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A Bayesian state-space size-structured population dynamics model for northern hake

Margarita María Rincón [1] * Santiago Cerviño [2] **
Samu Mäntyniemi [3] *** José Castro [2] Javier Ruiz [1]

[1] Instituto de Ciencias Marinas de Andalucía, Consejo Superior de Investigaciones Científicas, ICMAN-CSIC, Puerto Real, Cádiz, Spain
[2]Instituto Español de Oceanografía, IEO, Vigo, Spain. [3]Fisheries and Environmental Management Group, University of Helsinki, Finland

Abstract

In fisheries research bayesian state-space models have been proved to be very useful because of their capacity to include new data while measuring the uncertainty associated to biological and physical processes. The ECOKNOWS (Effective use of ecosystem and biological knowledge in fisheries) project proposes to use bayesian analysis in a general population dynamics model GPDM as a powerful tool to include biological and physical information in management strategies. Results of a preliminary Bayesian model adapting this model to northern hake population dynamics are presented here. The model intends to reproduce as far as possible the structure and main assumptions of the current ICES model. Actually there are some parameters with convergence problems but we are developing a new version considering informative priors for the biological processes which are supposed to ameliorate the estimations.

Introduction

European hake (*Merluccius merluccius*) is widely distributed over the Northeast Atlantic shelf, from Norway to Mauritania, with a larger density from the British Islands to the south of Spain (Casey and Pereiro, 1995; Murua, 2010) and in the Mediterranean and Black sea. ICES assumes two different stock units, being the Northern stock distributed northwards than Iberian peninsula, in ICES Division IIIa, Subareas IV, VI and VII and Divisions VIIIa,b,d. Northern hake is caught by different countries (Spain, France, Ireland, UK, etc) and different fleets (trawlers, gillnetters, longlinners, etc) in a mixed fishery where the other main species are megrims, anglerfishes, neprhops, etc. The mean landings in recent years are around 45 thousand tonnes in the first decade of XXI century although these have risen to 73 thousand tonnes in 2010 (ICES, 2012). Discards are around 2 thousand tonnes in recent years. Catch data from 1978 are used for assessment purposes.

*margarita.rincon@icman.csic.es
**santiago.cervino@vi.ieo.es
***samu.mantyniemi@helsinki.fi

Fleet	Selection	ICES fleet	Discards	Retention
1	Double Normal	SPTRAWL7	Yes	Logistic
2	Double Normal	FRNEP8	Yes	Logistic
3	Double Normal	SPTRAWL8	Yes	Logistic
4	Logistic	TRAWLOTH+OTHERS	No	
5	Double Normal	GILLNET+LONGLINE	No	

Table 1: Fleets in hake Bayesian GPDM.

Hake is an important species for the fishing activity in the area and also has an important role in the ecosystem as top predator. Despite this their biology has many unknowns making difficult an accurate assessment. Allometric length-weight relationship ($W(g) = 0.00513 * L(cm)^{3.074}$) and maturity-at-length logistic parameters ($L_{50} = 42.85\,cm$ and $slope = -0.2$) are assumed to be constant on time as used in the ICES assessment. Hake growth is relatively unknown. Studies developed in the first years of XXI century showed that hake grows about two times faster than assumed under previous otolith ring interpretation (de Pontual et al., 2003, 2006; Piñeiro et al., 2007). Since age interpretation was wrong and there is not an alternative to assign ages, ICES decided to move to a length based assessment model with SS3 (Methot, 2000). Since the tagging information reported growth rates about two times faster than previously assumed the natural mortality rate was corrected following Hewitt and Hoenig (2005) from 0.2 to 0.4 year -1. For modelling purposes M was set as 0.4; the growth follows Von Bertalanffy functions with $Linf$ as 130 and k estimated by the model was 0.177 $year^{-1}$.

ECOKNOWS (Effective use of ecosystem and biological knowledge in fisheries) is a FP7-KBBE project in the topic "Improving fisheries assessment methods by integrating new sources of biological knowledge". The main aim of the project is to develop models that use all the available biological information which is likely to be useful for the management of specific stocks in a bayesian statistical context. Classical statistical methods do not allow combining existing information with new data. Bayesian statistics, uses prior knowledge, that is knowledge we have before we start to analyze any new data. If the new data includes more information about the parameters, then the Bayesian calculus combines the prior information with the new information in a process that can be called scientific learning (Gelman et al., 2003; Congdon, 2003). The ECOKNOWS project provides the support for the development of a General Population Dynamic Model which will be adapted to simulate the ICES model used to the hake dynamics and this model will be used to implement the hake biological knowledge coming from other hake species related with growth, mortality or reproduction.

The goal of this work is to develop a Bayesian model for Northern hake able to deal with the biological process. In this first stage we will present the current status and future development of the Bayesian model. Our aim is that the model presented reproduces as far as possible the structure and main assumptions of the current ICES model.

Materials and methods

The data used for this work were extracted from the input file used in the ICES assessment with SS3. This data ranges from 1978 to 2010 split by quarters and considers 7 fleets and 4 surveys. 3 of the fleets have also discards. These data consist on total landings in weight and length distribution for all fleets and surveys. Length distributions available are grouped by 2 cm length classes from 4 to 100 cm. The approach to develop this Bayesian model begins with a simpler data grouping. The current version uses 10 years (2001-2010), four quarters, 19 length groups (1, 5, 10, 15, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 60, 70, 80, 100) and 5 fleets (Table 1).

