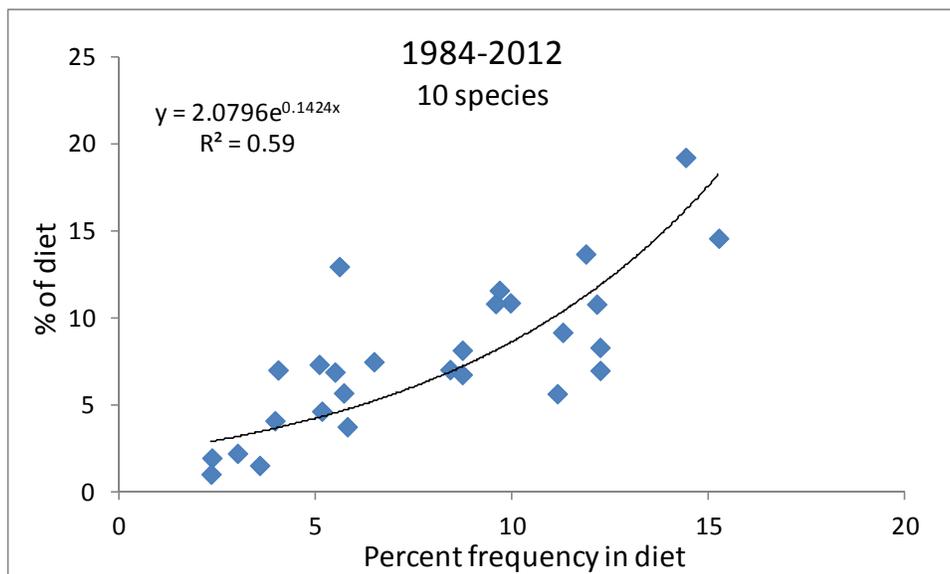
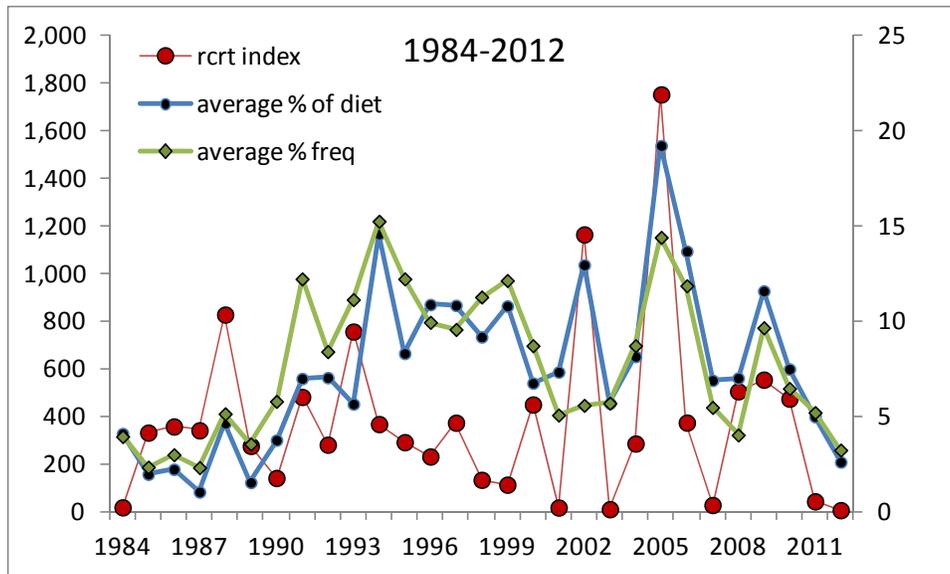
Appendix C2. Figure 7. Average annual % frequency of shrimp in diets of 10 predators with and without missing data filled in for some predators in some years.



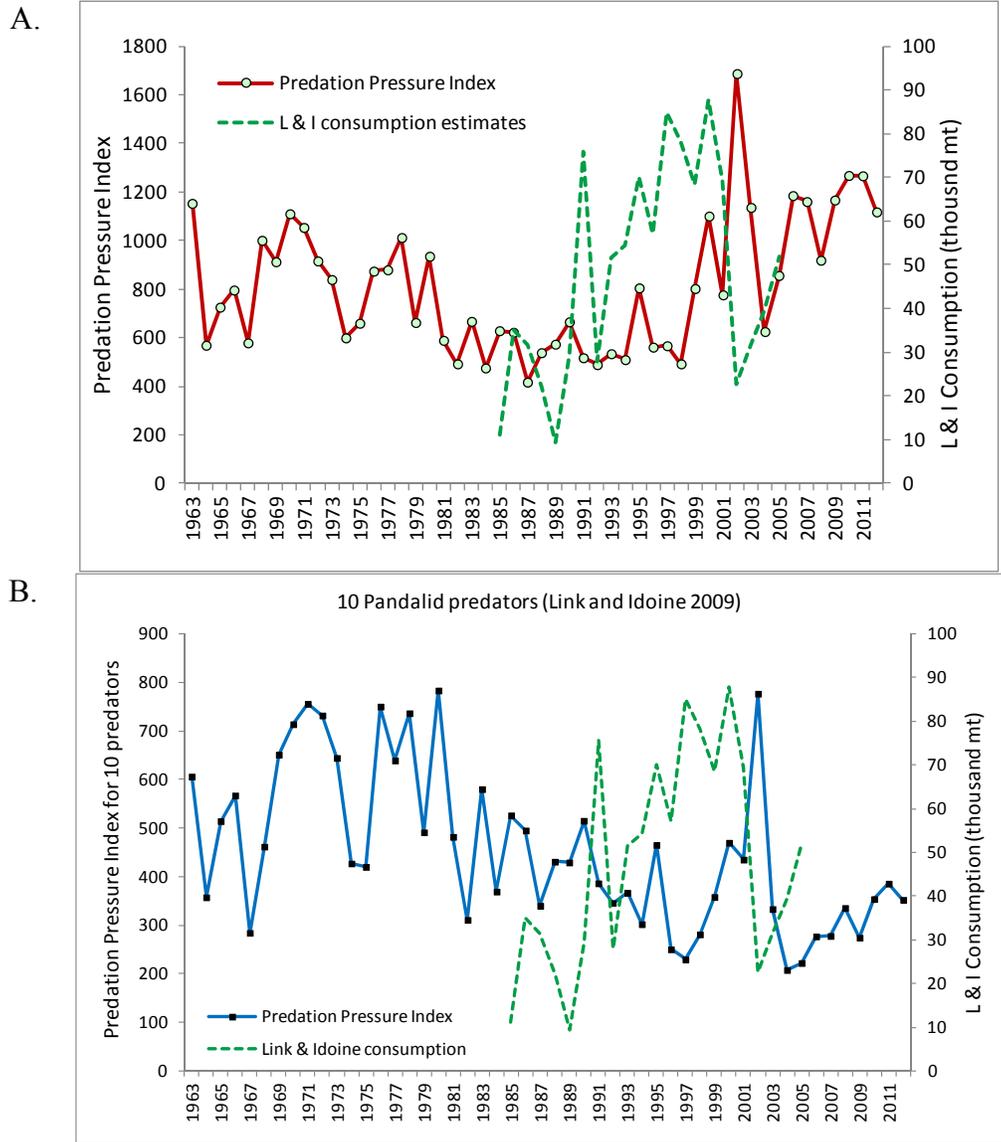
Appendix C2. Figure 8. Comparison of PPI calculated using average % frequency of Pandalids in diet for each predator (averaged over time) vs. using annual % frequency of Pandalids in diet for each predator.



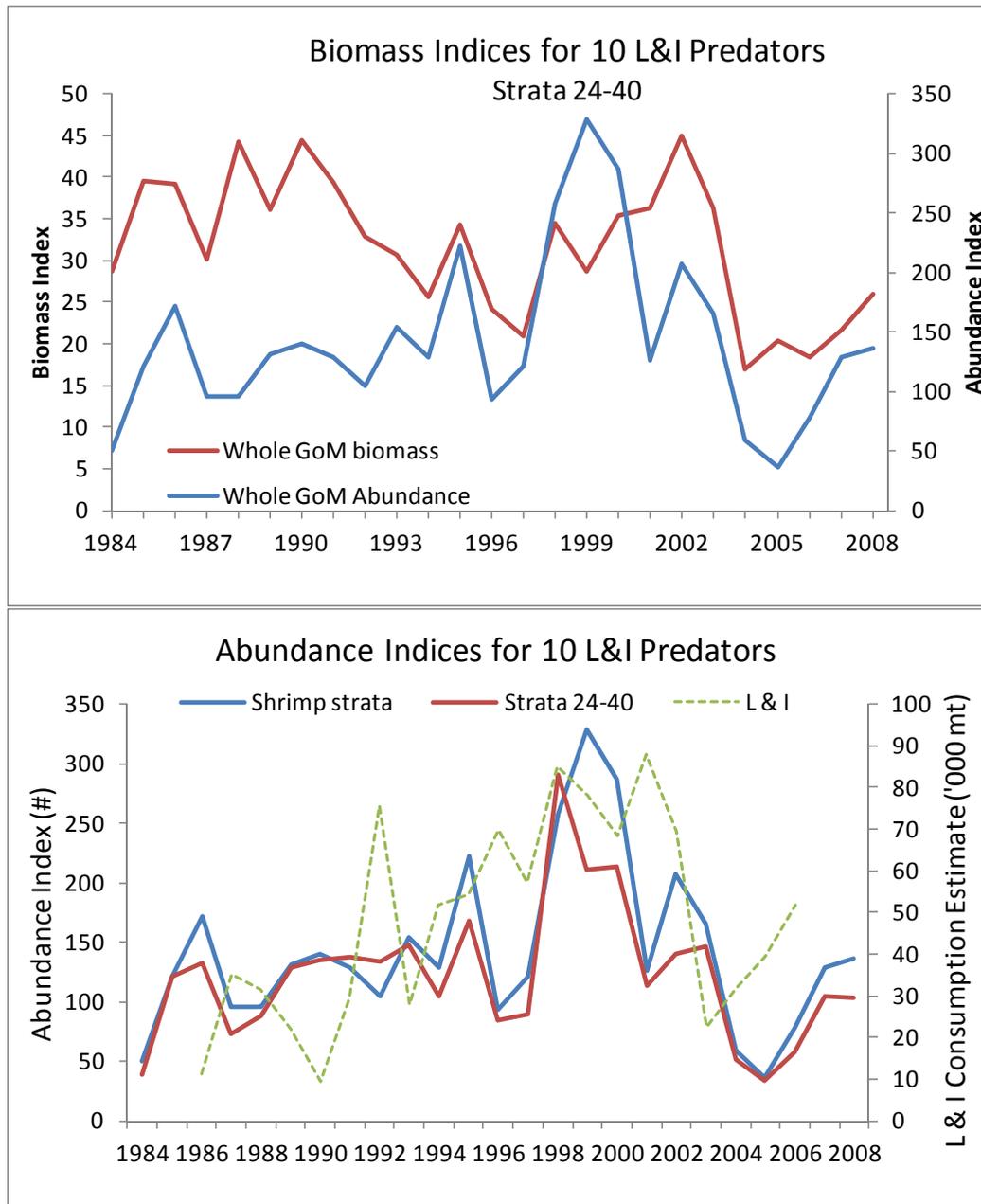
Appendix C2. Figure 9. Relationship between PPI(2) (annual % frequency) and shrimp recruitment index from summer shrimp surveys.



