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Depletion models with successive pulses of Humboldt squid (*Dosidicus gigas*)  
in coastal waters off Central Chile

*Ignacio Payá*

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## Depletion models with successive pulses of Humboldt squid (*Dosidicus gigas*) in coastal waters off Central Chile.

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### Summary

Due to its short life span, squid stocks are often assessed with intra-annual depletion models. However, there were no descriptions about this type of depletion processes in Chile. Therefore, frequency at length of the mantle and fishing yields were analyzed during weeks. A general migration pattern with the arrival of squids in November and their migration in October next year was identified. This pattern showed variations including the sequential arrival of two or three squid pulses before the migration of the cohort in October. Therefore, a weekly depletion model was implemented and programmed in AdModel Builder. It was fitted to the relative index of abundance generated by the CPUE standardization from artisanal boats. The model included a prior distribution of the natural mortality with a mean at 1.5 and known standard deviation. The model was adjusted separately for 2014, 2015, and 2016, and generated natural mortality estimates between 0.5 and 0.72. The biomass level varied between 350-400 thousand t, in 2015 and 2016, and 1.8 million t in 2014. Estimation of potential biomass (without fishing) at the end of the depletion period allowed to estimate biomass escapement percentages around 56 to 94%, which were higher than the 40% of escapement recommended to maintain the sustainability of a stock. However, it is likely that squids that can escape from the catch in Chile are captured in spawning areas in the EEZ of Peru and close to them but in the SPRFMO area. Also, squid that recruit to Chile are large individuals that have escape the fishing in the SPRFMO area and in EEZ of Peru. Therefore, it is proposed to integrate all the Information at a regional level and to develop a scheme of intra-annual stock assessment through depletion models.

## Contents

1. INTRODUCTION .....	2
2. MATERIAL AND METHODS.....	3
2.1 Data collection .....	3
2.2. Depletion Model.....	4
3. RESULTS .....	7
3.1 Depletion model in 2014 .....	7
3.2 Depletion model in 2015.....	11
3.3 Depletion model in 2016.....	15
4. DISCUSSION.....	18
5. REFERENCES.....	20

## 1. INTRODUCTION

Squid landings used to be very low in Chile. However, they increased significantly from 2004 reaching 296 thousand tons in 2005. After that they decreased and have been fluctuating around 150 thousand tons (Figure 1). The first annual catch quota was established in 180 thousand tons for 2012 and it was based on a precautionary approach and the historical average of the catches. In 2013, this quota was increased to 200 thousand tons and has been kept constant since then. From 2014, 80% of the catch quota is allocated to the small-scale fleet and 20% to the industrial fleet. Annual landings have not reached the catch quotas in any of the years. Industrial fleet has reached its quota share but artisanal fishermen did not.

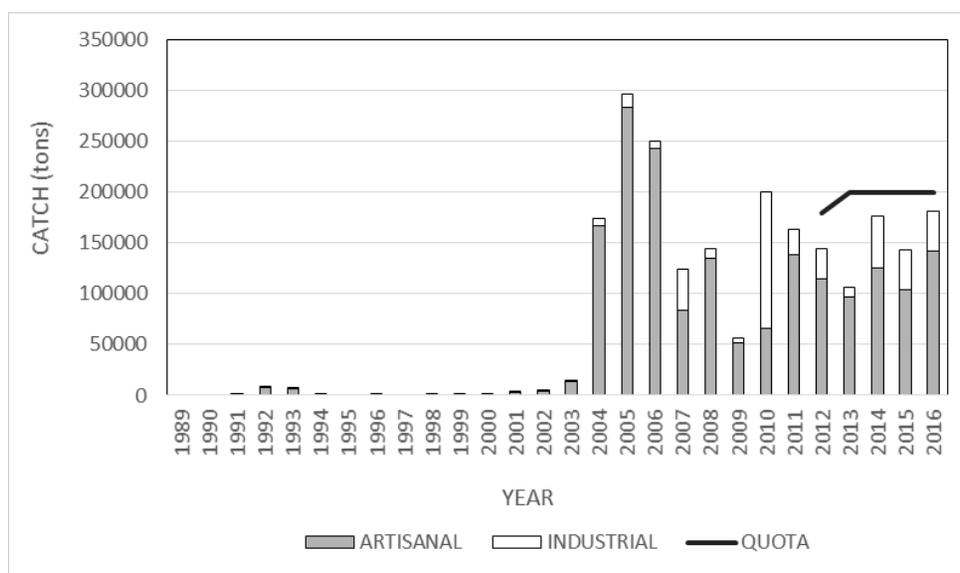


Figure 1. Total landings per sector and global catch quota.

Zúñiga et al. (2008) found a regular seasonal pattern in the catches from 2002 to 2005, and postulated the existence of two cohorts in a year. Payá et al. (2015) found that large squids (>60 cm ML) enter the Chilean coastal area and remains there until October of the next year. His hypothesis was based on the analysis of the modal progression of mantle sizes and on the modeling of monthly variation of relative abundance (standardized cpue).

In 2015, Payá (2016) implemented and applied the intra-annual depletion model on a weekly scale and with two recruitment pulses to the squid Chilean fishery. This model was similar to the model that Payá (2007a) introduced in the Falkland Islands-Malvinas squid (*Loligo*) stock assessment and that it still in use to manage this fishery.

This contribution summarizes the experiences of applying the depletion model with pulses (Payá 2007a) to the squid fishery in Chile from 2014 to 2016.

## 2. MATERIAL AND METHODS

### 2.1 *Data collection*

#### Data

Fishery statistics of the small-scale fleet per boat and fishing trip are collected by the National Fisheries and Aquaculture Service (SERNAPESCA). Industrial catches come from fishing logbooks that the industrial fleet reports to SERNAPESCA.

Mantle length-frequency data and individual weights per week and per fishery type are sampled by IFOP's scientific observers in small-scale landing centers and onboard industrial vessels.

#### Weekly index of abundance

Since stock assessments have been conducted following an annual stock assessment and management cycle, depletion models have been applied annually and independently (Payá 2015 a 2017).

The index of abundance is based on catch rates of small-scale vessels because of the following reasons: a) small-scale catches cover most of the annual quota (80% of catch quota); b) small-scale catches are carried out throughout the year, while industrial catches are conducted during the first quarter of the year; and c) small-scale catches come from three regions that cover from 29° to 38°S, while industrial catches come from a reduced area around 36°S.

For each year separately, CPUE intra-annual variability models were fit. The CPUE were the tons catch per fishing trip ( $t/vcp$ ). The models included week and region as fixed effects and overall length boat as continued covariate. The response variable was transformed through logarithm to stabilize variance, thus defining identity as the link function.

$$\eta_{i,j,k} = \alpha + \sum_h \beta_h T_{h,i,j,k} + \sum_q \gamma_q S_{q,i,j,k} + \phi L_i + \varepsilon_{i,j,k}$$

where,  $i$  stands for vessel,  $j$  week,  $k$  region, and  $L$  vessel's length.  $\mathbf{T}$  is a matrix of  $n \times h$  that represents the week's predictors,  $\mathbf{S}$  is a matrix of  $n \times q$  that represents predictors in relation to the region,  $\phi$  is the length's coefficient, and  $\{\alpha, \beta, \gamma, \Phi\} = \Theta$ , are the model's coefficients to be estimated, and  $\varepsilon$  are the random errors normally distributed with a mean of zero.

### Length to weight relationship

The whole individual weight ( $W$ ) to mantle length ( $ML$ ) model was fit to samples of combined sexes. The variables were transformed through logarithm to linearize the potential model between the whole weight and the mantle length, and to stabilize the variance. The identity was defined as the link function. Exploratory variables included the year and the log continuous variable ( $ML$ ) (logarithm of mantle length). According to these specifications, the model of  $\log(W)$  on the scale of the linear predictor  $\eta$  was:

$$\eta_{i,j} = \alpha + \sum_h \beta_h T_{h,ijk} + \phi \ln(ML_i) + \varepsilon_{i,j}$$

where,  $i$  represents the individual, and  $j$  the year.  $\mathbf{T}$  is a matrix of  $n \times h$  that represents the year's predictors,  $\phi$  is the coefficient of the mantle's length logarithm,  $\{\alpha, \beta, \phi\} = \theta$  are the coefficients of the model to be estimated, and  $\varepsilon$  are the random errors normally distributed with a mean of zero.