Model description

Process model

Spawning

At the beginning of each month the female population is assumed to spawn once each quarter. They are supposed to produce a number of eggs computed with the following dot product:

$$Eggs_t = (\mathbf{\Phi_t} \cdot N_t \mathbf{eggs_t})$$

Where $\mathbf{\Phi_t} = (\phi_{t,1}, \ldots, \phi_{t,k})$ denotes the relative size class frequencies allocating the population N_t in K length classes and $\mathbf{eggs_t} = (e_{t,1}, \ldots, e_{t,K})$, is the number of eggs per kilogram spawned by a mature female of length class K (aprox 1000 eggs by kilogram). In order to calculate the kilograms equivalent to a determined length, the weight-length relationship with $a = 0.00000531$ and $b = 3.074$ was used.

Recruitment and population dynamics

Recruitment is determined by K_{bh} and α parameters in the following Beverton-Holt model:

$$R_t = \frac{K_{bh} Eggs_t}{\frac{K_{bh}}{\alpha} + Eggs_t}$$

The recruits are incorporated to the change in total population size equation as:

$$N_{t+1} \approx p_t N_t + R_{t+1}$$

Where N_t and p_t are the number of individuals into the stock and the expected survival at time t, respectively, while R_{t+1} is the number of recruits at time $t+1$.

Growth

Growth of individuals is assumed to take place instantly in the beginning of each month. Each individual has the possibility of stay in the same length class or move higher. This movement is modelled through a transition matrix $\mathbf{g_t} = (g_{t,i,j})_{K \times K}$, where $g_{t,i,j}$ denotes the probability of and individual to move from length class i to length class j at time t. A normally distributed growth from each length class is assumed following the von Bertanlanffy growth function, such that length at time t is $l_t = Linf * (1 - exp(-k_g * (t - t_0)))$, where k_g is a parameter for somatic growth rate and $Linf$ is maximum size (see Appendix A in Mantyniemi 2013).

After growth, vector $\mathbf{\Phi_t}$ becomes $\mathbf{\Phi_t^{(G)}} = \mathbf{\Phi_t} \times \mathbf{g_t}$ describing a modified size distribution of the population.

Mortality and survival

A fish in length class $k, k = 1, \ldots, K$, after growth could be caught by fleet $j, j = 1, \ldots, F$, or to survive, with respective probabilities given by Baranov (see for example Quinn and Deriso, 1998) as follows:

$$\begin{aligned} \gamma_{t,k,j} &= \frac{F_{t,k,j}}{\sum_{j=1}^{F} F_{t,k,j} + M} (1 - e^{-(\sum_{j=1}^{F} F_{t,k,j} + M)}) \phi_{t,k}^{(G)} \\ p_t &= \sum_{k=1}^{K} (1 - e^{-(\sum_{j=1}^{F} F_{t,k,j} + M)}) \phi_{t,k}^{(G)} \end{aligned}$$

With $M = 0.1$ as the natural mortality and

$$F_{t,k,j} \approx propF_j \cdot Fsel_{k,j} \cdot F, \tag{1}$$

the fishing mortality for the $j-th$ fleet, where $propF_j$ is a parameter for the proportion of fishing mortality corresponding to fleet j, $Fsel_{k,j}$ is the fishing selectivity for fleet j and F the parameter for total fishing mortality.

When the hake is caught it has two posibilities, to be landed with probability $\gamma_{t,k,j} Rsel_{k,j}$ or to be discarded with probability $\gamma_{t,k,j}(1 - Rsel_{k,j})$, both determined by the retention pattern of the $j-th$ fleet, $Rsel_{k,j}$.

Then the proportion of landed fish and discarded fish from all death fish, q_t^l and q_t^d, is computed respectively, as:

$$q_t^l = \frac{1}{1-p_t}\sum_{j=1}^{F}\sum_{k=1}^{K}\gamma_{t,k,j}Rsel_{k,j} = \frac{1}{1-p_t}\sum_{j=1}^{F}q_{t,j}^l$$

$$q_t^d = \frac{1}{1-p_t}\sum_{j=1}^{F}\sum_{k=1}^{K}\gamma_{t,k,j}(1-Rsel_{k,j}) = \frac{1}{1-p_t}\sum_{j=1}^{F}q_{t,j}^d$$

Fishing selectivity, survey selection and retention patterns

Table 1 summarizes the descriptions of the functions chosen for the fishing selectivity, $Fsel_{k,j}$, survey selection, $Ssel_{k,s}$ and retention patterns, $Rsel_{k,j}$, for each fleet. The particular case of northern hake includes 5 fleets for fishing selectivity and retention ($F = 5$) and 3 different ones for survey selectivity. Fishing selectivity for fleets 1,2,3 and 5 is modelled with a double normal function while for fleet 4, a logistic function was used. Retention applies only for the first three fleets and each one is modelled with a logistic function, for the other two fleets the retention is assumed constant equal to 1. The double normal selection function is defined by parameters τ_{1j}, τ_{2j} and $l_j, j = 1, 2, 3, 5$, as follows:

For $\mathbf{M} = (M_1, \ldots, M_K)$ a vector with the midpoints of each length class k

$$Fsel_{k,j} = \begin{cases} e^{-\tau_{1j}(M_k - l_j)^2} & \text{if } M_k < lj, \\ e^{-\tau_{2j}(M_k - l_j)^2} & \text{if } M_k \geq lj, j = 1, 2, 3, 5 \end{cases}, \tag{2}$$

The logistic function with parameters α_j^f and $\beta_j^f, j = 4$ or α_j^r and $\beta_j^r, j = 1, 2, 3$ is used for fishing selectivity and retention, respectively:

$$\begin{aligned} logit(Fsel_{k,j}) &= \beta_j^f(M_k - \alpha_j^f), j = 4 \\ logit(Rsel_{k,j}) &= \beta_j^r(M_k - \alpha_j^r), j = 1, 2, 3 \end{aligned}$$

The survey selection patterns are modelled as double normal analogously to equation (2) , with parameters $I\tau_{1s}, I\tau_{2s}$ and $Il_s, s = 1, 2, 3$.