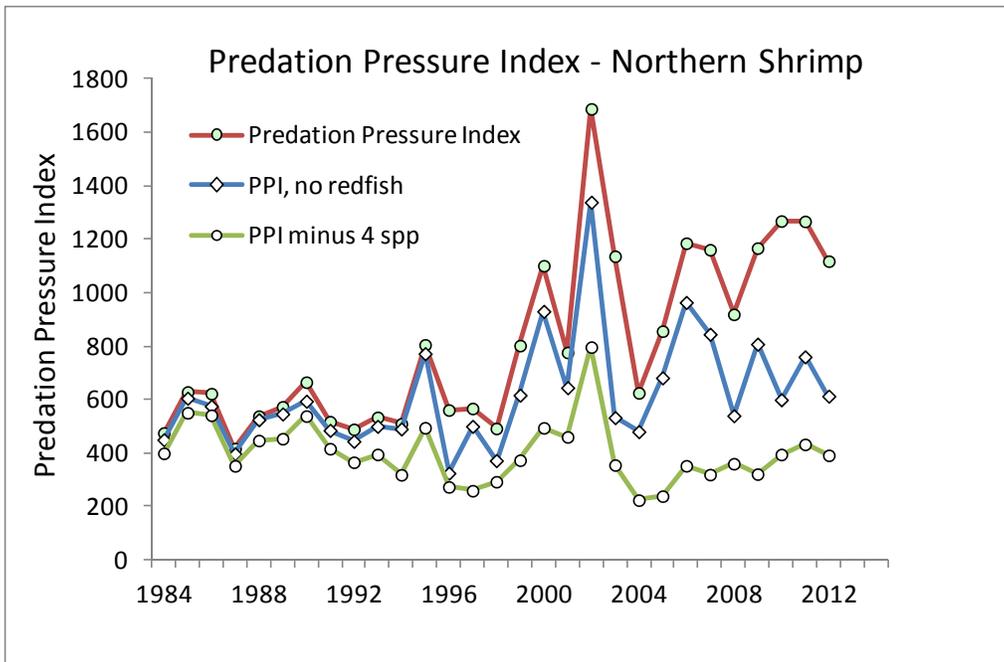
Appendix C2. Figure 10. Top: time series of recruitment indices from summer shrimp survey, % frequency of Pandalids in diet of top 10 predators, and % by volume of Pandalids in diet (unweighted). Bottom: relation between % frequency of Pandalids in diet and % by volume of Pandalids in diet.



Appendix C2. Figure 11. Comparison of predation pressure index (PPI) based on fall survey biomass indices with estimates of *P. borealis* consumption from Link and Idoine (2009) (L&I). ( A.) PPI using 21 identified predators vs. consumption based on 10 predators estimated by L&I; (B.) PPI using only the 10 species identified by L&I vs. consumptions estimates.



Appendix C2. Figure 12. (A) Biomass and abundance for 10 L&I predators for entire Gulf of Maine; (B) abundance indices of the 10 L&I predators for the western Gulf of Maine shrimp assessment strata and the entire Gulf of Maine (strata 01240-01400), with L&I consumption estimates overlaid.



Appendix C2. Figure 13. PPI vs. PPI with redfish not included, and PPI without redfish, dogfish, herring and haddock.

### Appendix C3. Technical documentation for Collie-Sissenwine Analysis (CSM, Version 4) stock assessment model

CSA is a relatively simple two-bin stock assessment model that estimates abundance, fishing mortality and recruitment using total catch numbers and survey data (Collie and Sissenwine 1983; Conser 1995). The “recruit” group in the model consists of animals that will recruit at or during the current time step. The “post-recruit” group contains all older individuals. Typically, both groups are assumed fully available to the fishery but this assumption can be relaxed in practice if fishing mortality rates are viewed as rates for fully recruited animals.

CSA (Version 4) used in this assessment was completely reprogrammed in AD-Model Builder during 2013 and is available with a graphical user interface in the NOAA Fisheries Toolbox at <http://nft.nefsc.noaa.gov/>. The update uses maximum likelihood rather than weighted sums of squares to estimate parameters. Multiple survey indices of two types can be used and the user must supply survey and year specific CVs that measure the precision of survey and catch observations. Pope’s approximation is no longer used to simulate the population because accuracy of the approximation degrades at high mortality rates and because Baranov’s catch equation (which assumes continuous fishing) works well for pulse fisheries in most cases. As in previous versions, natural mortality in each year is specified by the user and not estimable in the model. The updated model does not allow for process errors because their original formulation was problematic and did not improve model performance, they can be difficult to estimate objectively, and because they are no longer required with high fishing mortality rates to avoid negative abundance estimates and numerical problems (Mesnil 2003 and p. 39 in ASMFC 2006).

#### Population dynamics

Abundance in each year  $N_y$  is:

$$N_y = P_y + R_y$$

where  $R_y$  is the number of new recruits to the model in year  $y$  and  $P_y$  is the abundance of all older individuals. Post-recruits are related to total abundance in the previous year:

$$P_y = N_{y-1}e^{-Z_{y-1}}$$

where  $Z_y = F_y + M_y$  is the instantaneous annual rate for total mortality, and  $F_y$  and  $M_y$  are instantaneous annual rates for fishing and natural mortality. Stock biomass is calculated:

$$B_y = N_y b_y$$

where  $b_y$  is a mean weight per individual.

Post-recruits in the first year, recruitments and fishing mortality rates are parameters that can be estimated in the model. Natural mortality rates and mean weights are specified by the user and may change over time.

## Observations

Predicted catch in number is calculated:

$$\hat{C}_y = \frac{F_y}{Z_y} N_y (1 - e^{-Z_y})$$

Catch weight is:

$$W_y = \hat{C}_y w_y$$

where  $w_y$  is the mean weight of individuals in the catch as specified by the user.

There are two types of surveys in the model. A “recruit/post-recruit” survey involves paired indices (one for recruits and the other for post-recruits) derived from the same survey. “Aggregate” surveys involve a single index (for recruits plus post-recruits, recruits only or post-recruits only, but see below in the latter case) from each survey. Recruit/post-recruit surveys involve an assumption about catchability of recruits relative to post-recruits. The aggregate approach is the same as used in most other stock assessment models but using a single selectivity parameter for recruits that can be estimated in the model (the selectivity of post-recruits is assumed equal to one and recruit selectivity can be larger or smaller).<sup>1</sup> Multiple surveys of either type can be used in the same model run. It is probably better, however, to use only one recruit/post-recruit pair at a time because relative catchability assumptions have a very strong effect on model estimates. Relative catchability assumptions for multiple surveys may conflict and cause serious problems with model fit.

Recruit/post-recruit survey data are pairs of survey indices and are derived from a single survey. Post-recruit indices are predicted:

$$\hat{p}_y = q_p P_y$$

where  $q_p$  is a catchability coefficient. Recruit indices are predicted:

$$\hat{r}_y = s_p q_p R_y$$

where  $s_p$  is a relative catchability parameter for recruits relative to post-recruits. Relative catchability is specified by the user while the catchability for post-recruits  $q_p$  is a parameter that can be estimated in the model.

Aggregate surveys are predicted:

$$\hat{u}_y = Q(gR_y + P_f)$$

where  $g$  and  $Q$  are selectivity and catchability parameters that can be estimated in the model.

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<sup>1</sup> To implement an aggregate survey for post-recruits only, set the recruit selectivity parameter to zero. To implement an aggregate survey for recruits only, fix or estimate the recruit selectivity parameter to be a value much larger than one.

## Goodness of fit

Parameters are estimated to minimize the negative log likelihood of the data. The negative log likelihood used to measure goodness of fit to the catch data assumes that measurement errors are log normal :

$$\mathcal{L} = \sum_y \left\{ \ln(s) + 0.5 \left[ \frac{\ln(C_y) - \ln(\hat{C}_y)}{s} \right]^2 \right\}$$

where  $s$  is a log scale standard deviation based on an assumed CV measurement errors in the catch data that are supplied by the user:

$$s = \sqrt{\ln(CV^2 + 1)}$$

The negative log likelihood for goodness of fit to a survey index also assumes log normal errors but the standard deviation may vary from year to year and among surveys. Using an aggregate survey as an example:

$$\mathcal{L} = \sum_y \left\{ \ln s_y + 0.5 \left[ \frac{\ln(u_y) - \ln(\hat{u}_y)}{s_y} \right]^2 \right\}$$

The annual variances are calculated from CVs for measurement errors in each survey observation that are supplied by the user.

The total negative log likelihood used to estimate parameters is:

$$\mathcal{L}_{total} = \sum_j \omega_j \mathcal{L}_j$$

where the  $\omega_j$  are user specified weights for each type of data in the model. The user specified weights are normally one except during sensitivity or other types of diagnostic analyses.

The user can “tune” variances used in goodness of fit calculations by adjusting the assumed CVs. In particular, the assumed CVs may be adjusted over the course of several runs until the implied CV based on residuals approximately matches the assumed value:

$$CV_{implied} = \sqrt{e^{s^2} - 1}$$

and  $s^2$  is the variance of the log scale residuals.

Variances for model parameters and other model estimates can be calculated in CSA by asymptotic approximation or MCMC analysis. The software produces a comma delimited database file containing data, estimates and diagnostics as well as a separate output file for likelihood profile analysis. The NOAA Fisheries Tool Box GUI produces a number of useful

graphics and diagnostics. An R program that creates graphics and additional diagnostics is also available on the Tool Box website.

### References

Atlantic States Marine Fisheries Commission. 2000. American lobster stock assessment report for peer review. Stock Asses. Rep. No. 00-01 (Supplement). Atlantic States Marine Fisheries Commission, Washington, DC

Atlantic States Marine Fisheries Commission. 2006. American lobster stock assessment report for peer review. Stock Assessment Report No. 06-03 (Supplement). Atlantic States Marine Fisheries Commission, Washington, DC. 366p.

Collie, J. S. and Sissenwine, M.P. 1983. Estimating population size from relative abundance data measured with error. Can. J. Fish. Aquat. Sci. 40:1871-1879.

Conser, R.J. 1995. A modified DeLury modeling framework for data limited assessment: bridging the gap between surplus production models and age-structured models. A working paper for the ICES Working Group on Methods of Fish Stock Assessment. Copenhagen, Denmark.