Estimation of model parameters was conducted through generalized linear models (Nelder y Wedderburn 1972). The selection of the best model was based on the lowest AIC value (Akaike Information Criterion, Akaike 1973).

Statistical analyses were conducted with  $R$  (R Development Core Team 2009), using *nlme* package.

## 2.2. Depletion Model

### Depletion model with a single squid group

The main assumption to apply this model is that there is a homogeneous group of squid that, when captured, show a depletion of their relative abundance. The depletion model was adjusted following the formulation of depletion models used for Falkland Islands - Islas Malvinas *Loligo* squid assessment (Rosemberg *et al.* 1990 and Payá 2007b). The decrease of the abundance during a fishing season is modeled as follows:

$$N_{t+1} = [(N_t e^{-0.5M/52}) - C_t] e^{-0.5M/52}$$

where  $t$  represents the time interval (weeks),  $N$  the abundance in number of individuals,  $M$  is natural mortality and  $C$  the catch in number of individuals. Considering a total of 52 weeks a year, mortality within a week is  $M/52$ . Catch in number of individuals was estimated as follows:

$$C_t = \frac{Y_t}{\bar{W}_t}$$

where  $Y$  is the total squid landing in the country that includes both industrial and small-scale fleets.

The mean weight,  $\bar{W}$  was calculated as:

$$\bar{W}_t = \frac{\sum_1^{nl} f_{l,t} a l_{l,t}^b}{\sum_1^{nl} f_{l,t}}$$

where  $f$  is the frequency at length of the mantle  $l$  is the week  $t$  and  $a$  and  $b$  are the parameters of the size-weight ratio. The final average weight was obtained as the average of weights per small-scale and industrial fleet weighed by the catch of each fleet.

Biomass per interval was obtained multiplying abundance by the mean weight.

$$B_t = N_t \bar{W}_t$$

The model predicts the abundance index,  $\hat{I}$ , as:

$$\hat{I}_t = N_t q$$

where  $q$  is the catchability coefficient.

The observed abundance index,  $I$ , was calculated as:

$$I_t = \frac{CPUE^s}{\bar{W}_t}$$

where  $CPUE^s$  is the standardized CPUE (tons by fishing trip) and  $\bar{W}$  is the mean weight.

The model was fitted to the data by maximizing the likelihood of the data, assuming a lognormal distribution:

$$L_d = -0.5nl \ln(2\pi) - \sum_{t=tni}^{tfin} \ln(\sigma) - 0.5 \sum_{t=tni}^{tfin} \left( \frac{\ln(I_t) - \ln(\hat{I}_t)}{\sigma} \right)^2$$

where  $I$  is the observed abundance index,  $\hat{I}$  the estimated abundance index,  $t_{ini}$  the initial week,  $t_{fin}$  the final week. There are two cohorts in a year, the first one that arrived in November of the previous year and leaves the area in October of the current year, and the second one that arrives in November of the current year (Payá *et al.* 2014a). The starting and final weeks of the depletion event was defined based on CPUE depletion and mean weight increase.

Because of the uncertainty of natural mortality value, a prior distribution for this parameter was also included in the model:

$$L_{prior} = -0.5n\ln(2\pi) - \ln(\sigma_M) - 0.5 \left( \frac{\ln(M_{prior}) - \ln(M)}{\sigma_M} \right)^2$$

where  $M_p$  and  $\sigma_M$  are the mean and standard deviation. Three cases were analyzed: 1)  $M_p$  was set at 1.5 based on Payá *et al.* (2014) and  $\sigma_M = 0.1$ ; 2)  $M$  fixed at 1.0; 3)  $M$  fixed at 1.5.

The total likelihood was:

$$L_{tot} = L_{data} + L_{prior}$$

In order to estimate the potential biomass percentage that escapes in the week  $t_{fin}$ , potential biomass that would have existed without fishing was calculated,  $PB_{t_{fin}}$ :

$$PB_{t_{fin}} = N_{t_{ini}} e^{-(t_{fin}-t_{ini})M/52} W_{t_{fin}}$$

, and the escape percentage, escapement, in  $t_{fin}$  as follows:

$$Escapement_{t_{fin}} = \frac{B_{t_{fin}}}{PB_{t_{fin}}} 100$$

The model was programmed by Payá (2015 and 2016) in AdModel Builder (Fournier *et al.* 2012) and called CHUSMODEL based on Chilean Humboldt Squid Depletion Model (see details in ANNEX). Uncertainties were calculated using standard deviations of the estimated parameters from the Hessian Matrix.

### Depletion model with successive pulses

This modification of the model includes the sequential arrival of squid groups or pulses. This type of model of several pulses was developed and applied for the first time on the Falkland/Malvinas *Loligo* squid by Payá (2007b), who also identified the groups in the light of the changes of the mean weights, since individuals of a same group must grow, so if the mean weight is maintained or reduced, it means that a new group entered. This group identification criterion is still currently applied

and has been related to environmental variables by Winter and Arkhipkin (2015). Modeling by groups or pulses is still used and has been subsequently called as disturbances of the depletion process (Roa-Ureta, 2012). The basic idea is that during the week the arrival of a new group of squid is identified, the parameter  $N_{ini_{ng}}$  is added, corresponding to the abundance of this new group (ng), modifying the equation of that week in particular.

$$N_{t+1} = [((N_{ini_{ng}} + N_t)e^{-0.5M/52}) - C_t]e^{-0.5M/52}$$

The main assumption is that all squid groups have the same catchability, which is supported by the index of abundance comes from a standardized CPUE in which the area and length effects have been excluded. The rest of the model variables such as the adjustment to the data is done like in the model with a single group of squid.

### 3. RESULTS

#### 3.1 Depletion model in 2014

The beginning of the depletion was established in week 5 based on the start of the CPUE drop (Figure 2). The entry of the second pulse was established in week 27, with the CPUE increase and weight drop. The end of the second pulse depletion was established in week 35 with the entry of a new squid group of a smaller size that did not show depletion but a continuous CPUE increase.

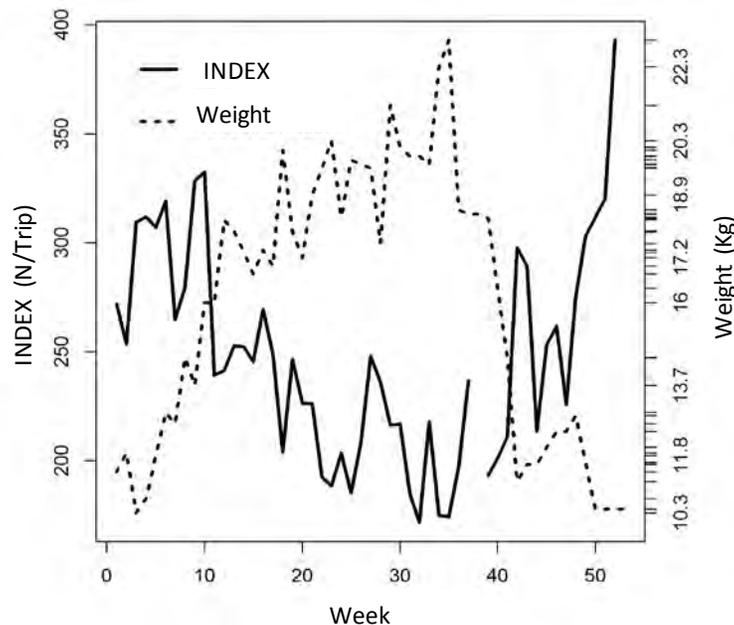


Figure 2. Weekly variation of the index of abundance (CPUE) and the individual weight, in 2014. The model fitted well to the data, without any trend in residuals through estimates (Figure 3). Biomass was estimated in 1,9 million tons in week 35 (Figure 4).