Observational model

Landings and discards in numbers

Landings and discards at time t, l_t and dis_t, respectively, are assumed to follow a beta-binomial distribution.

$$\begin{aligned} l_t &\sim Betabin(q_t^l, 1 - q_t^l, d_t) \quad t = 1, \ldots, T \\ dis_t &\sim Betabin(q_t^d, 1 - q_t^d, d_t) \quad t = 1, \ldots, T \end{aligned}$$

For q_t^l and q_t^d as defined before and $d_t \approx N_t(1 - p_t)$ representing all the death fishes (by natural and fishing mortality) at time t.

Proportion of landings and discards by fleet

From available data for landings and discards numbers by fleet, the vector of proportions $\mathbf{Pl_t} = (Pl_{t,1}, \ldots, Pl_{t,F})$ and $\mathbf{Pd_t}$, respectively, are calculated. They are modelled with a Dirichlet-Multinomial distribution.

$$\begin{aligned} \mathbf{Pl_t} &\sim DM(l_t, \frac{1}{q_t^l}(q_{t,1}^l, \ldots, q_{t,F}^l)) \quad t = 1, \ldots, T \\ \mathbf{Pd_t} &\sim DM(dis_t, \frac{1}{q_t^d}(q_{t,1}^d, \ldots, q_{t,F}^d)) \quad t = 1, \ldots, T \end{aligned}$$

For speed up computational time the Dirichlet approximation described in Mantyniemi 2012 was implemented.

Length Distribution of landings and discards by fleet

Vector of length distribution of landings by fleet, $\mathbf{Ll_{t,j}} = (Ll_{t,j,1}, \ldots, Ll_{t,j,K})$, and discards, $\mathbf{Ld_{t,j}}$, are presented in percentages, and assumed to be multinomially distributed.

$$\begin{aligned}\mathbf{Ll_{t,j}} &\sim Multi(100, \frac{1}{q^l_{t,j}}(\gamma_{t,1,j} Rsel_{1,j}, \ldots, \gamma_{t,K,j} Rsel_{K,j}))\\ \mathbf{Ld_{t,j}} &\sim Multi(100, \frac{1}{q^d_{t}}(\gamma_{t,1,j}(1 - Rsel_{1,j}), \ldots, \gamma_{t,K,j}(1 - Rsel_{K,j}))\end{aligned}$$

Survey indexes

Estimations of the population by length through surveys are available for some quarters with three different fleets $I_{t,s}, s = 1, 2, 3$. They are assumed lognormally distributed with a coefficient of variation $CV = 0.2$, as follows:

$$I_{t,k,s} \sim LN(log(q_s N_t \phi_{t,k} Ssel_{k,s}) - log(CV^2+1)/2, 1/log(CV^2+1)) \quad k = 1, \ldots, K, s = 1, 2, 3.$$

Prior distributions

Function	**Priors**
Initial abundance	log(N[1])~N(dnorm(muN,s2N), muN=0, s2N=10000
F	F~dunif(0,0.5)
Fleet 1-Selection Double normal	tau11~dunif(0,0.3), tau21~dunif(0.0005,0.01) l11~dunif(20,40)
Fleet2 - Selection Double normal	tau12~dunif(0.002,0.3), tau22~dunif(0.002,0.3) l12~dunif(10,30)
Fleet3 -Selection Double normal	tau13~dunif(0,0.3), tau23~dunif(0.00005,0.01) l13~dunif(20,60)
Fleet 4- Selection Logistic	alphaFsel~dnorm(-40,1/400)T(-60,-10) betaFsel~dunif(0.1,0.99)
Fleet 5- Selection Double normal	tau15~dunif(0.002,0.01), tau25~dunif(0.0005,0.005) l15~dunif(50,90)
Fleet 1 retention pattern – Logistic	alphaGsel[1]~dnorm(-27,0.01), betaGsel[1]~dunif(0.001,3)
Fleet 2 retention patters – logistic	alphaGsel[2]~dnorm(-27,0.01) betaGsel[2]~dunif(0.001,3)
Fleet 3 retention pattern - logistic	alphaGsel[3]~dnorm(-27,0.01) betaGsel[3]~dunif(0.001,3)
Survey1- double normal	Itau11~dunif(0.0001,0.01), Itau21~dunif(0.0005,0.005) Il11~dunif(40,80), q1~dunif(5e-5,10e-3)
Survey2- double normal	Itau12~dunif(0.001,0.5), Itau22~dunif(0.001,0.1) Il12~dunif(1,30), q2~dunif(10e-3,10e-1)
Survey3- double normal	Itau13~dunif(0.001,0.5), Itau23~dunif(0.00001,0.1) Il13~dunif(5,30), q3~dunif(10e-5,10e-3)
Growth (Logit)	Gk = mink+(maxk-mink)*pk, mink=0.025; maxk = 0.075; logit pk ~ dnorm(0,1)
Beverton-Holt	log(K)~dnorm(muK,s2K), muK=log(0.2), s2K=25

The prior distributions have been chosen uninformative but with plausible boundaries in order to allow parameters to move in a wide range of values.