## Appendix C4. Parameter estimates from CSA final model.

index	name	value	std.dev	index	name	value	std.dev	index	name	value	std.dev	index	name	value	std.dev
1	logrhat	6.91	0.33	61	logqhat	-0.6304	0.1614	121	f_calc	0.11	0.02	181	totnum	2213.8	537.5
2	logrhat	7.06	0.28	62	logqhat	-1.9209	0.2062	122	f_calc	0.33	0.08	182	totnum	5695.7	1174.0
3	logrhat	6.77	0.30	63	logqhat	0.0540	0.3174	123	f_calc	0.49	0.11	183	totnum	9145.7	1772.6
4	logrhat	6.56	0.29	64	logphat1	6.8974	0.4082	124	f_calc	0.55	0.18	184	totnum	4647.5	946.6
5	logrhat	6.79	0.31	65	logsrx[2]	0.0000	0.0002	125	f_calc	0.13	0.05	185	totnum	2880.1	623.1
6	logrhat	7.05	0.24	66	logsrx[3]	-6.9077	0.1925	126	f_calc	0.00	0.00	186	totnum	2552.4	546.4
7	logrhat	6.66	0.25	67	rhat	998.0	328.8	127	qhat	0.53	0.09	187	totnum	2183.4	387.0
8	logrhat	6.33	0.26	68	rhat	1166.9	332.0	128	qhat	0.15	0.03	188	totnum	885.9	219.3
9	logrhat	6.25	0.26	69	rhat	873.8	266.3	129	qhat	1.06	0.33	189	totnum	315.9	112.9
10	logrhat	6.76	0.30	70	rhat	705.9	206.1	130	phat	989.68	403.97	190	totnum	153.4	58.5
11	logrhat	6.95	0.29	71	rhat	887.2	272.8	131	phat	1177.70	342.27	191	totbio	14.47	3.49
12	logrhat	6.92	0.25	72	rhat	1148.7	270.0	132	phat	1289.30	334.76	192	totbio	19.82	4.21
13	logrhat	6.49	0.29	73	rhat	778.0	196.9	133	phat	1126.60	305.96	193	totbio	19.56	4.12
14	logrhat	6.75	0.36	74	rhat	560.3	147.7	134	phat	1223.30	320.03	194	totbio	16.66	3.83
15	logrhat	6.75	0.34	75	rhat	518.2	136.9	135	phat	1264.90	319.52	195	totbio	14.84	3.20
16	logrhat	5.76	0.32	76	rhat	864.5	261.3	136	phat	1330.60	332.97	196	totbio	18.37	3.67
17	logrhat	6.46	0.34	77	rhat	1042.0	299.5	137	phat	1127.90	293.97	197	totbio	19.86	4.23
18	logrhat	6.01	0.37	78	rhat	1016.9	254.8	138	phat	999.42	275.46	198	totbio	16.10	3.74
19	logrhat	7.08	0.28	79	rhat	657.9	190.0	139	phat	962.49	266.14	199	totbio	13.65	3.34
20	logrhat	6.65	0.42	80	rhat	855.3	304.5	140	phat	1092.60	295.76	200	totbio	11.98	2.74
21	logrhat	7.45	0.29	81	rhat	853.5	289.7	141	phat	1031.50	288.23	201	totbio	15.12	2.85
22	logrhat	8.39	0.23	82	rhat	317.0	101.7	142	phat	600.48	220.71	202	totbio	16.69	3.15
23	logrhat	8.69	0.22	83	rhat	640.8	220.4	143	phat	312.69	151.93	203	totbio	10.22	2.01
24	logrhat	6.43	0.39	84	rhat	407.6	149.0	144	phat	525.85	235.60	204	totbio	7.54	2.14
25	logrhat	6.85	0.29	85	rhat	1183.2	330.7	145	phat	841.41	221.47	205	totbio	9.62	2.13
26	logrhat	6.99	0.28	86	rhat	769.1	324.5	146	phat	507.00	155.61	206	totbio	9.93	2.26
27	logrhat	7.16	0.21	87	rhat	1721.9	505.7	147	phat	483.17	146.02	207	totbio	8.22	2.02
28	logrhat	5.61	0.41	88	rhat	4386.8	1007.8	148	phat	515.08	135.05	208	totbio	6.73	1.64
29	logrhat	4.40	0.39	89	rhat	5943.9	1335.3	149	phat	526.59	140.54	209	totbio	9.17	2.07
30	logrhat	2.65	0.46	90	rhat	620.7	243.2	150	phat	491.95	179.47	210	totbio	9.01	2.43
31	logf_calc	-1.47	0.26	91	rhat	944.3	274.6	151	phat	1308.90	364.90	211	totbio	16.62	3.91
32	logf_calc	-1.56	0.24	92	rhat	1084.6	300.9	152	phat	3201.80	691.58	212	totbio	34.65	7.01
33	logf_calc	-1.32	0.24	93	rhat	1286.9	274.1	153	phat	4026.70	851.99	213	totbio	63.30	12.11
34	logf_calc	-1.92	0.25	94	rhat	274.2	113.3	154	phat	1935.80	461.58	214	totbio	39.53	8.07
35	logf_calc	-1.72	0.24	95	rhat	81.7	32.0	155	phat	1467.80	353.04	215	totbio	26.06	5.67
36	logf_calc	-1.42	0.23	96	rhat	14.2	6.5	156	phat	896.52	264.28	216	totbio	22.26	4.78
37	logf_calc	-1.54	0.24	97	f_calc	0.23	0.06	157	phat	611.77	173.23	217	totbio	15.80	2.95
38	logf_calc	-1.59	0.25	98	f_calc	0.21	0.05	158	phat	234.16	98.54	218	totbio	6.81	1.69
39	logf_calc	-1.88	0.26	99	f_calc	0.27	0.06	159	phat	139.24	56.51	219	totbio	2.92	1.07
40	logf_calc	-1.69	0.25	100	f_calc	0.15	0.04	160	phat	76.89	29.34	220	totbio		
41	logf_calc	-0.89	0.23	101	f_calc	0.18	0.04	161	totnum	1987.7	459.9				
42	logf_calc	-0.32	0.26	102	f_calc	0.24	0.05	162	totnum	2344.7	494.3				
43	logf_calc	0.04	0.30	103	f_calc	0.21	0.05	163	totnum	2163.1	450.3				
44	logf_calc	-0.80	0.36	104	f_calc	0.20	0.05	164	totnum	1832.5	414.2				
45	logf_calc	-1.66	0.24	105	f_calc	0.15	0.04	165	totnum	2110.5	446.0				
46	logf_calc	-1.11	0.26	106	f_calc	0.18	0.05	166	totnum	2413.6	475.2				
47	logf_calc	-1.69	0.28	107	f_calc	0.41	0.10	167	totnum	2108.6	443.9				
48	logf_calc	-2.69	0.26	108	f_calc	0.73	0.19	168	totnum	1688.1	379.4				
49	logf_calc	-2.06	0.25	109	f_calc	1.05	0.31	169	totnum	1517.6	360.1				
50	logf_calc	-1.32	0.32	110	f_calc	0.45	0.16	170	totnum	1827.0	411.7				
51	logf_calc	-1.97	0.26	111	f_calc	0.19	0.05	171	totnum	2134.6	397.6				
52	logf_calc	-3.06	0.22	112	f_calc	0.33	0.09	172	totnum	2048.4	373.1				
53	logf_calc	-2.43	0.21	113	f_calc	0.18	0.05	173	totnum	1258.3	224.7				
54	logf_calc	-1.84	0.22	114	f_calc	0.07	0.02	174	totnum	1168.0	336.6				
55	logf_calc	-2.24	0.23	115	f_calc	0.13	0.03	175	totnum	1379.4	300.5				
56	logf_calc	-1.12	0.25	116	f_calc	0.27	0.09	176	totnum	1158.4	256.6				
57	logf_calc	-0.72	0.22	117	f_calc	0.14	0.04	177	totnum	1147.8	288.8				
58	logf_calc	-0.60	0.32	118	f_calc	0.05	0.01	178	totnum	890.8	218.2				
59	logf_calc	-2.05	0.38	119	f_calc	0.09	0.02	179	totnum	1698.3	399.3				
60	logf_calc	-16.22	0.38	120	f_calc	0.16	0.04	180	totnum	1295.7	363.8				

## **Appendix C5. Changes to Gulf of Maine Northern Shrimp Data Since the 2007 SAW**

Landings data from the NMFS landings database (derived from dealer reports) were queried in 2009 (and again in 2012 without change), and the northern shrimp landings for 1958 through 1999 were updated for the 2013 assessment. See Appendix C5 Table 1 for a comparison. Most changes were small, with a mix of additions and reductions. The greatest change was the addition of 373 mt to the 1996 landings.

Landings data for 2000 through 2006 were queried from the federal and Maine state harvester report data in 2011, and are compared with data from the 2007 SAW in Appendix C5 Table 1. All data differences were additions, with the greatest being the addition of 465 mt in 2000 (which had previously been based on the dealer database) and an additional 446 mt in 2006 (the terminal year at the time of the 2007 SAW), probably due to the receipt of additional, late 2006 harvester reports.

The numbers of vessels in the fishery for recent years (since 1997) was also reported in the 2007 SAW report. In 2011, corrections were made to these data. 1997 through 1999 were compared with the data reported in the 1997 through 1999 NSTC stock assessment reports and one minor modification was made. For 2000 through 2006, the vessel counts were re-calculated from the harvester report database. The most notable differences were for 2003, in which the number of vessels had been over-reported by about 12% in the earlier report, possibly because of double counting of vessels that were in both the federal and Maine state databases, and for 2006, the terminal year for the 2007 report, in which vessels were under-reported by about 17%, probably because of late harvester reporting (Appendix C5 Table 2).

The numbers of trips in the fishery were also re-calculated for 2000 through 2006. In the 2007 report, trap trips for 2000-2006 had not been included, so the total number of trips increased about 15% to 30%. The total trips for 1987 were also adjusted to include a few out-of-season experimental trips, to be consistent with other years (Appendix C5 Table 3).

During 2013, the NSTC reviewed all the port sample data from 1985 through 2012, in an effort to standardize and computerize all data, particularly for Maine, by reviewing raw data sheets and older databases. Data for samples that had not been computerized were found and added, and others were corrected. A few samples that were found to be incomplete in the databases (some lengths missing or the catch or sample weights missing) and for which no raw data sheets could be found were eliminated. The biggest change was the addition of several samples for 1993, which resulted in a 10% increase in the number of shrimp measured for that year (Appendix C5 Table 4).

The NSTC also reviewed and changed the way the port sample data were expanded to landings to estimate the total number of shrimp in catches. In the past, all the samples for each state-month-gear were pooled, and the average weight of a shrimp was calculated by dividing the total weight of the samples by the total number of northern shrimp in those samples, for each state, month, and gear. Then the landings for that state-month-gear were divided by the average weight of one shrimp, to estimate the total number of shrimp in the landings, for each season. In 2013, the NSTC recalculated these estimates for 1985-2013, by first expanding each sample to that sample's catch weight before pooling by state, month and gear. This resulted in larger catches being more heavily weighted in the calculation. This had a relatively small effect,

without trend, on the calculation of the mean weight of a shrimp, however. The greatest change was a 6% increase in the mean weight in 1999. (Appendix C5 Table 5).

The changes noted above to the landings data, corrections to the port sample data, and the re-weighting of the sample data, all resulted in changes to the estimated number of shrimp in the landings, used in the CSA model input. Most notable were increases in the 2000-2006 estimates, closely aligned with the increases in reported landings described above, with the largest increase of 19% in 2006 (the terminal year) (Appendix C5 Table 6).

Maine pounds per hour towing data from port interviews were unchanged, except that the 1999 value was corrected from 152 lbs/hr to 147 lbs/hr because of the addition of data for 27 more interviews.

Pounds per trip changed somewhat because of the changes to the total landings and the number of trips described above. Pounds per trip generally declined for 2000-2006 in the 2013 assessment because of the inclusion of trap trips, which usually have a lower mean catch rate per trip than trawl trips (Appendix C5 Table 7).

Minor corrections were made to the ASMFC summer survey data. For the 1985 survey, the retransformed age 1.5 number per tow was corrected from 337 to 332, the >22mm number per tow from 1,184 to 1,169, and the total number per tow from 1,849 to 1,825. For the 2006 survey, the retransformed age 1.5 number per tow was corrected from 423 to 374, the >22mm number per tow from 2,703 to 2,773, and the total number per tow from 9,996 to 9,998.

Appendix C5. Table 1. Northern shrimp landings data (mt) as reported in the 2007 SAW report compared with the 2013 assessment.

	2013		2007 SAW		Difference (mt)	% of 2013
	annual	seasonal	annual	seasonal		
1958	2.2		2.3		-0.1	-4.5%
1959	7.8		7.7		0.1	1.3%
1960	40.9		40.9		0.0	0.0%
1961	30.8		30.9		-0.1	-0.3%
1962	175.7		176.0		-0.3	-0.2%
1963	254.7		254.4		0.3	0.1%
1964	422.5		422.5		0.0	0.0%
1965	949.3		955.0		-5.7	-0.6%
1966	1,766.4		1,766.4		0.0	0.0%
1967	3,171.2		3,171.1		0.1	0.0%
1968	6,610.2		6,610.0		0.2	0.0%
1969	12,824.3		12,823.9		0.4	0.0%
1970	10,669.5		10,669.3		0.2	0.0%
1971	11,129.6		11,129.3		0.3	0.0%
1972	11,095.0		11,094.9		0.1	0.0%
1973	9,404.7		9,404.8		-0.1	0.0%
1974	7,944.7		7,944.7		0.0	0.0%
1975	5,286.6		5,286.7		-0.1	0.0%
1976	1,022.4		1,022.3		0.1	0.0%
1977	381.2		387.2		-6.0	-1.6%
1978	3.3		0.0		3.3	100.0%
1979	438.7		486.5		-47.8	-10.9%
1980	332.8		339.1		-6.3	-1.9%
1981	1,073.9		1,071.2		2.7	0.3%
1982	1,574.3		1,574.5		-0.2	0.0%
1983	1,573.9		1,566.5		7.4	0.5%
1984	3,226.9		3,226.8		0.1	0.0%
1985		4,131.9		4,130.9	1.0	0.0%
1986		4,635.0		4,635.0	0.0	0.0%
1987		5,266.0		5,253.2	12.8	0.2%
1988		3,035.6		3,031.3	4.3	0.1%
1989		3,315.4		3,315.4	0.0	0.0%
1990		4,662.5		4,661.6	0.9	0.0%
1991		3,585.3		3,571.4	13.9	0.4%
1992		3,460.0		3,443.6	16.4	0.5%
1993		2,142.9		2,142.9	0.0	0.0%
1994		2,915.2		2,914.8	0.4	0.0%
1995		6,456.6		6,466.4	-9.8	-0.2%
1996		9,539.4		9,166.1	373.3	3.9%
1997		7,119.5		7,079.1	40.4	0.6%
1998		4,166.8		4,174.4	-7.6	-0.2%
1999		1,865.9		1,816.1	49.8	2.7%
2000		2,855.0		2,389.5	465.5	16.3%
2001		1,331.0		1,329.1	1.9	0.1%
2002		452.7		423.7	29.0	6.4%
2003		1,344.4		1,211.00	133.4	9.9%
2004		2,131.4		1,948.70	182.7	8.6%
2005		2,610.1		2,553.20	56.9	2.2%
2006		2,322.7		1,876.60	446.1	19.2%