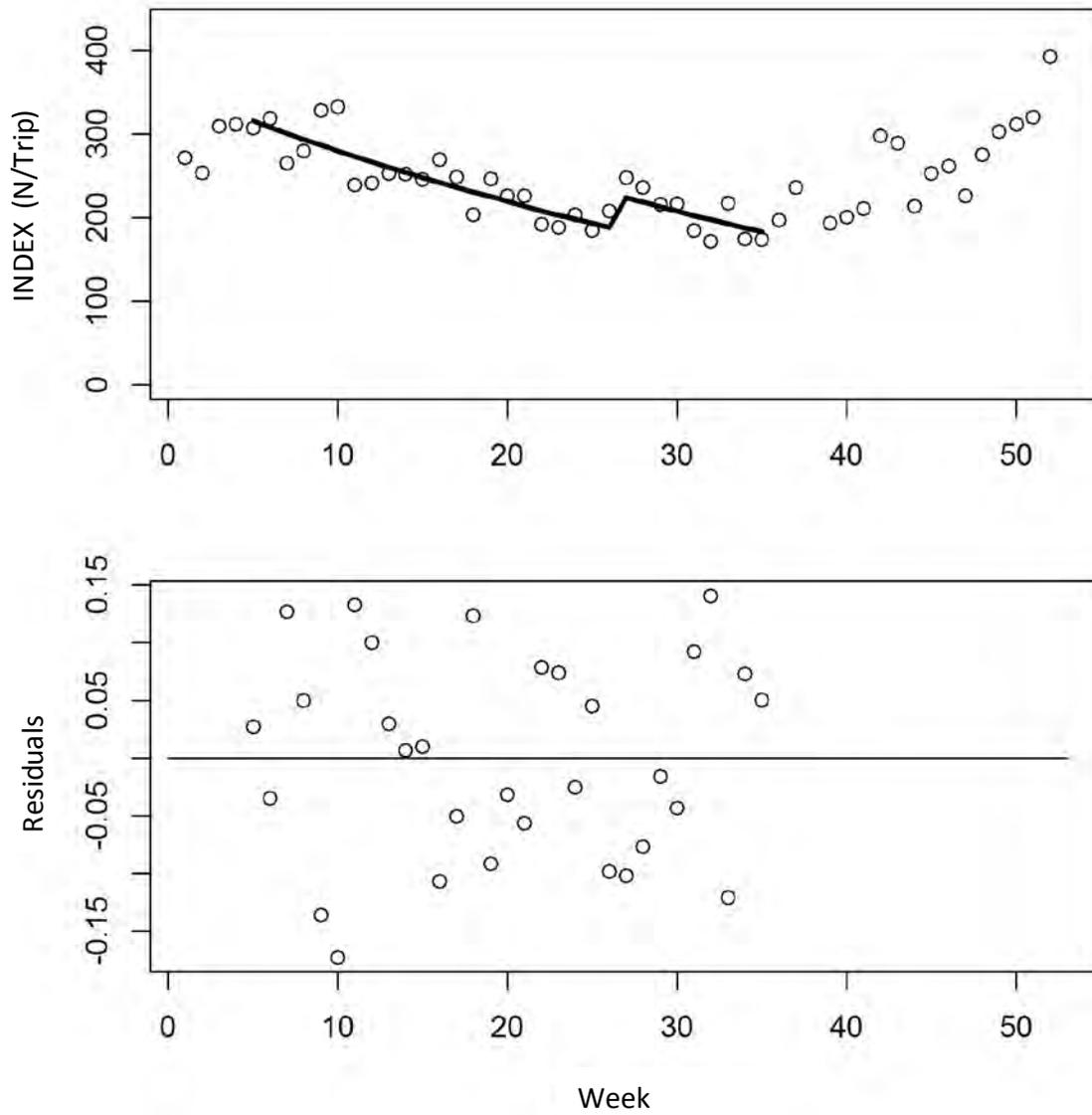


Figure 3. Fits of depletion model to abundance index (up) and its residuals (down). 2014.

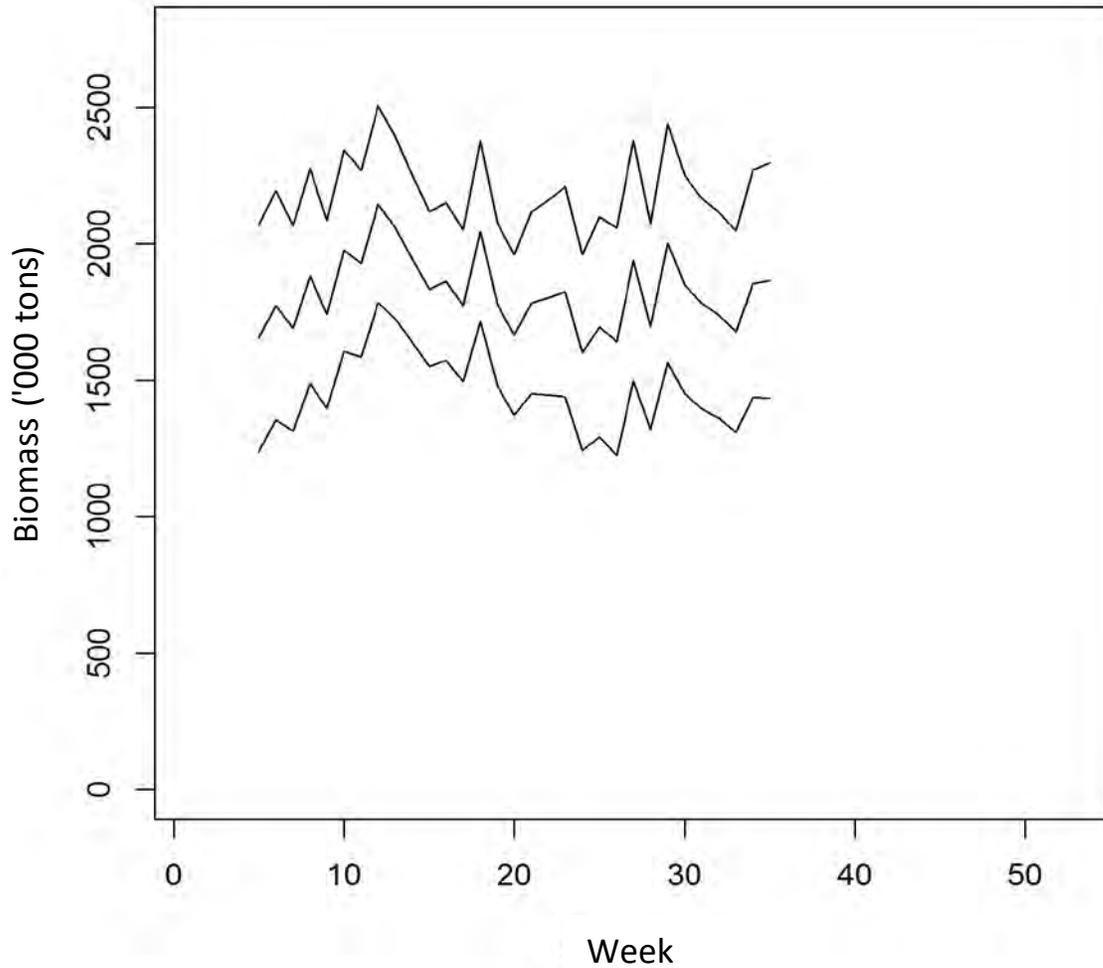


Figure 4. Biomasses, mode with lower and upper limits at 95% of confidence. 2014.

Catch of 144 thousand tons in 2014, would have allowed the escapement of 95% of the potential biomass in week 35 (Figure 5). Considering 40% of the potential biomass, as a desired escapement criterion, the catch quota of 200 thousand tons allowed to widely surpass this recommended escapement level.