Preliminary results

The results presented here correspond to 520000 iterations. The first 20000 for adaptation without thinning and after that a thinning of 100 was applied. The total run takes 562.68 hours.

Observed-expected (total numbers)

GPDM works minimizing the catch and discards in numbers in every time step. The plot 1 shows how this fit performs. We can see a good performance fitting discards and similarities with landings, except for year 2009 where the model overestimate the values. The coherence between the time series data and the estimations could be interpreted as a partial validation of the model definition.

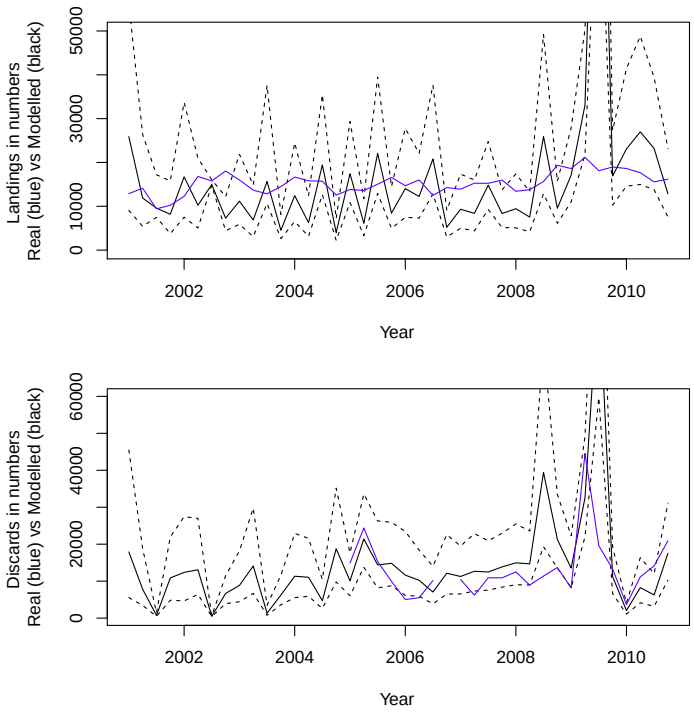

Figure 1: Comparison between modelled and real quaterly data for landings and discards in numbers (thousands). Blue line corresponds to real numbers transformed from ICES landings biomass data using the lenght at weight relationship. Solid black line corresponds the modelled median and dotted lines represent the 0.05 and 0.95 percentiles.

Model results

Selection and Retention plots

Selection and retention patterns are displayed in Figures 2 and 3, respectively. The model reproduces propperly the selection and retention patterns compared with ICES estimations, except for the discards of fleet SPTRAWL8, which is coherent with the mixing problems associated to the parameters involved, alphaGsel[3] and betaGsel[3], see Appendix I.

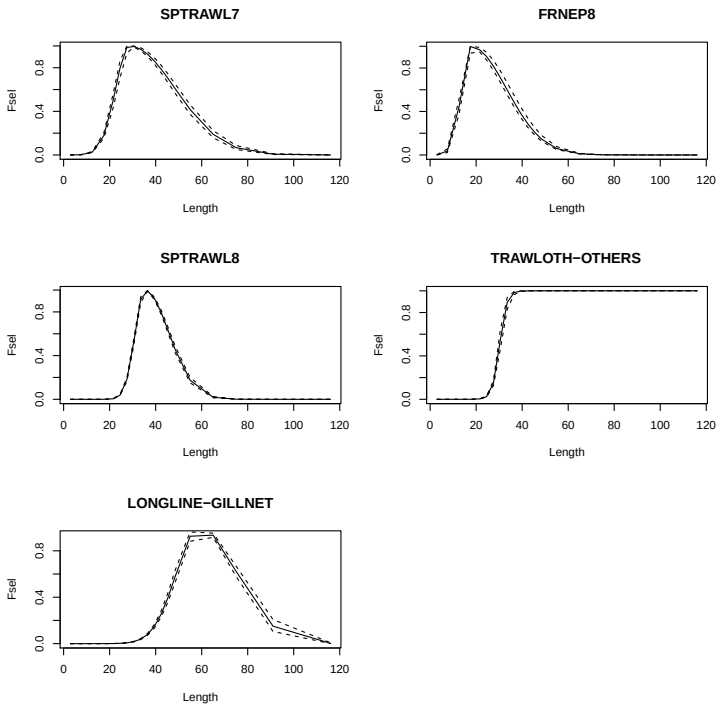

Figure 2: Modelled selection patterns for the five fleets considered. Black solid line corresponds to the median while dotted black lines represent the 0.05 and 0.95 percentiles

Growth plots

The modelled von-Betallanfy growth curve corresponding to the dotted and red line in left panel of Figure 4 was calculated assuming $Linf = 130$. The somatic growth rate k_g was estimated following a logit normal prior distribution bounded by 0.025 and 0.075. This curve result very similar to the ICES estimation (black solid line) even when the posterior distribution for the annual somatic growth rate parameter is bimodal (Right panel of Figure 4). Traceplot for quaterly parameter k_g in Appendix I shows two chains witouth mixing but with a very small difference between their means. The first one around 0.0425 and the other one around 0.0445. When they are transformed into annual values they result also in different but closer values, which lead us to conclude that an annual somatic growth rate between 0.17 and 0.178 will be adequate to model the growth dynamics as done in ICES.