Appendix C5. Table 2. Northern shrimp fishery numbers of vessels in the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1997	311	310	1	0.3%
1998	260	260	0	0.0%
1999	238	238	0	0.0%
2000	304	285	19	6.3%
2001	275	288	-13	-4.7%
2002	198	200	-2	-1.0%
2003	222	248	-26	-11.7%
2004	192	190	2	1.0%
2005	197	197	0	0.0%
2006	144	119	25	17.4%

Appendix C5. Table 3. Northern shrimp fishery numbers of trips in the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1987	12,497	12,285	212	1.7%
1988	9,240	9,240	0	0.0%
1989	9,561	9,561	0	0.0%
1990	9,758	9,758	0	0.0%
1991	7,968	7,968	0	0.0%
1992	7,798	7,798	0	0.0%
1993	6,158	6,158	0	0.0%
1994	5,990	5,990	0	0.0%
1995	10,465	10,465	0	0.0%
1996	11,791	11,791	0	0.0%
1997	10,734	10,734	0	0.0%
1998	6,606	6,606	0	0.0%
1999	3,811	3,811	0	0.0%
2000	4,554	3,335	1,219	26.8%
2001	4,133	3,599	534	12.9%
2002	1,304	1,010	294	22.5%
2003	3,022	2,157	865	28.6%
2004	2,681	2,277	404	15.1%
2005	3,866	3,091	775	20.0%
2006	2,478	1,646	832	33.6%

Appendix C5. Table 4. Numbers of shrimp measured from port samples, as reported in the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1985	6,032	5,998	34	1%
1986	6,415	6,259	156	2%
1987	5,699	5,603	96	2%
1988	6,393	6,079	314	5%
1989	8,885	9,351	-466	-5%
1990	8,132	8,248	-116	-1%
1991	15,058	14,611	447	3%
1992	10,225	10,111	114	1%
1993	12,852	11,556	1,296	10%
1994	12,221	11,076	1,145	9%
1995	14,270	13,977	293	2%
1996	28,320	27,903	417	1%
1997	35,033			
1998	23,916			
1999	22,529			
2000	11,458			
2001	14,714	15,091	-377	-3%
2002	5,243	5,243	0	0%
2003	11,805	11,596	209	2%
2004	10,972	10,432	540	5%
2005	19,539	19,539	0	0%
2006	16,218	16,314	-96	-1%

Appendix C5. Table 5. Mean weight of a shrimp (g) in the landings, as used by CSA in the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1985	11.6	11.7	-0.1	-0.9%
1986	12.6	12.8	-0.3	-2.2%
1987	12.4	12.4	0.1	0.5%
1988	13.8	13.3	0.5	3.8%
1989	11.2	11.7	-0.5	-4.4%
1990	10.7	10.5	0.1	1.2%
1991	10.7	11.2	-0.4	-4.2%
1992	12.9	13.1	-0.2	-1.6%
1993	11.5	11.0	0.5	4.0%
1994	11.1	10.8	0.3	2.8%
1995	10.3	10.5	-0.2	-2.1%
1996	11.0	11.5	-0.4	-4.0%
1997	9.9	10.0	0.0	-0.1%
1998	11.5	11.2	0.4	3.2%
1999	9.0	8.4	0.6	6.3%
2000	10.9	11.4	-0.5	-4.4%
2001	9.4	9.4	-0.1	-0.6%
2002	9.6	9.5	0.1	0.9%
2003	10.5	10.7	-0.2	-1.4%
2004	9.6	9.8	-0.2	-1.7%
2005	10.9	10.9	0.0	-0.3%
2006	11.4	11.5	0.0	-0.2%

Appendix C5. Table 6. Estimated numbers of shrimp (millions) in landings, as used by CSA in the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1985	356	353	3	1%
1986	369	361	8	2%
1987	424	425	-1	0%
1988	220	228	-8	-4%
1989	296	284	12	4%
1990	437	442	-5	-1%
1991	335	320	15	4%
1992	268	262	6	2%
1993	187	195	-8	-4%
1994	263	270	-7	-3%
1995	627	615	12	2%
1996	865	799	66	8%
1997	716	711		
1998	361	374		
1999	207	215		
2000	261	209		
2001	142	141	1	1%
2002	47	44	3	6%
2003	128	114	14	11%
2004	221	199	22	10%
2005	240	234	6	3%
2006	203	164	39	19%

Appendix C5. Table 7. Mean pounds per trip from the 2007 SAW report compared with the 2013 assessment.

	<u>2013</u>	<u>2007 SAW</u>	<u>Difference</u>	<u>% of 2013</u>
1991	992	988	4	0.4%
1992	978	974	4	0.4%
1993	767	767	0	0.0%
1994	1,073	1,073	0	0.0%
1995	1,360	1,362	-2	-0.1%
1996	1,784	1,714	70	3.9%
1997	1,462	1,454	8	0.6%
1998	1,391	1,317	74	5.3%
1999	1,079	1,067	12	1.1%
2000	1,382	1,444	-62	-4.5%
2001	710	740	-30	-4.2%
2002	765	831	-66	-8.6%
2003	981	1,029	-48	-4.9%
2004	1,753	1,821	-68	-3.9%
2005	1,488	1,541	-53	-3.5%
2006	2,066	2,252	-186	-9.0%

## Appendix C6. Additional Model Runs Conducted during SARC58 Review

The Panel requested additional runs of the UME and CSA model at the workshop to explore the effects of data weighting on the fit to the indices and model estimates of F.

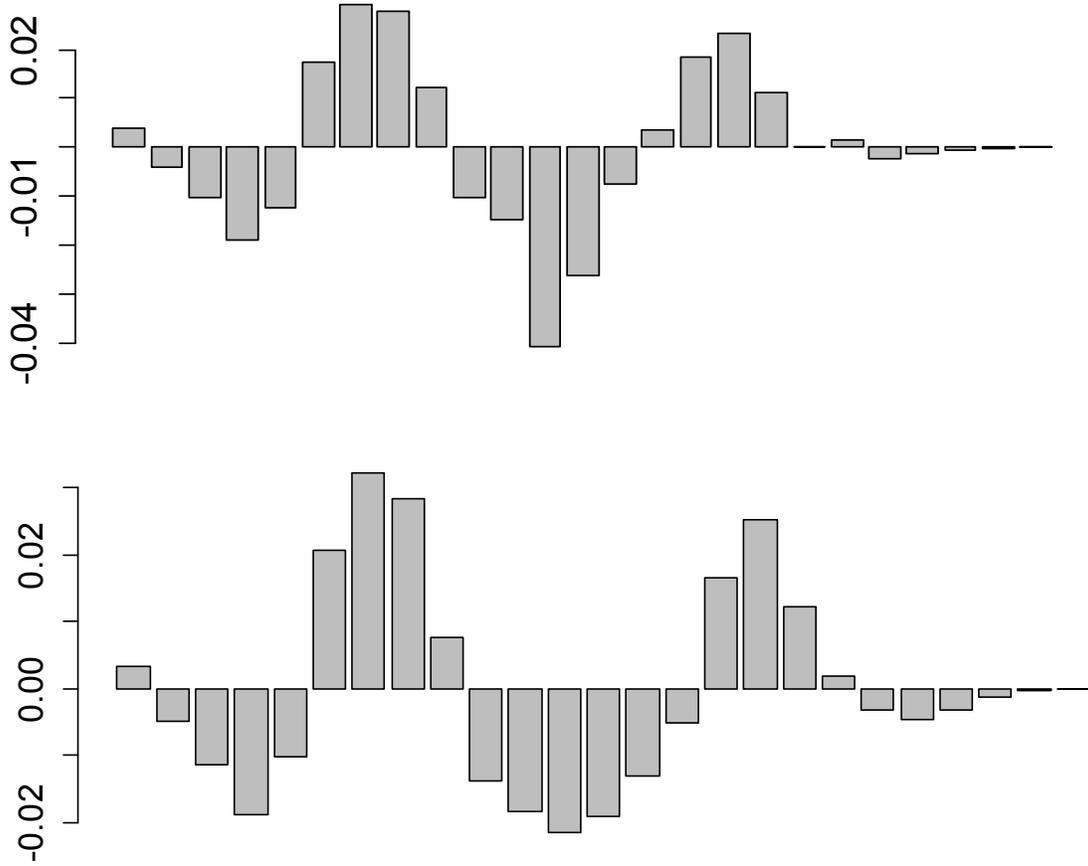
Table C6.1 Requested and additional weighting schemes for the UME model. All runs were done with  $M=0.5$  for all size classes.

Base Model	Panel Request
<b>Survey <math>\lambda = 1</math></b>	Survey $\lambda = 2$
<b>Total catch <math>\lambda = 1</math></b>	Total catch $\lambda = 0.5$
<b>Size comp. <math>\lambda = 1</math></b>	Size comp. $\lambda = 1$
<b>Survey CVs = CSA adjusted</b>	Survey CVs = CSA adjusted
<b>Catch CV = 0.05</b>	Catch CV = 0.05

Table C6.2. Base model and additional weighting schemes considered for the CSA model.

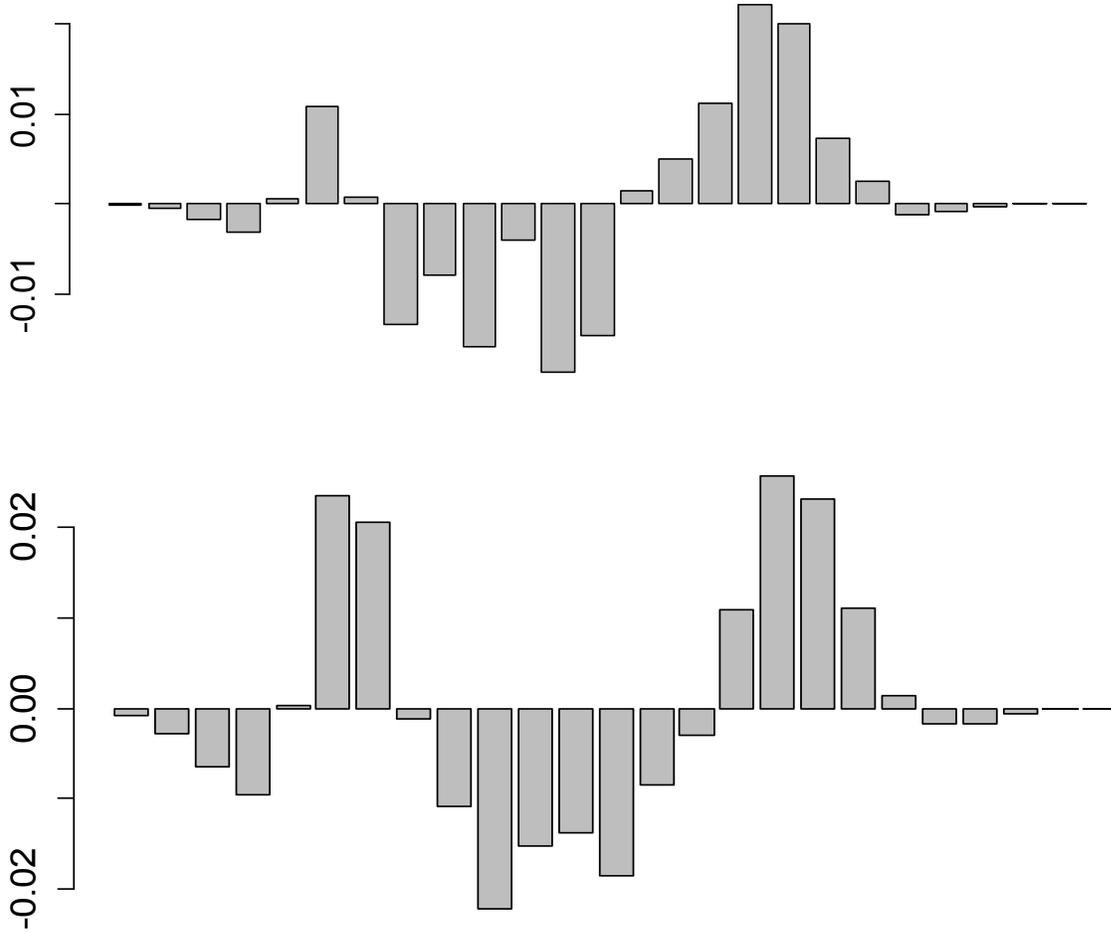
Base Model	Additional Runs	
<b>All survey <math>\lambda = 1</math></b>	Shrimp survey $\lambda = 2$	Shrimp survey $\lambda = 2$
<b>Total catch <math>\lambda = 1</math></b>	Total catch $\lambda = 0.5$	Total catch $\lambda = 0.01$
<b>Survey CVs = CSA adjusted</b>	NEFSC survey $\lambda = 1$	NEFSC survey $\lambda = 1$
<b>M=PPI</b>	Survey CVs = CSA adjusted	Survey CVs = CSA adjusted
<b>Catch CV = 0.05</b>	M=PPI	M=PPI
	Catch CV=0.2	Catch CV=0.2