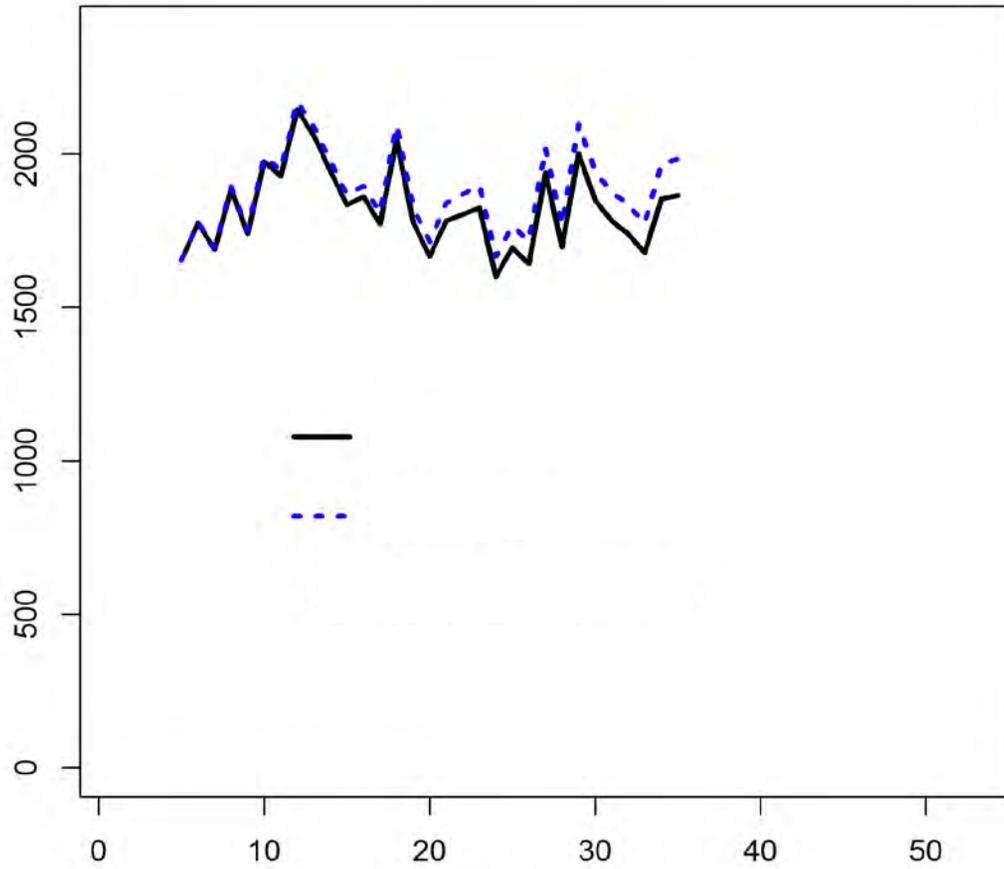


Figure 5. Surviving biomass to fishing and potential biomass that would have existed without fishing. The escapement or survival percentage in relation to biomass and potential biomass in week 35 is indicated. 2014.

### 3.2 Depletion model in 2015

Based on the changes in the mean weights and abundance index, three pulses or squid groups were identified. The first was present from the beginning of the year; the second arrived in week 8; and the third arrived in week 19 and remained until week 31. From week 32, new squid groups enter with lower mean weights and falling (Figure 6).

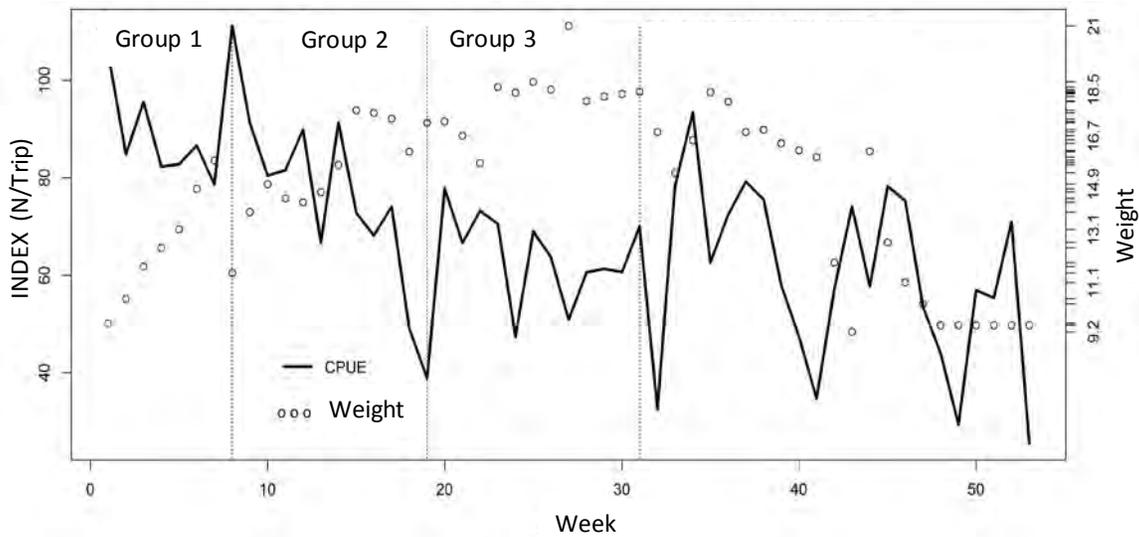


Figure 6. Identification of the arrival of different squid groups during the year, based on the mean weight variation (points) and abundance index (line). 2015.

The model adjusted well to the 2015 data (Figure 7).