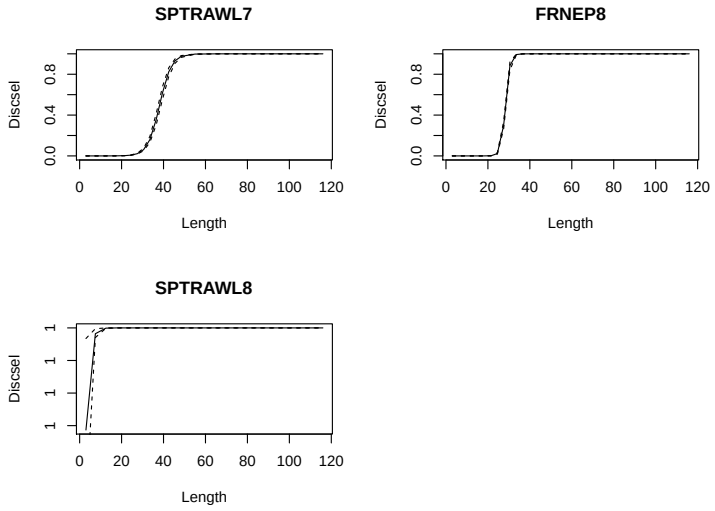

Figure 3: Modelled retention patterns for the fleets discarding. Black solid line corresponds to the median while dotted black lines represent the 0.05 and 0.95 percentiles

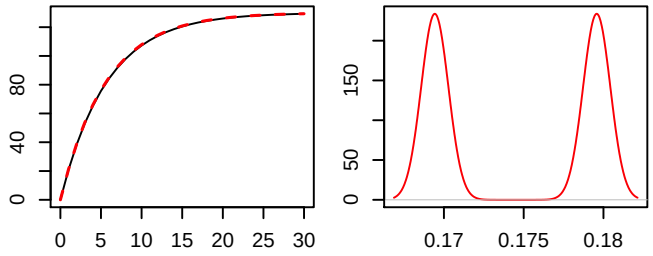

Figure 4: Left:Comparison between modelled von-Bertallanfy growth curve (dotted and red) and the one estimated by ICES (black). Right: Posterior distribution for the annual somatic growth rate parameter, k_g.

Summary plots and tables (Recruits, SSB, landings, discards and fishing mortality)

Tables 2 and 3 shows a comparison between modelled (solid black line) and ICES estimations (dotted line) of recruitment, SSB, landings, discards and fishing mortality by year $\mathbf{F}_a$. This data is plotted in Figure 5. The comparison shows an inconsistency with ICES results. While recruitment is coherent, the landings and stock spawning biomass is less with a higher fishing mortality. We think this discrepancy is mainly driven by the lack of convergence of some parameters and problems in the definition of the fishing mortality. This problems are explained below in the Discussion section. A detailed quaterly output for the same variables is displayed in Figure 6.

	ICES Recr.	Mod.Recr.	ICES SSB	Mod.SSB	ICES F	Mod.F
2001	317173	226314	36791	8928	0.72	2.6
2002	265151	214509	37888	6277	0.78	5.1
2003	145895	117508	38161	4247	0.78	2.8
2004	334983	609397	43609	3473	0.78	2.1
2005	224857	213164	42802	21206	0.87	0.75
2006	303304	382818	36530	6750	0.72	3
2007	454286	351191	45909	4166	0.61	0.68
2008	381687	769588	56968	6874	0.47	0.58
2009	99576	376328	85181	19975	0.4	0.53
2010	176248	291357	131075	41404	0.39	0.49

Table 2: Comparison between ICES estimations and GPDM medians of Recruitment(thousands), SSB (tonnes) and Fishing mortality F

	ICES land.	Mod.land.	ICES disc.	Mod.disc
2001	36675	17979		9663
2002	40107	26484		6617
2003	43162	8958	2170	3746
2004	46417	6564	2169	4161
2005	46550	12063	4988	8878
2006	41467	7211	2974	5357
2007	45098	5861	3774	6357
2008	47823	6101	4076	10084
2009	58975	46569	3445	33760
2010	73125	53908	1476	15874

Table 3: Comparison between ICES estimations and GPDM medians of landings and discards (tonnes)

Supplementary material

Diagnostics (Gelman plots, traces, posteriors) are presented in Appendix I. An acceptable level of convergence is achieved when: Gelman plots should tend towards 1; traces should be random and horizontal with overlapping in all chains; and posteriors. Posteriors represent the distribution of the parameter.

The modelled length frequency of the population at each quarter is displayed in Appendix II.

Computation

The model have been run in the Centre of Supercomputing of Galicia (CESGA) using the SVG cluster with an AMD Opteron and AMD Bulldozer Processors. The software used was R 2.14.1 (R Development Core Team, 2011) and JAGS 3.3.0 (Just another Gibbs sampler) (Plummer, 2013). The code is written in R linking with the MCMC sampler through the package *rjags* (Plummer, 2012).