# NEFSC Albatross

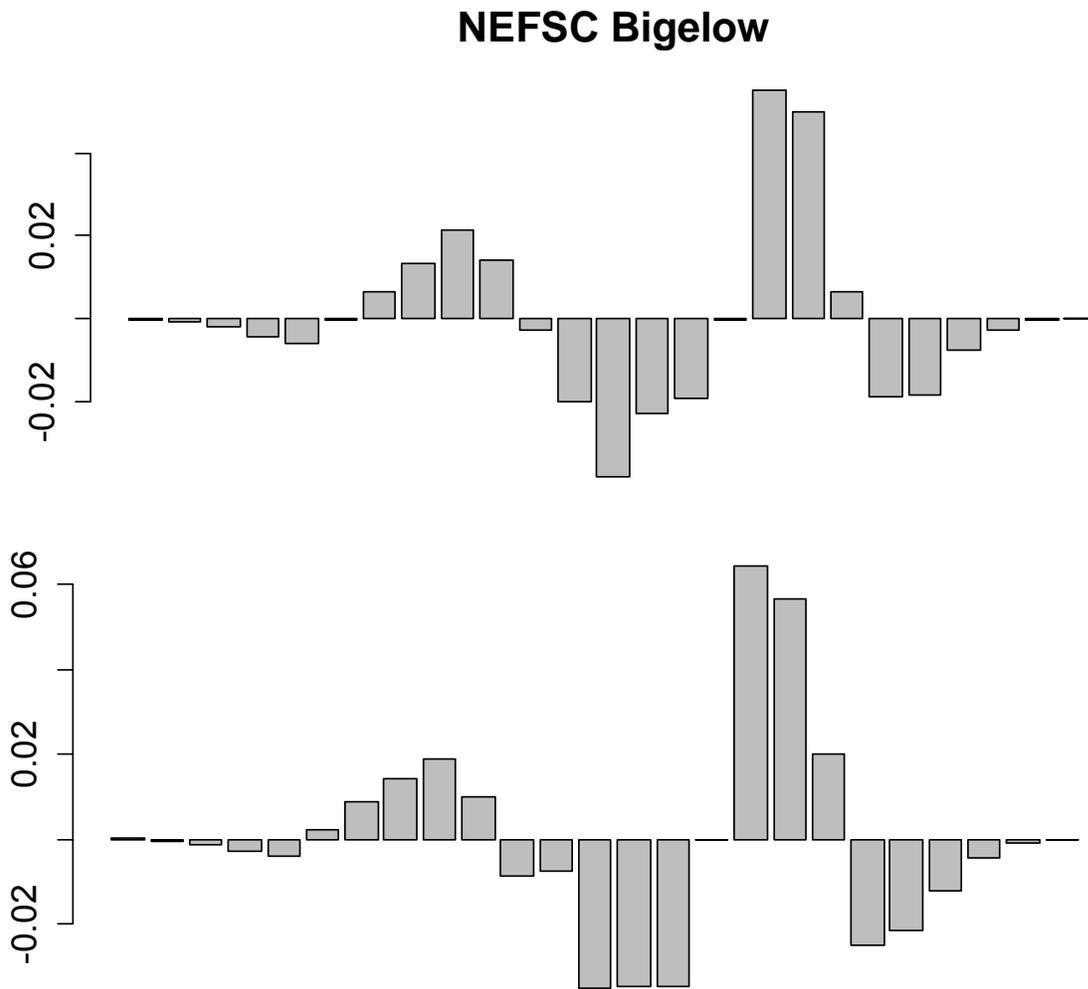


Appendix C6. Figure 1. Average proportion-at-size residuals for the NEFSC Albatross survey (observed - predicted) for the UME base model configuration (top) and the Panel's requested configuration (bottom).

## Summer Shrimp

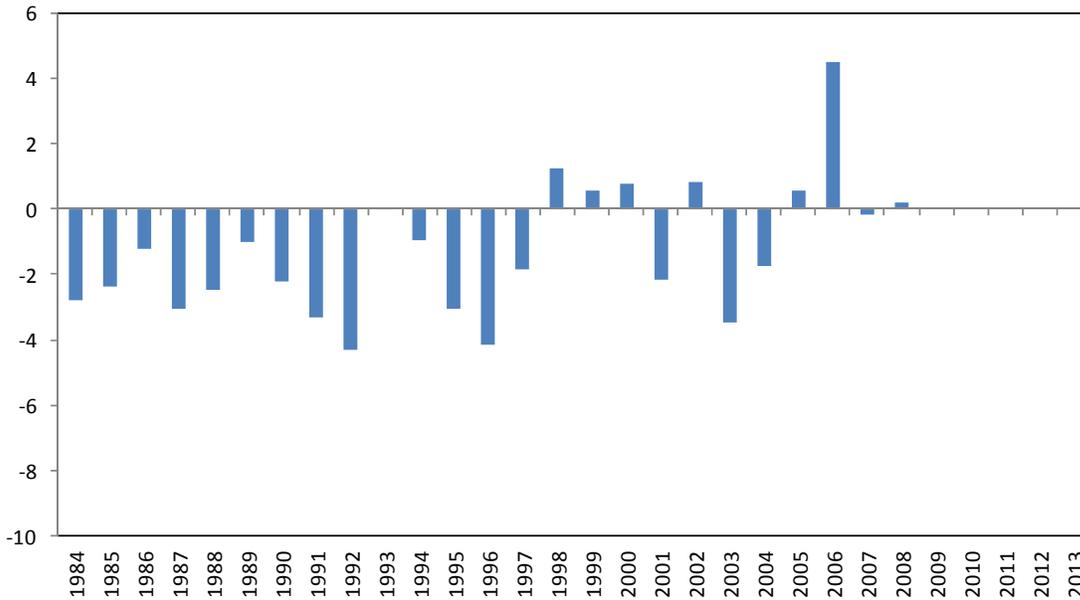
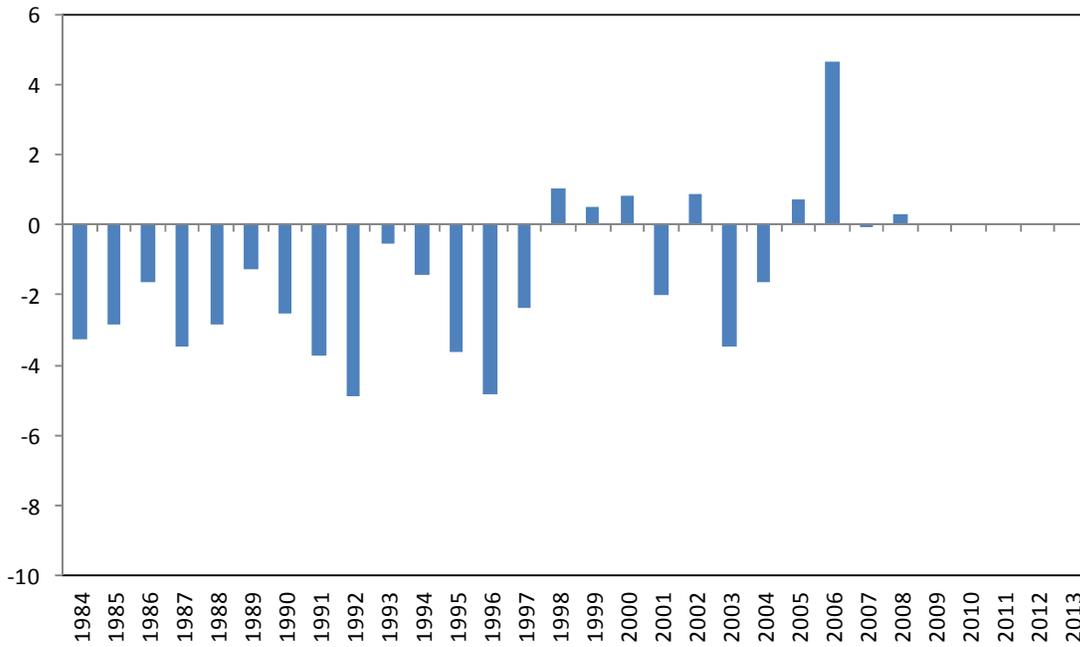


Appendix C6. Figure 2. Average proportion-at-size residuals for the ASMFC summer shrimp survey (observed - predicted) for the UME base model configuration (top) and the Panel's requested configuration (bottom).



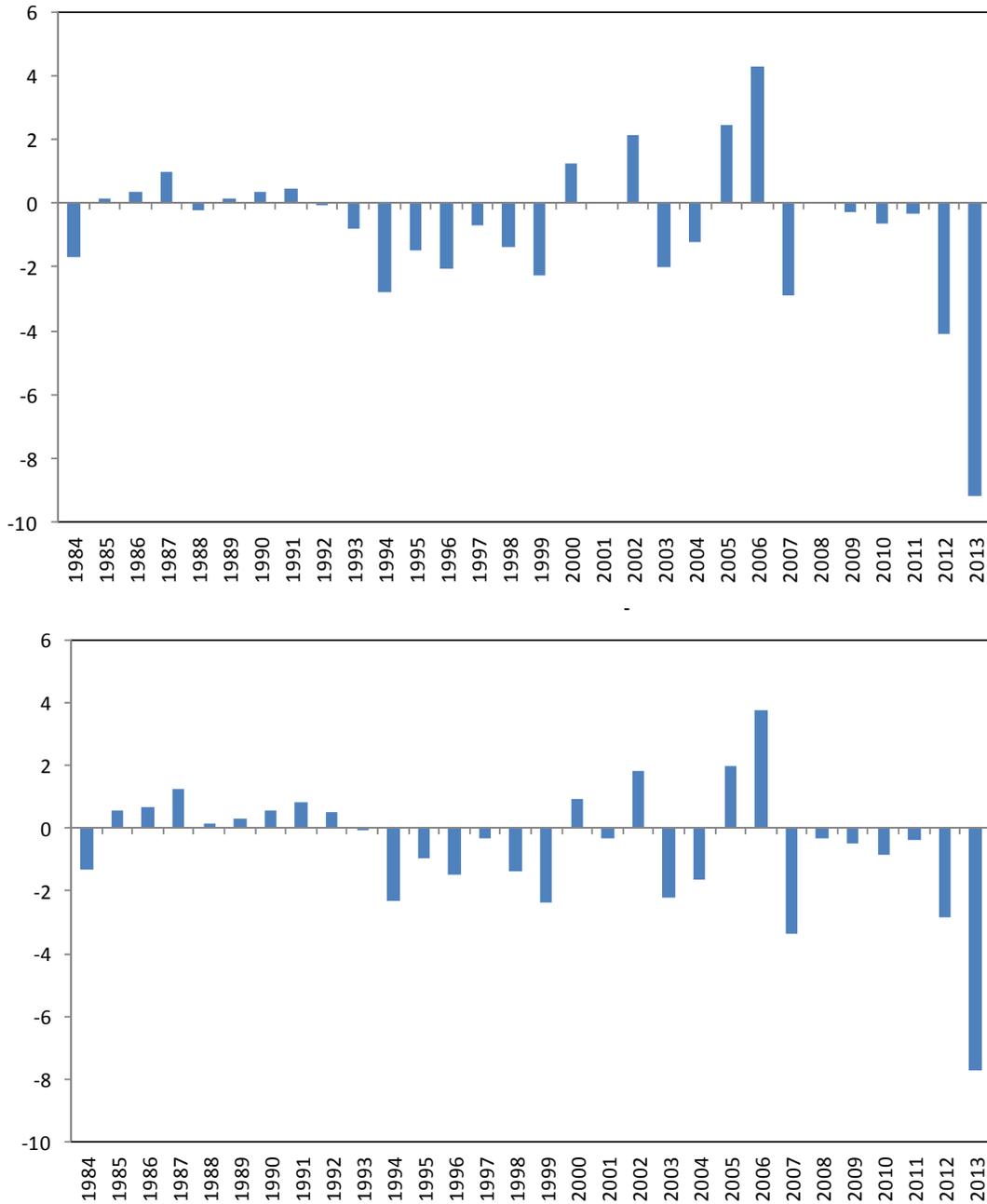
Appendix C6. Figure 3. Average proportion-at-size residuals for the NEFSC Bigelow survey (observed - predicted) for the UME base model configuration (top) and the Panel's requested configuration (bottom).