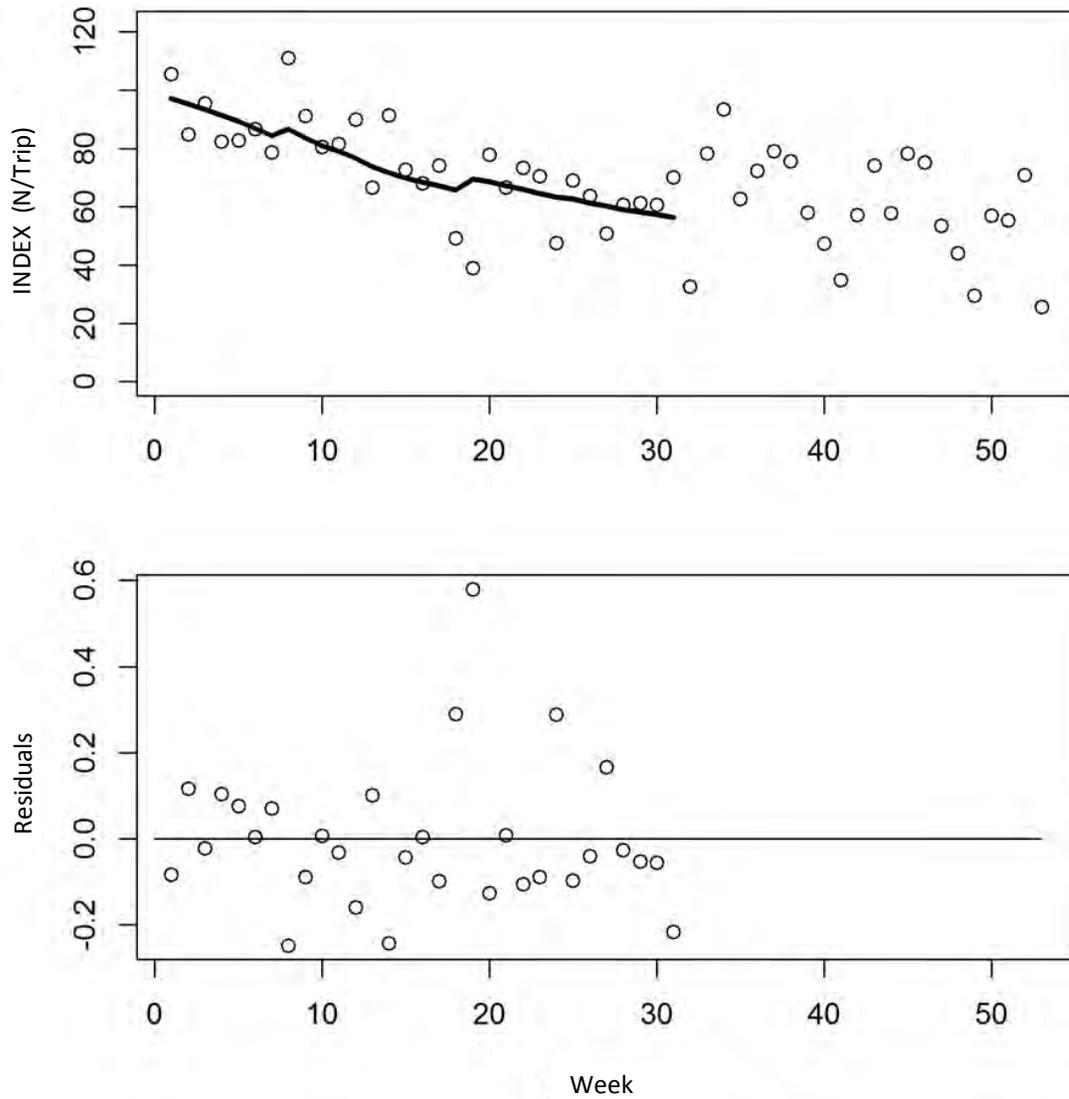


Figure 7. Fits of depletion model with three groups to the CPUE (up) and its residuals (down). 2015.

The depletion model with three groups estimated  $M$  equals to 0.5 and a relatively stable biomass during the weeks, since the decrease of abundance in number was compensated by the rapid growth in weight (Figure 8). Escapement in biomass was estimated at 70% (Figure 9).

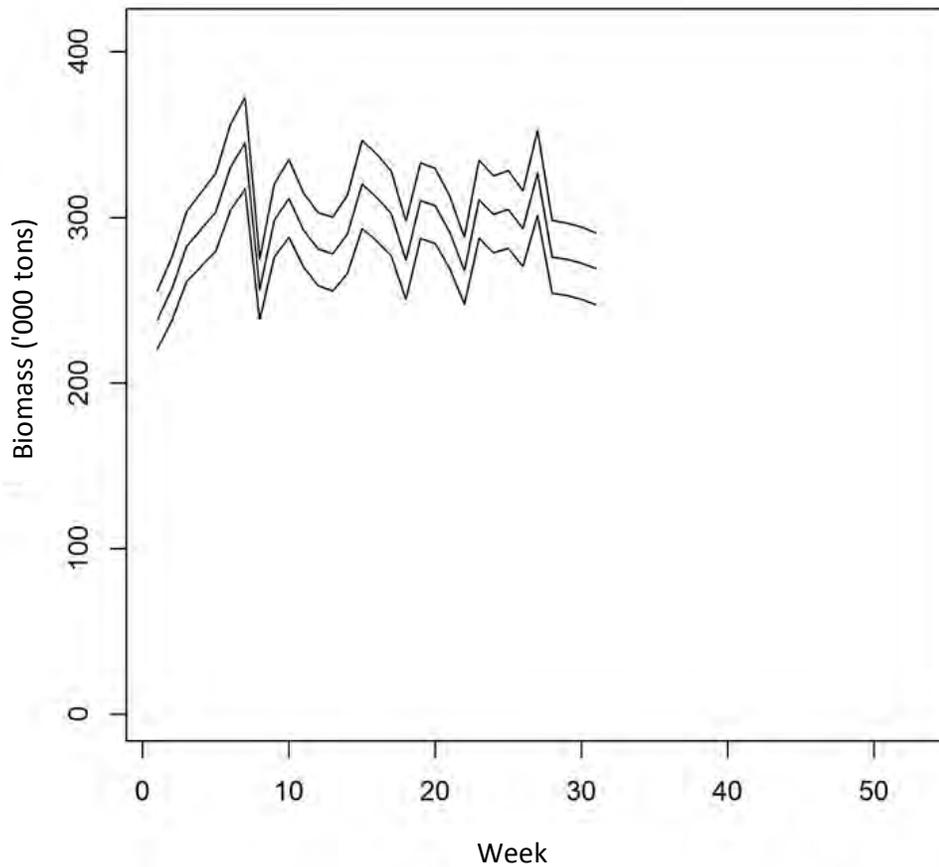


Figure 8. Biomasses, mode with lower and upper limits at 95% of confidence, estimated with the depletion model with three squid groups. 2015.

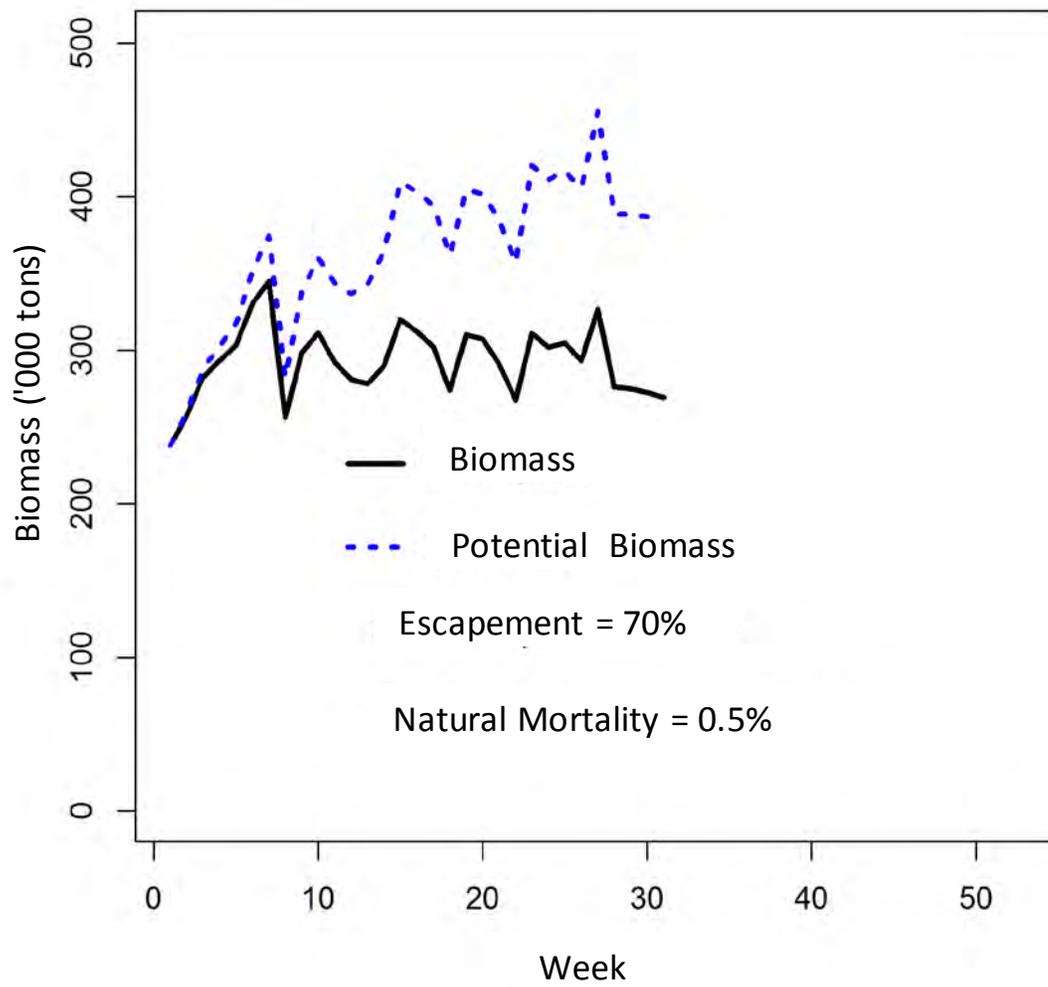


Figura 9. Potential biomass and biomasses with fishing. Depletion model with three squid groups. 2015.

### 3.3 Depletion model in 2016

Three pulses or squid groups were identified. The first group was present from the beginning of the year; the second arrived in week 12; and the third arrived in week 25. They remained until week 40. From week 41, a fourth squid group of lower mean weights entered (Figure 10).