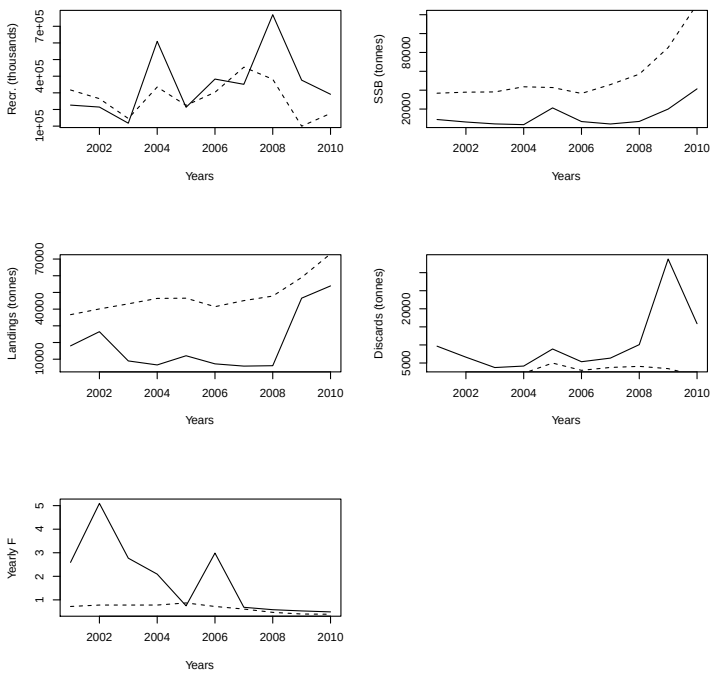

Figure 5: Comparison between modelled (solid black line) and ICES estimations (dotted line) by year

Discussion and future work

As a starting point, a general rule to develop models is doing it simple and to evolve eventually towards a complexity level that allows answering the relevant questions. As stated before, this requires having a model similar (at least in their main assumptions) than the model that ICES uses to provide advice (ICES, 2012). The model and data described before accomplished this requirement; however the Bayesian implementation has huge computational requirements expending many days for a single run. This makes the initial model development impossible in a feasible time since every run provide the clues for the next runs. The current ICES model has 33 years split in quarters, i.e. 132 time steps; 94 length groups from 1 to 130 cm (every 1 cm until 40 cm; every 2 cm until 100 cm and every 10 cm until 130 cm) and 7 fleets, 3 of them with discards. This model structure is not feasible for the GPDM development process so we decided to simplify the data making bigger groups.

In the initial run the time period were reduced to 10 years (from 2001 to 2010); the length groups were reduced to 13 and the fleets were reduced to 1. This simple structure allowed us to compile the model, to identify problems in the code, to improve the definition of un-informative priors and to define Bayesian settings such us the iterations number, the adaptation period, the burning and the thinning. However after extending the iterations the model did not converge.

In a second stage we extended the fleets from 1 to 5 as described in table 1. The 3 fleets with discards were kept and the other 4 were joined making 2 new fleets. The model was extended to deal with discards and also to estimate the discards in the time steps without discard observations. The convergence problems remained. The runs with this data structure were used to modify the non-informative priors, allowing to a better model performance, particularly with some priors that do not allow covering the full parameter range, something that a priori is difficult constraint. The fact that the growth parameter (Von Bertalanffy

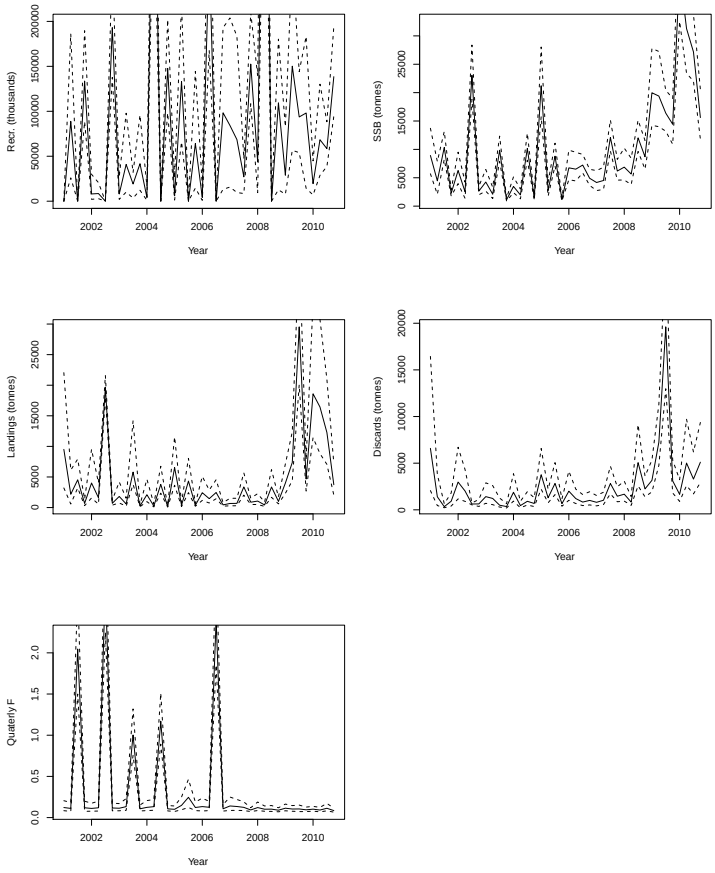

Figure 6: Modelled percentiles 0.5 (Solid black line), 0.05 and 0.95 (Dotted lines) by quarter

k_g) did not converge suggest us that increasing the number of length classes could allow a better performance of growth model. In this third stage we did 2 alternative length groups: (1) with 19 length classes and (2) with 27 length groups. The second one, with 27 length groups and 200000 iterations dies after 450 hours, the limit of time we have in the CESGA supercomputers to run process. With the first one we got good values for the growth parameter (Von Bertalanffy k_g) so we decided to use this for future development of the model. We took this code but we implemented it with more iterations (500000) looking for convergence, this time we used a new processor (AMD bulldozer) and we ask for an special permission in CESGA for 600 hours. This is the run whose results are presented here.