### NEFSC Albatross



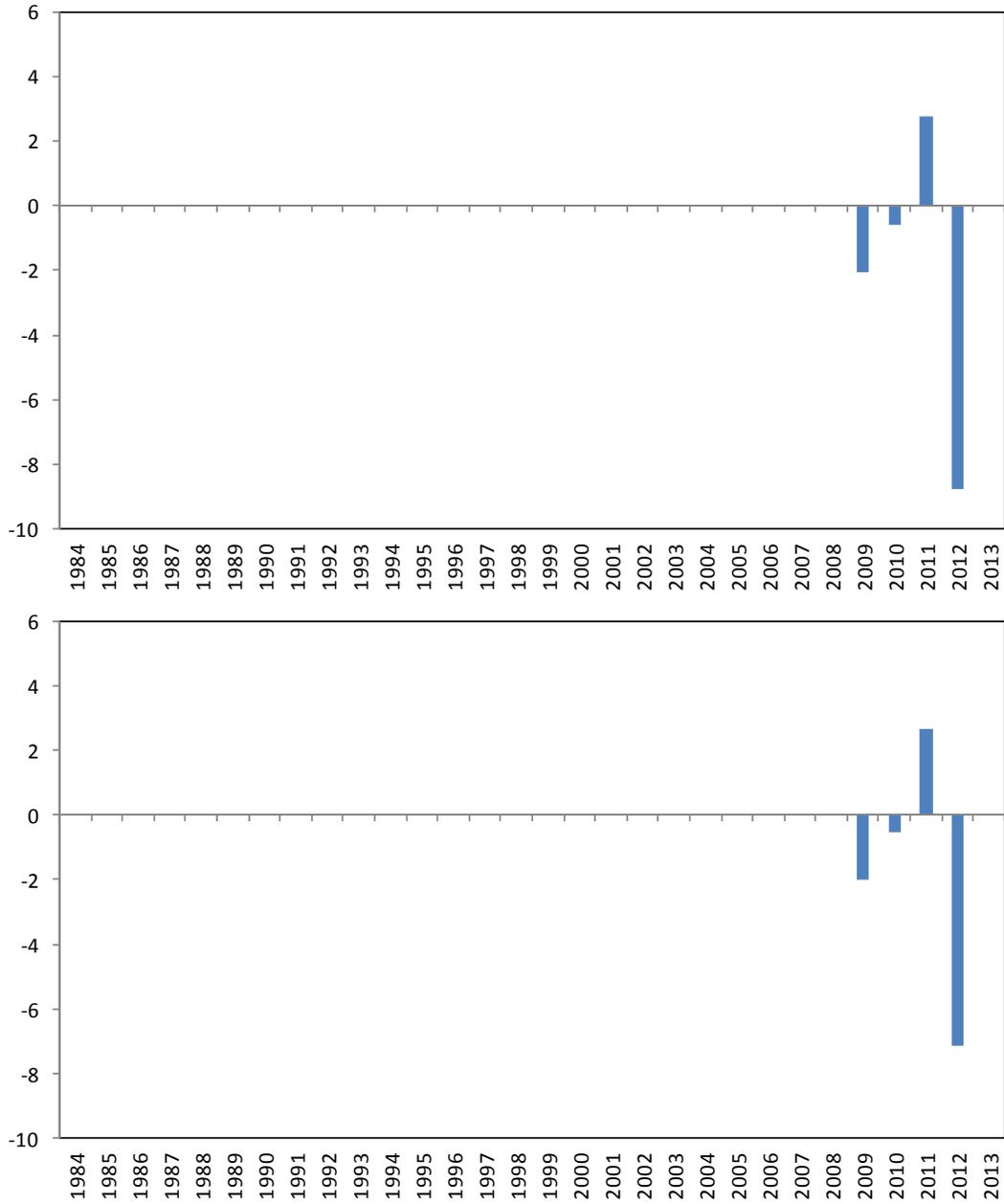
Appendix C6. Figure 4. Standardized residuals for the NEFSC Albatross index for the UME base model configuration (top) and the Panel's requested configuration (bottom).

## Summer Shrimp



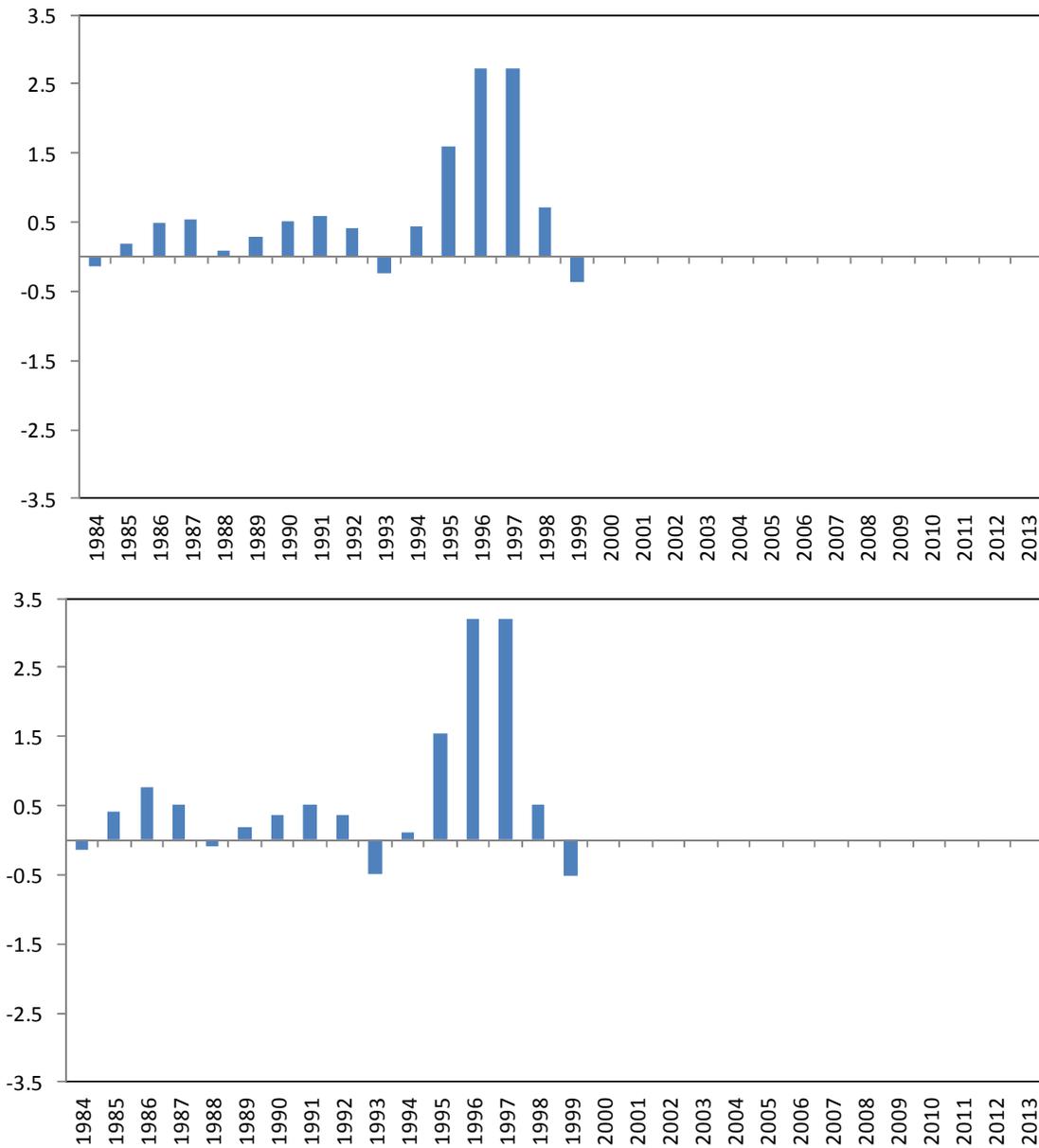
Appendix C6. Figure 5. Standardized residuals for the ASMFC summer shrimp survey index for the UME base model configuration (top) and the Panel's requested configuration (bottom).

# NEFSC Bigelow



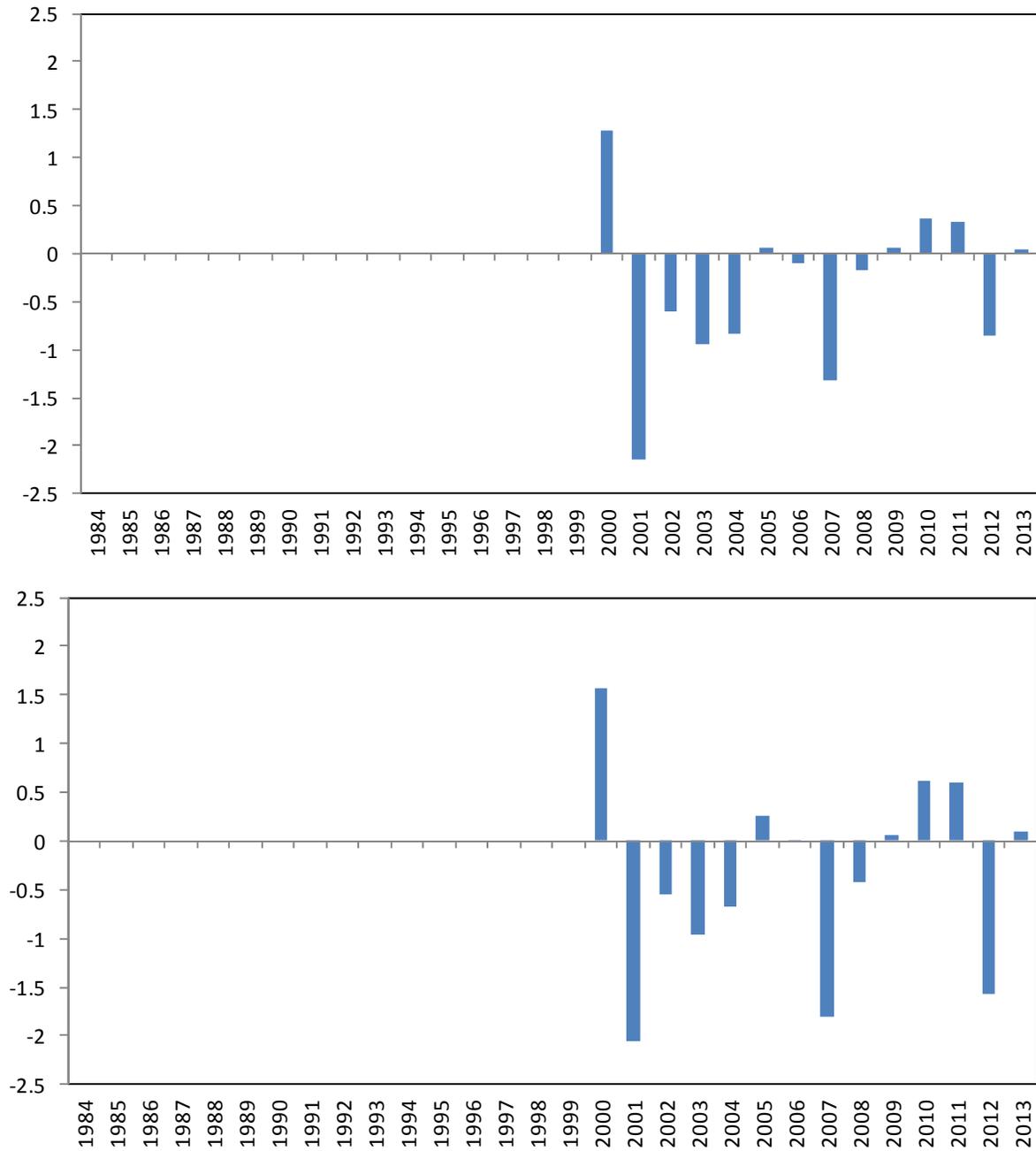
Appendix C6. Figure 6. Standardized residuals for the NEFSC Bigelow survey index for the UME base model configuration (top) and the Panel's requested configuration (bottom).