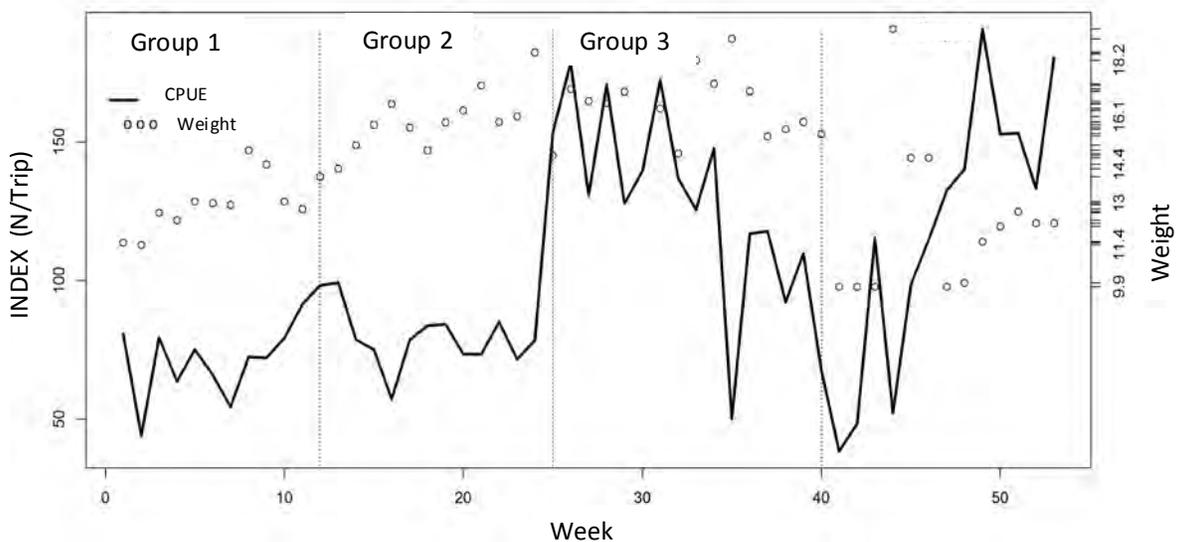


Figure 10. Identification of the arrival of different squid groups during the year, based on the variation of the mean weight (points) and abundance index (line). 2016.

In 2016, unlike previous years, models with three pulses included the estimations of different catchability coefficients for each pulse. The model selected was case 1, which estimated  $M$  at 0.72. The model fitted to data, but with some trend in residuals, since the third pulse generated many positive residuals (Figure 11).

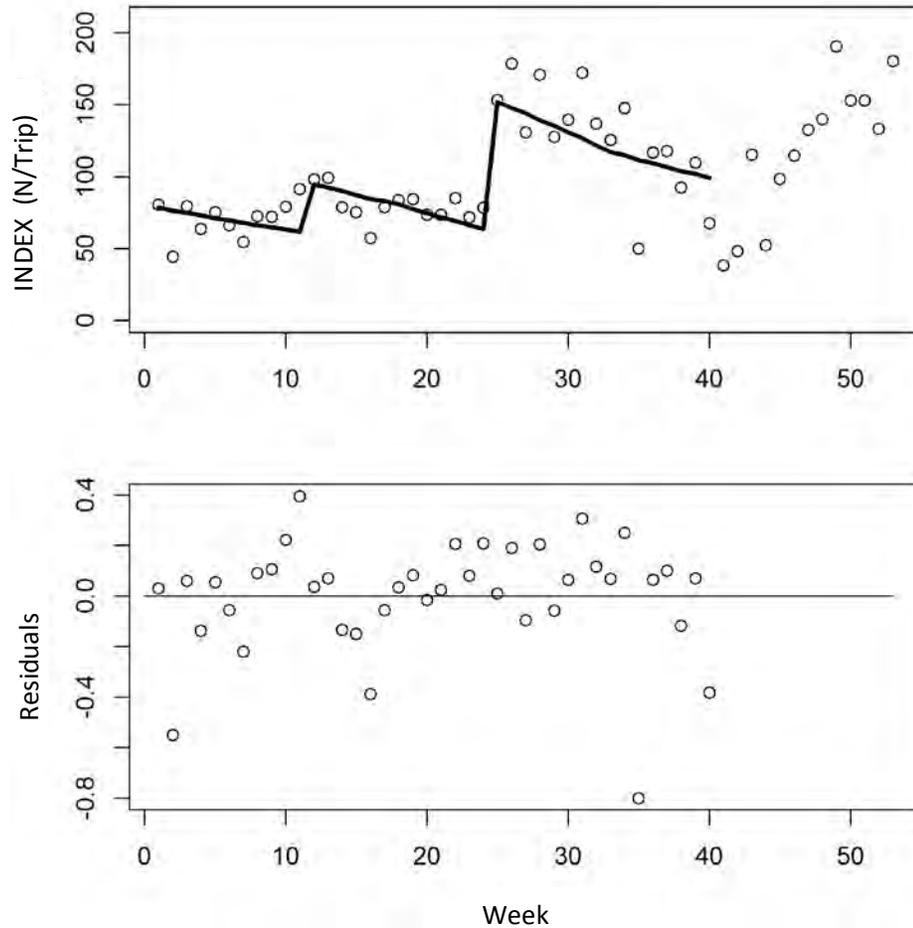


Figure 11. Fits of the depletion model with three groups with different catchability coefficients each. Fit to abundance index (up) and residuals (down). 2016.

Biomass showed a sustained decrease, with minor fluctuations due to the variation of mean weights (Figure 12). Abundance of groups 2 and 3 were not statistically different from zero and, therefore, the changes of the CPUE were generated by the changes of catchability.

Potential biomass without fishing showed a decreasing trend during the year; however, catches allowed the escapement of 56% in week 40 (Figure 13).

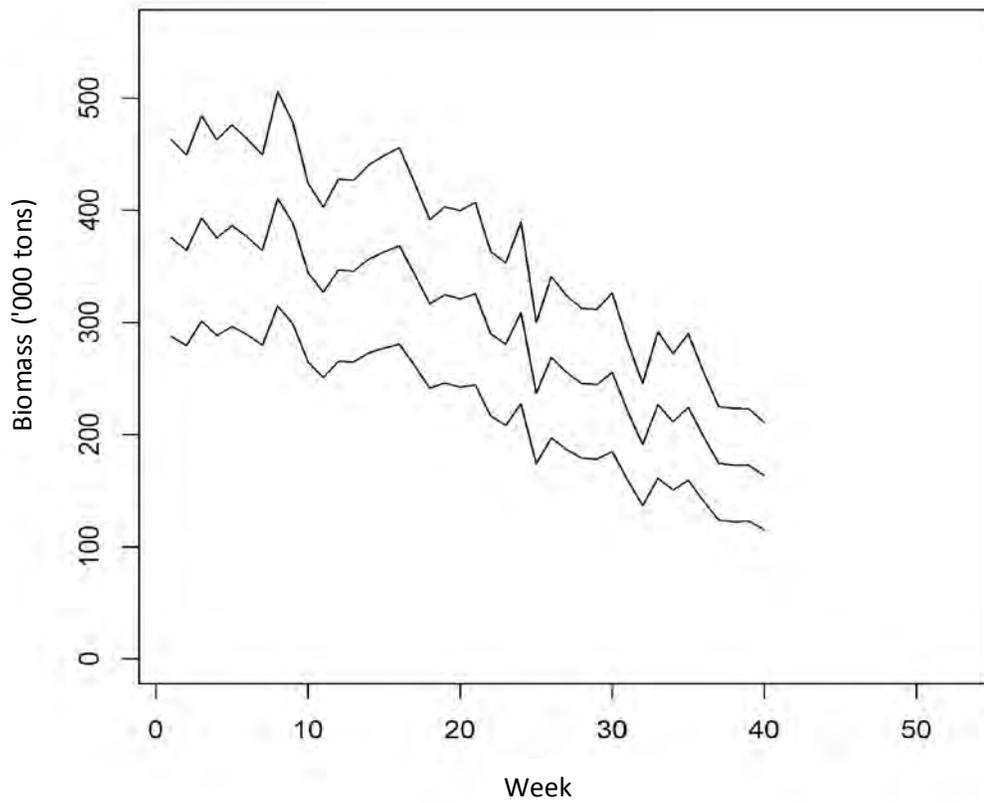


Figure 12. Biomasses, mode with lower and upper limits at 95% of confidence, estimated with the depletion model with three squid groups. 2016