This run has been running for 23.4 days and even so the time was not enough to get convergence. Diagnostic analysis in Appendix I shows that some parameters have more difficulties to converge than others. Most of the chains that are not mixing enought, remain very close, which gives an idea about the range of the values being coherent with the results and with ICES estimations. The more problematic parameters are k_g, K_{bh}, alphaGsel[3] and betaGsel[3]; and the annual fishing mortality parameter $\mathbf{F}_a, a = 1, \ldots, 10$, plotted in Figure 5. The first group failed in the convergence process while the fishing mortality parameter has problems of definition. Convergence problems could be solved when biological-based priors will be incorporated. Adding information of the processes involved are supposed to improve the internal mechanics of the model. Also a bigger number of iterations could help, but considering that actually it spends 562.68 hours for 500000 iterations, it will be an expensive solution in terms

of computational cost.

In order to compare with ICES estimations, $\mathbf{F}_a$ was calculated as the sum of the fishing mortality corresponding to each fleet and each size class bigger than 15 cm and less than 80 cm ($15 \leq k \leq 80$) divided by the total number of classes matching this conditions, as follows :

$$\mathbf{F}_a = \sum_{k=4}^{17} \sum_{j=1}^{5} \frac{F_{a,j,k}}{14} \tag{3}$$

with $F_{a,j,k} = \sum_{t=1+4(a-1)}^{4a} F_{t,k,j}$ the fishing mortality in year $a, a = 1, \ldots, 10$, for fleet $j, j = 1, \ldots, 5$, at size class $k, k = 1, \ldots, 19$, and $F_{t,k,j}$ as defined in equation (1).

The proportion of fishing mortality corresponding to each fleet, $propF_j$, is defined constant in time and we think that this assumption is incorrect driving to the following means and standard deviations for $propF_j, j = 1, \ldots, 5$, output:

```
        Mean         SD
1 0.09682728 0.01380948
2 0.07017254 0.01024625
3 0.11818517 0.01603182
4 0.08031845 0.01150752
5 0.63449656 0.02546795
```

When the mean of the observed catch proportion by fleet was:

```
    Fleet 1    Fleet 2    Fleet 3    Fleet 4    Fleet 5
0.17232600 0.05267043 0.26924902 0.23228009 0.27350134
```

It could be seen how the fishing mortality proportion by fleet results higher for the fleet 5 which is inconsistent with observed data. As a consequence of this, considering the equation (1), $\mathbf{F}_a$ results also in an overestimation. This could explain the incompatibilities in Figure 5.

Hake GPDM has a problem of convergence. As future work, we will try to re-define $propF_j$ dependent on the time step and we will include relevant biological knowledge to the priors in order to improve mixing and achieve convergence.

Acknowledgements

We gratefully thank CESGA (Galician Supercomputing Center) for providing access to the SVG System. This work was supported by projects ECOKNOWS (FP7-244706). Margarita M. Rincon was funded by P09-RNM-5358 of the Junta de Andalucia.

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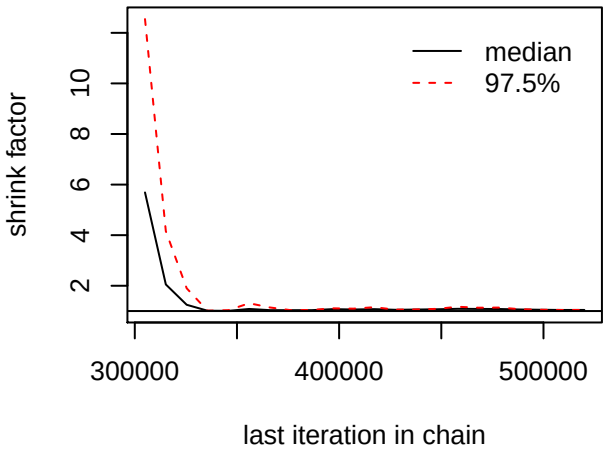
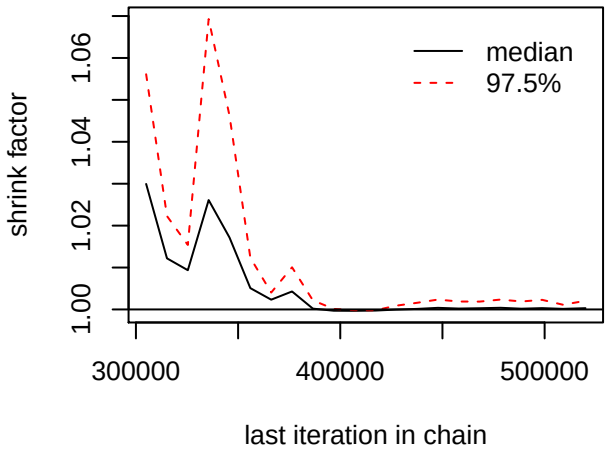
APPENDIX I− Diagnostics
Gelman plots for General parameters