### Mixed



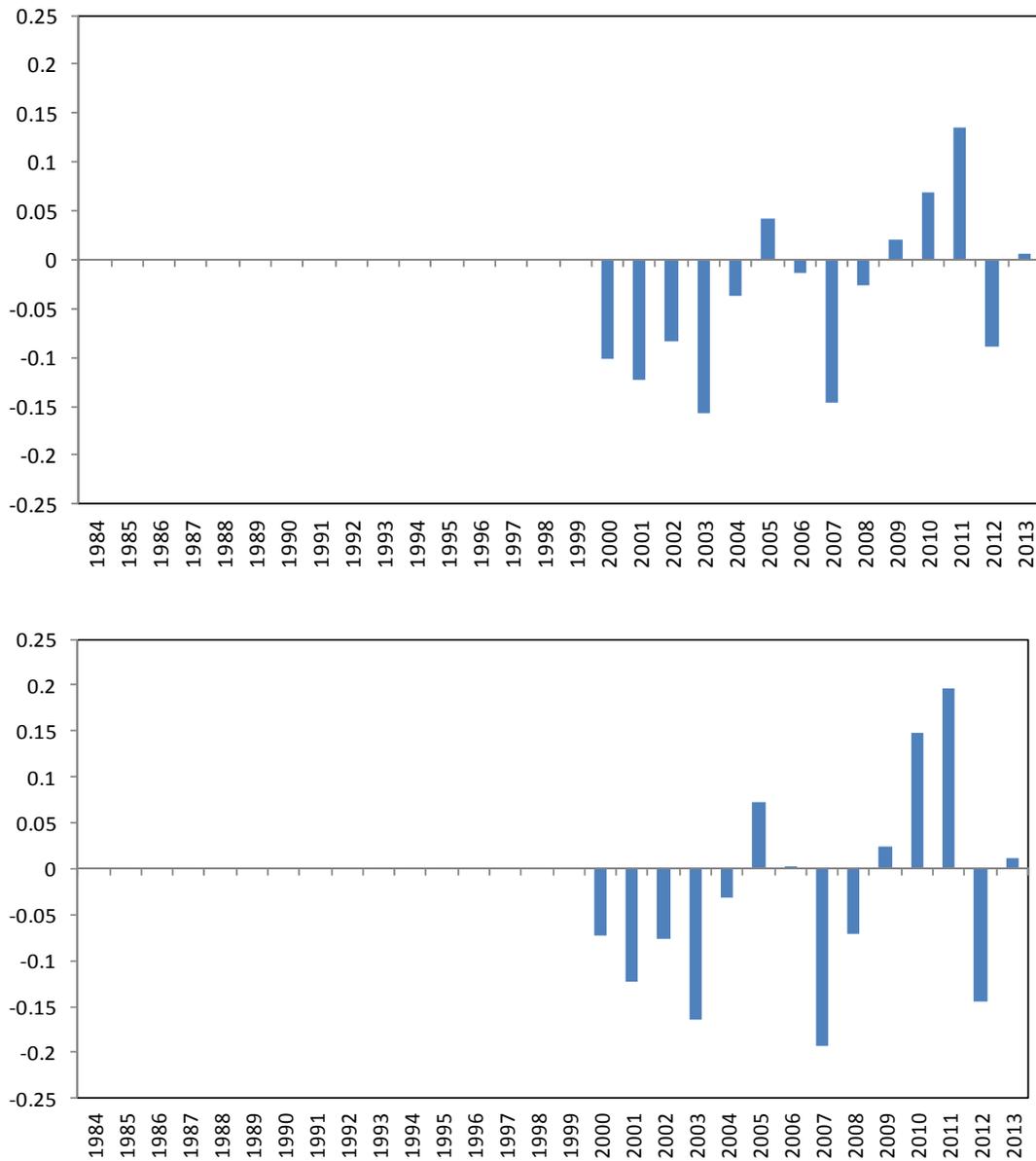
Appendix C6. Figure 7. Standardized residuals for total catch from the mixed fleet for the UME base model configuration (top) and the Panel's requested configuration (bottom).

## Trawl

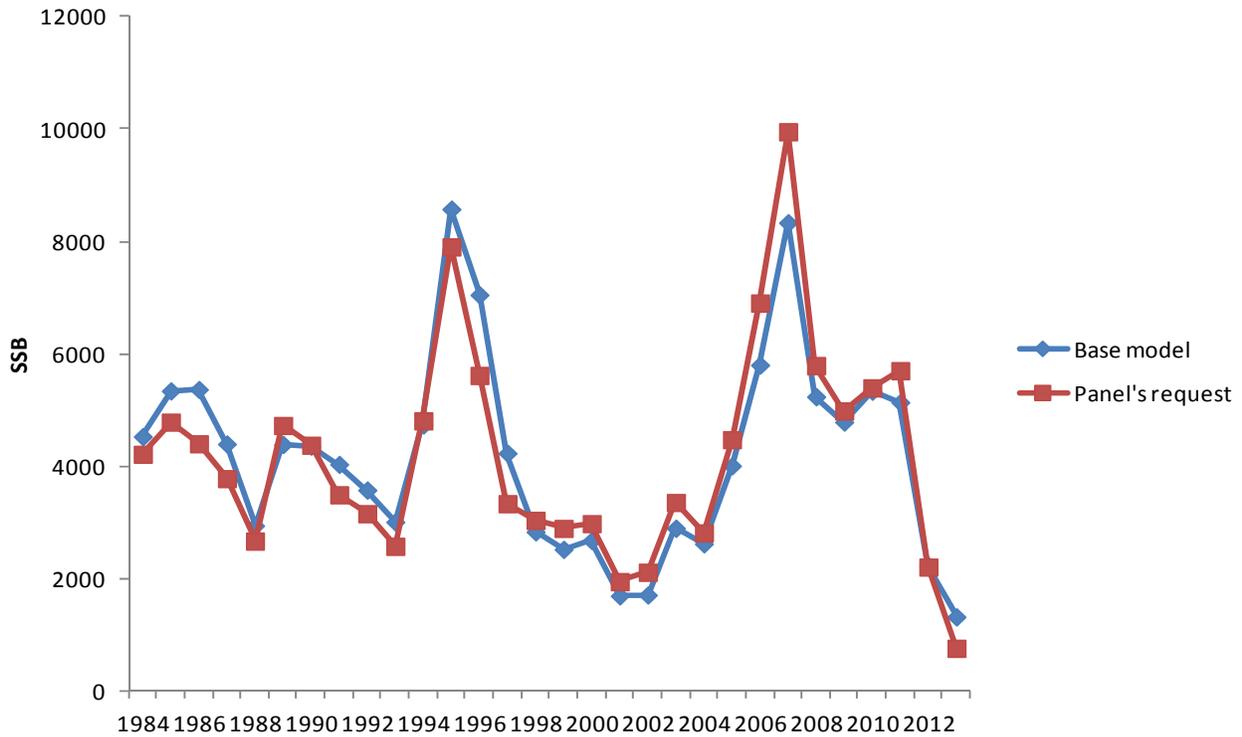
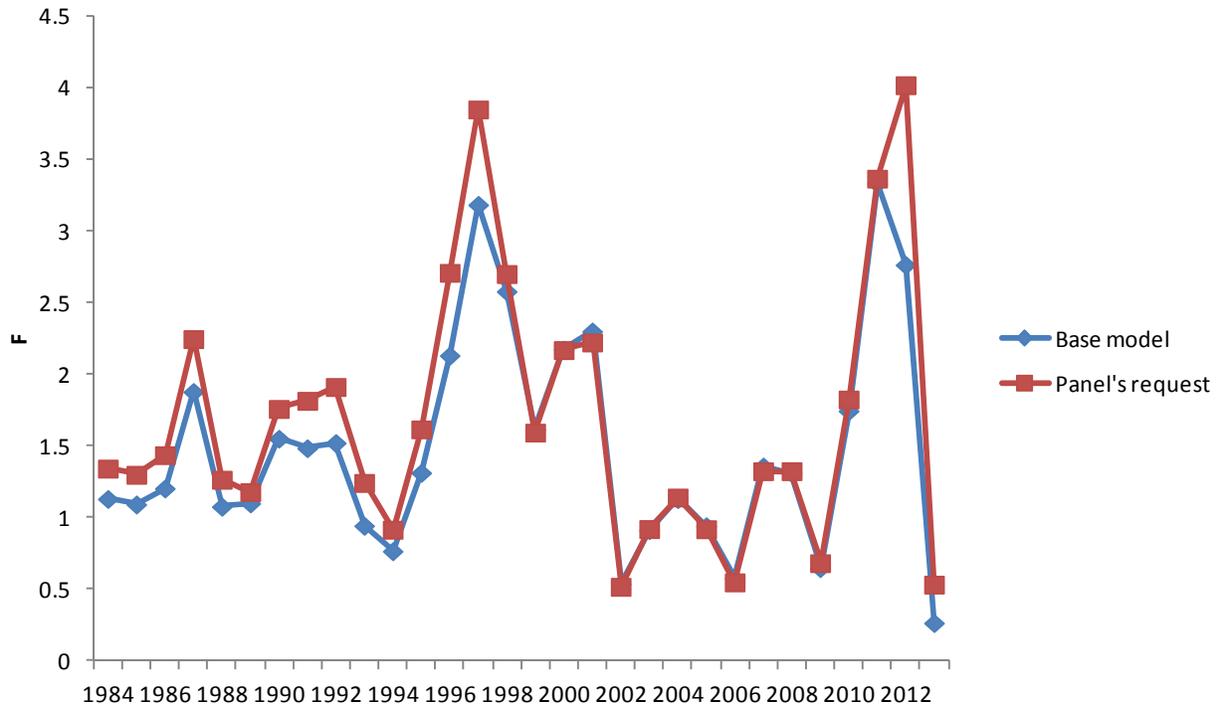


Appendix C6. Figure 8. Standardized residuals for total catch from the trawl fleet for the UME base model configuration (top) and the Panel's requested configuration (bottom).

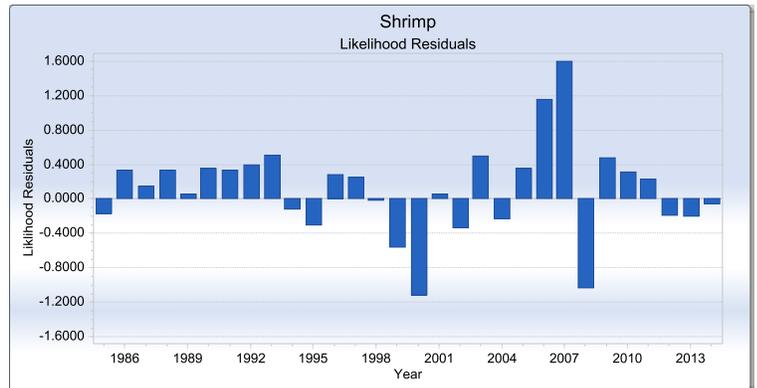
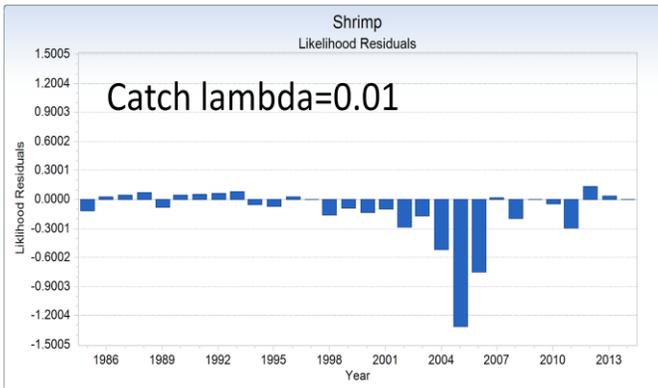
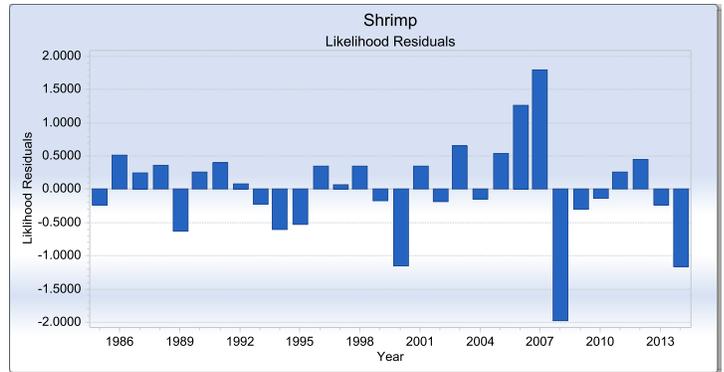
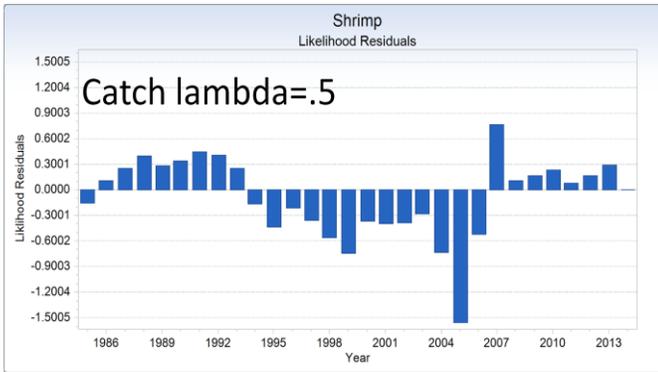
## Trap