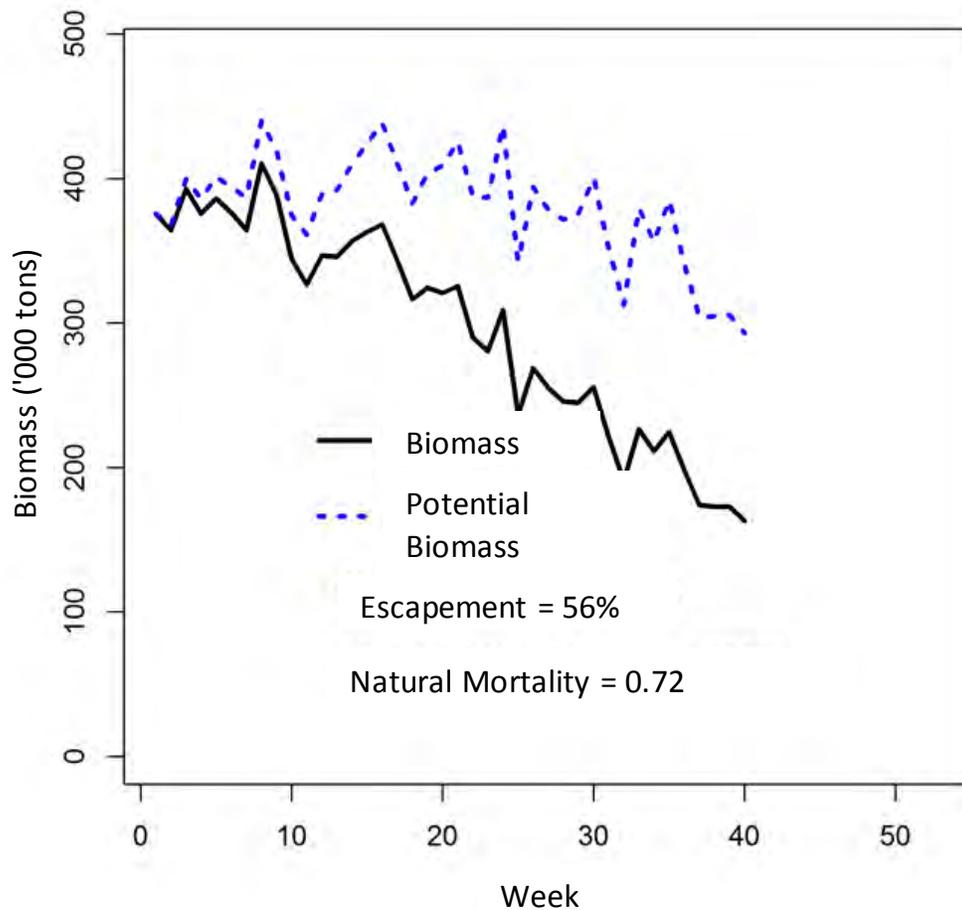


Figure 13. Potential biomass and biomasses with fishing. Depletion model with three pulses. 2016.

#### 4. DISCUSSION.

Analysis of mantle length frequencies and abundance indices (standardized cpue) per week are essential to understand the intra-annual dynamics of squids. Although Zuñiga *et al.* (2008) were able to find seasonal patterns of monthly catches between 2002 and 2005, and to suggest the potential presence of two cohorts per year, their results are biased since they analyzed a very initial two-year period in the development of the squid fishery.

Squid depletion models indicate a high variability on a general pattern that consists of the arrival of squids in November and departure in October next year. This pattern may have variations because of the entry of two or three squid pulses before they leave in October, and before the arrival of a new

group of smaller squids in November. This type of patterns per pulses is very similar to the pattern described by Payá (2007b) for the Falkland Islands-Malvinas squid.

A key element to model depletions is to consider that local depletions or entry of squids from different areas may exist. This is frequent in the case of the Falkland-Islands-Malvinas squid, but so far there is no information detected in squid in Chile. Analyzes conducted by fishing coves and ports covering from 29 to 38°S indicate a clear synchrony in the progression of size structure and the decrease of fishing yields.

The natural mortality, as always, is a key parameter that affects biomass level and therefore the escapement percentages. Since squids have a short life span (1,5 to 2 years), they should have a high mortality (1-1,5 per year); however, when these values were used in the Humboldt squid depletion models, extremely high biomass were estimated. When the prior distribution of  $M$  was relaxed and allowed more flexibility to the model to estimate  $M$ , its values fluctuated between 0.5 and 0.7. At first sight, these values seem low if a constant natural mortality through the entire life history is considered, but they may be plausible if are only for large squids (>60 cm ML), such as those captured in Chile, and there is not extrapolation to all squid sizes. As in all stock assessment of any resource, natural mortality is a key parameter that is not always well estimated.

The different models indicate that between 2015 and 2016 biomass that made it to escape was higher than the recommended biomass (>40% of the potential biomass at the end of the period). This would only be correct if squids that migrate from the Chilean coast to spawn are concentrated in a place with no fishing, such as the EEZ of the Chilean oceanic islands, but it is highly likely that squids migrate to spawn in Peru, where there is the main known spawning area of squid and where there is commercial fishing. Therefore, it is very difficult to know which the biomass percentage that finally escapes to reproduce is.

On the other hand, in depletion models, the initial biomass depends on the level of recruitment that enters the fishing grounds. In other squid fisheries, such as the Falkland-Islands-Malvinas squid, the recruitment depends on the escapement in biomass from the past fishing season and on the environmental conditions (temperature) during spawning and development of paralarvae and pre-recruits. In Chile, recruitments that make it to commercial capture are from large squids (>60 ML), probably the survivors of fishing operations carried out within the SPRFMO area and Peru's EEZ. In conclusion, in order to know the status of the total squid stock and in particular the stock of large squids fished in Chile, it is necessary to include Information from catches conducted within the SPRFMO area and in EEZ of coastal countries.

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**A N N E X**

ADMB code of CHUSMODEL, Chilean HUmboldt Squid Depletion Model.

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Proper citation:

Payá. I. 2017. Estatus y posibilidades de explotación biológicamente sustentables de los principales recursos pesqueros nacionales al año 2018. Jibia, año 2018. ANEXO III. Código de CHUSMODEL, Chilean HUmboldt Squid Depletion Model. Instituto de Fomento Pesquero.

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1  ////////////////////////////////////////////////////////////////////
2  //                                                                    //
3  // Chilean Humboldt Squid depletion Model (CHUSModel)                //
4  // with 3 grups or cohorts                                           //
5  //                                                                    //
6  // Version 4.0                                                        //
7  // Ignacio Payá, 2017                                               //
8  //                                                                    //
9  // Proper citation:                                                 //
10 // Payá. I. 2017. Estatus y posibilidades de explotación           //
11 // biológicamente sustentables de los principales                  //
12 // recursos pesqueros nacionales al año 2018. Jibia, año 2018.     //
13 // ANEXO III. Código de CHUSMODEL, Chilean HUmboldt Squid         //
14 // Depletion Model. Instituto de Fomento Pesquero.                 //
15 //                                                                    //
16 ////////////////////////////////////////////////////////////////////
17
18
19 GLOBALS_SECTION
20   const double pi = 3.141592654;
21   #undef reporte
22   #define reporte(object) report <<"# "#object "\n" << object << endl;
23
24 TOP_OF_MAIN_SECTION
25   arrmblsize = 50000000;
26   gradient_structure::set_GRADSTACK_BUFFER_SIZE(1.e7);
27   gradient_structure::set_CMPDIF_BUFFER_SIZE(1.e7);
28   gradient_structure::set_MAX_NVAR_OFFSET(5000);
29   gradient_structure::set_NUM_DEPENDENT_VARIABLES(5000);
30
31 DATA_SECTION
32   // Read data file
33   init_int nc
34   init_matrix Mdata(1,nc,1,5) // Semanas t
35   number halfnlog2pi
36   number nu
37   ivector t(1,nc)
38   vector Y(1,nc)
39   vector W(1,nc)
40   vector C(1,nc)
41   vector l(1,nc)
42   !! ad_comm::change_datafile_name("CHUSMODEL3B.ctf");
43   init_int tini
44   init_int tini_2
45   init_int tini_3
46   init_int tfin
47   init_number minlogN

```