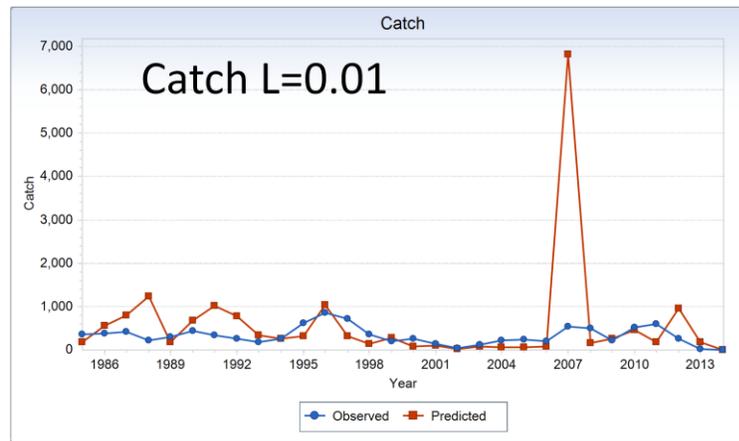
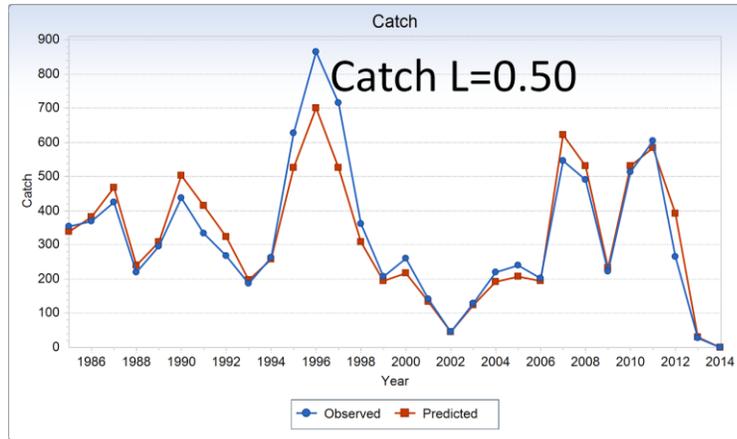
Appendix C6. Figure 9. Standardized residuals for total catch from the trap fleet for the UME base model configuration (top) and the Panel's requested configuration (bottom).



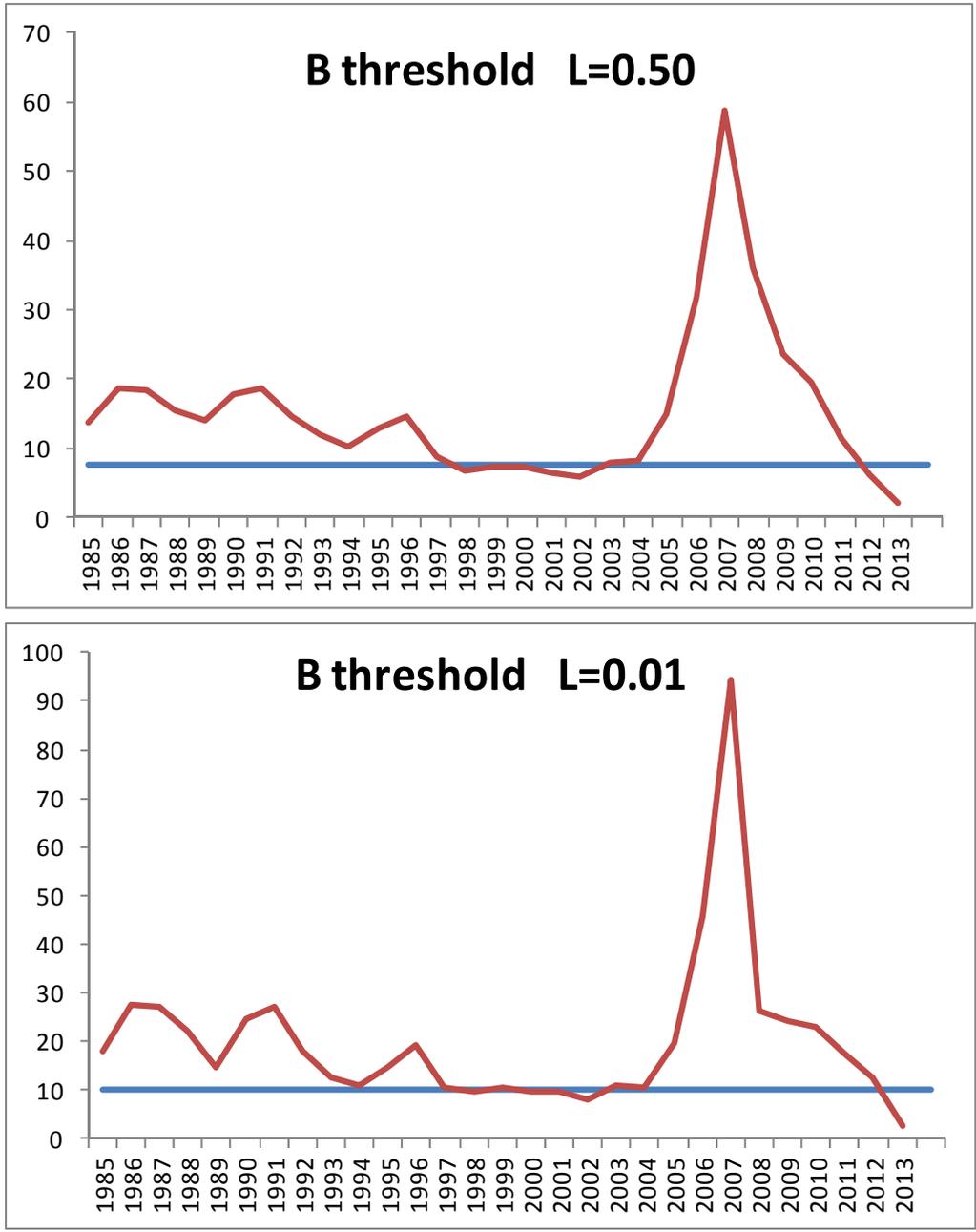
Appendix C6. Figure 10. Model estimates of F (top) and SSB (bottom) for the UME base model configuration and the Panel's requested configuration.



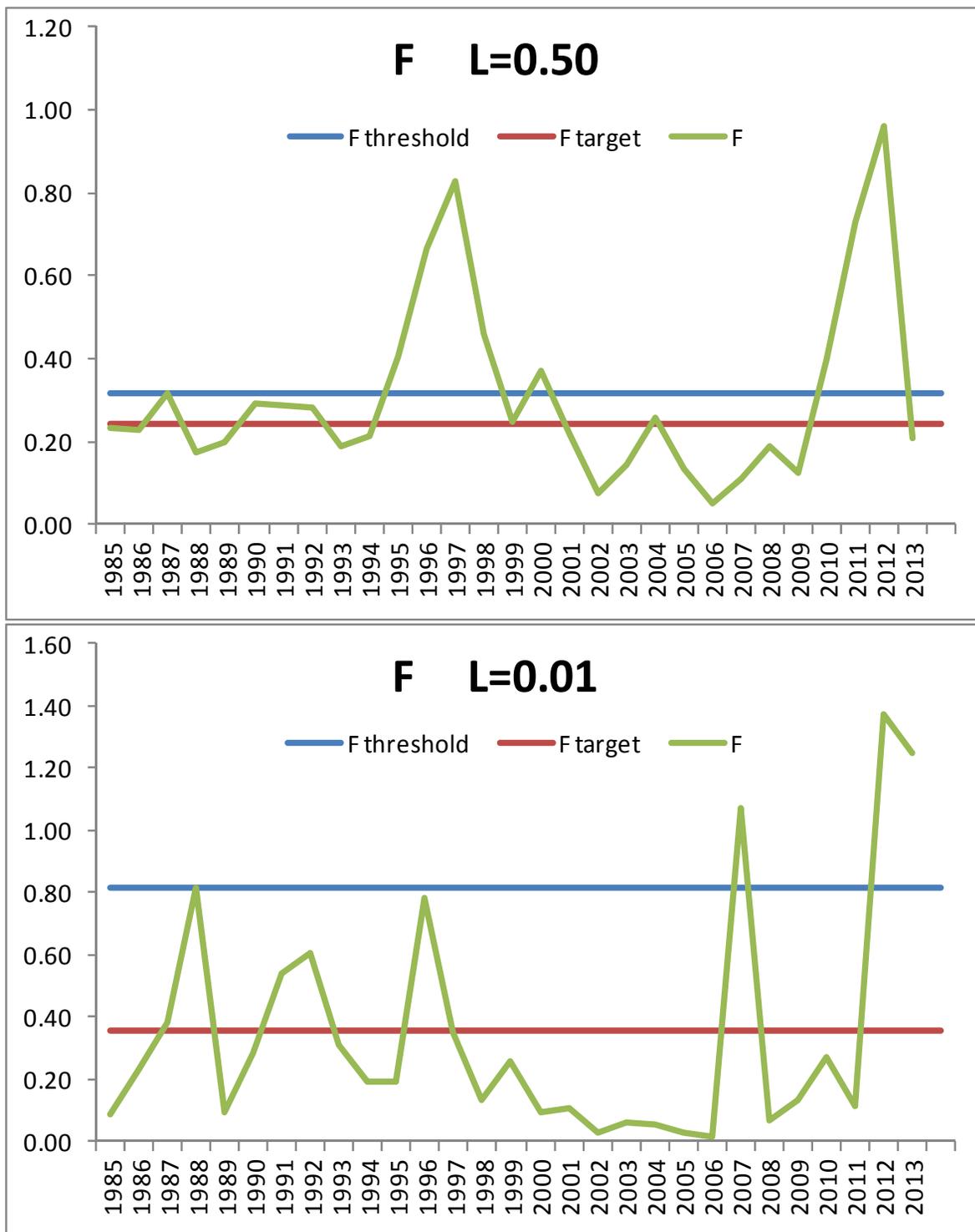
Appendix C6. Figure 11. Standardized residuals from the CSA model for the ASMFC summer shrimp survey index for recruits (left) and post-recruits (right), for different likelihood weights for total catch ( $\lambda=0.5$ , top, and  $\lambda=0.01$ , bottom).



Appendix C6. Figure 12. Observed and predicted total catch from the CSA model for different likelihood weights ( $\lambda$ ) on total catch.



Appendix C6. Figure 13. Biomass estimates from the CSA model compared to the biomass threshold estimates for total catch  $\lambda=0.5$  (top) and total catch  $\lambda=0.01$  (bottom).



Appendix C6. Figure 14. Fishing mortality estimates from the CSA model compared to the F target and threshold estimates for total catch  $\lambda=0.5$  (top) and total catch  $\lambda=0.01$  (bottom).