```

1   init_number maxlogN
2   init_number minlogq
3   init_number maxlogq
4   init_number minlogM
5   init_number maxlogM
6   init_int faseN
7   init_int faseq
8   init_int faseM
9   init_number sigmaM
10  init_number sigma
11  int neval
12
13  PARAMETER_SECTION
14  // Nini
15  init_bounded_number logNi(minlogN,maxlogN,faseN)
16  init_bounded_number logNi_2(minlogN,maxlogN,faseN)
17  init_bounded_number logNi_3(minlogN,maxlogN,faseN)
18  init_bounded_number logq1(minlogq,maxlogq,faseq)
19  init_bounded_number logq2(minlogq,maxlogq,faseq)
20  init_bounded_number logq3(minlogq,maxlogq,faseq)
21  init_bounded_number logM(minlogM,maxlogM,faseM)
22  // Derived
23  sdreport_number Ni
24  sdreport_number Ni_2
25  sdreport_number Ni_3
26  sdreport_number q1
27  sdreport_number q2
28  sdreport_number q3
29  sdreport_number M
30  number M_p
31  sdreport_vector N(1,nc)
32  sdreport_vector B(1,nc)
33  vector Bfit(1,nc)
34  vector lfit(1,nc)
35  vector logl(1,nc)
36  number RSS
37  sdreport_vector Bsp(1,nc)
38  vector Nsp(1,nc)
39  sdreport_number PorBioSobre
40  number likeprior
41  number likedata
42
43  // Objfun
44  objective_function_value f
45
46  PRELIMINARY_CALCS_SECTION
47  // Data

```

```

1   t= (ivector)column(Mdata,1);
2   Y= column(Mdata,2);
3   W= column(Mdata,3);
4   C= column(Mdata,4);
5   l= column(Mdata,5);
6   neval=0;
7   M_p=mfexp(logM);
8
9   PROCEDURE_SECTION
10  get_fit();
11  prior();
12  get_neglogL();
13
14  FUNCTION get_fit
15  RSS.initialize();Ni.initialize();q1.initialize();q2.initialize();q3.initialize();
16  Ni = mfexp(logNi);
17  Ni_2 = mfexp(logNi_2);
18  Ni_3 = mfexp(logNi_3);
19  q1 = mfexp(logq1);
20  q2 = mfexp(logq2);
21  q3 = mfexp(logq3);
22  M=mfexp(logM);
23  nu=0; N=0; B=0;Bsp=0;
24  for(int t=tini; t<=tfin; t++){
25    if (t==tini){
26      N(t)=Ni;
27      Nsp(t)=Ni;
28      B(t)=N(t)*W(t);
29      Bsp(t)=B(t);
30    }
31    else
32    {
33      if (t==tini_2){
34        N(t) = (( (Ni_2+N(t-1))*exp(-M/52/2))-C(t-1)) *exp(-M/52/2) ;
35        Nsp(t) = (Ni_2+Nsp(t-1)) *exp(-M/52) ;
36      }
37      else{
38
39        if (t==tini_3){
40          N(t) = (( (Ni_3+N(t-1))*exp(-M/52/2))-C(t-1)) *exp(-M/52/2) ;
41          Nsp(t) = (Ni_3+Nsp(t-1)) *exp(-M/52) ;
42        }
43        else{
44          N(t) = ((N(t-1)*exp(-M/52/2))-C(t-1))*exp(-M/52/2) ;
45          Nsp(t) = Nsp(t-1)*exp(-M/52) ;
46        }
47      }

```

```

1      B(t)=N(t)*W(t);
2      Bsp(t)=Nsp(t)*W(t);
3  }
4  if (N(t)<0.0) {N(t)=0.00001;}
5  if (Nsp(t)<0.0) {Nsp(t)=0.00001;}}
6
7  for(int t=tini; t<=tfin; t++){
8      if (l(t)>0){
9          nu=nu+1;
10         logl(t) = log(l(t)+0.0000001);
11         if(t<tini_2){
12             lfit(t) = q1*N(t);}
13         else if(t<tini_3){
14             lfit(t) = q2*N(t);}
15         else{lfit(t) = q3*N(t);}
16     }
17     RSS +=square( logl(t) - log(lfit(t)+0.0000001));}
18
19     PorBioSobre=B(tfin)/Bsp(tfin)*100;
20
21     if ( last_phase() ) neval+=1;
22     else neval=-2.;
23
24     FUNCTION prior
25     if (faseM>0) likeprior= 0.5*log(2*pi) + log(sigmaM) + square(log(M_p)-logM)/(2*sigmaM);
26     else likeprior=0;
27
28     FUNCTION get_neglogL
29     likedata = 0.5*nu*log(2*pi) + nu*log(sigma) + RSS/(2*sigma);
30     f = likedata + likeprior;
31
32     REPORT_SECTION
33     report << "##-----" << endl;
34     report << "## Chilean Humboldt Squid Depletion Model (CHUSModel)" << endl;
35     report << "## Ignacio Payá, 2017 " << endl;
36     report << "## version 4.0" << endl;
37     report << "## Three groups " << endl;
38     report << "## " << endl;
39     report << "## Citar como (Proper citation)" << endl;
40     report << "## " << endl;
41     report << "## Payá. I. 2017. Estatus y posibilidades de explotación" << endl;
42     report << "## biológicamente sustentables de los principales " << endl;
43     report << "## recursos pesqueros nacionales al año 2018. Jibia, año 2018. " << endl;
44     report << "## ANEXO III. Código de CHUSMODEL, Chilean HUmboldt Squid " << endl;
45     report << "## Depletion Model. Instituto de Fomento Pesquero. " << endl;
46     report << "##-----" << endl;
47     report << " " << endl;

```

```

1
2 report << "##-----" << endl;
3 report << "## Model fitting scenario and assumptions" << endl;
4 report << "##-----" << endl;
5 report << "##--1st Starting Week is: " << tini << endl;
6 report << "##--2nd Starting Week is: " << tini_2 << endl;
7 report << "##--3rd Starting Week is: " << tini_3 << endl;
8 report << "##--End Week is: " << tfin << endl;
9 report << "##--N phase is: " << faseN << endl;
10 report << "##--q phase is: " << faseq << endl;
11 report << "##--M phase is: " << faseM << endl;
12 report << "##--Likelihood of data is: " << likedata << endl;
13 report << "##--Likelihood of M Prior is: " << likeprior << endl;
14 report << "##--Whole Likelihood is: " << f << endl;
15 report << "##--CV M is: " << sigmaM/M << endl;
16 report << "##--CV RSS is: " << sigma/(RSS/nu) << endl;
17 report << " " << endl;
18
19 report << "##-----" << endl;
20 report << "## Model fit diagnostics" << endl;
21 report << "##-----" << endl;
22 report << "##--Number of function evaluations: " << neval << endl;
23     if( objective_function_value::gmax < 1.e-3 )
24         report << "##--MaxGrad = " << objective_function_value::gmax << ": model converged--
25 "<< endl << endl;
26
27     reporte(tini)
28     reporte(tini_2)
29     reporte(tini_3)
30     reporte(tfin)
31     reporte(t)
32     reporte(N)
33     reporte(W)
34     reporte(B);
35     reporte(Bsp);
36     reporte(lfit);
37     reporte(l);
38     reporte(Y);
39     reporte(C);
40     reporte(nu);
41     reporte(q1);
42     reporte(q2);
43     reporte(q3);
44     reporte(M_p);
45     reporte(M);
46     reporte(PorBioSobre);

```