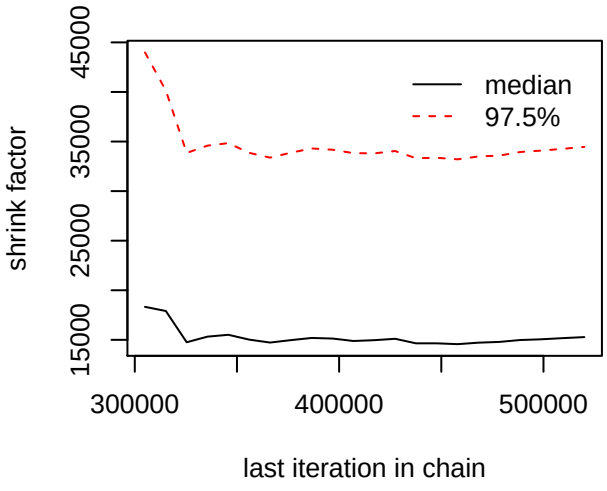
N[1]



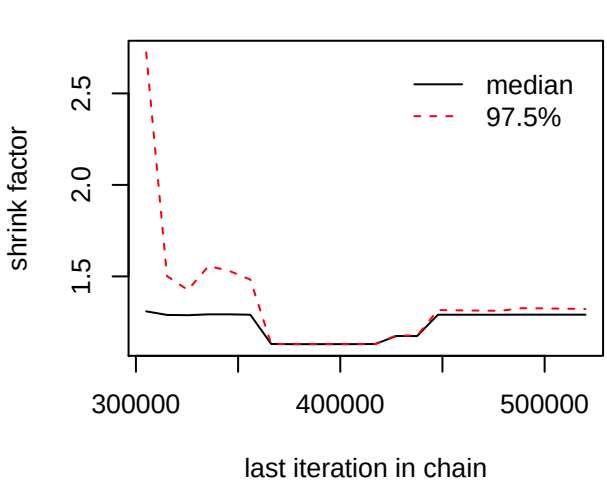
Fconstant



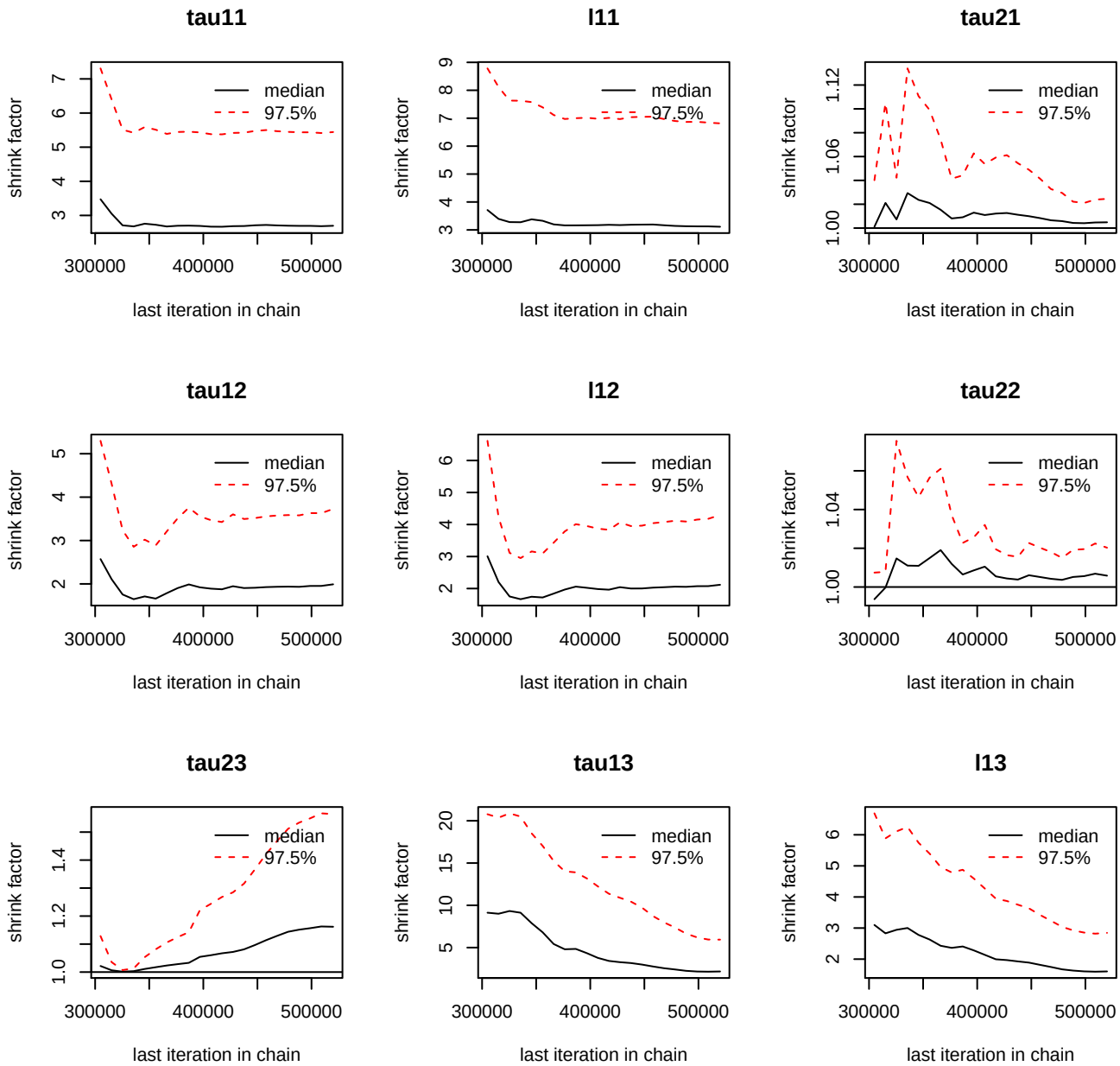
k_g



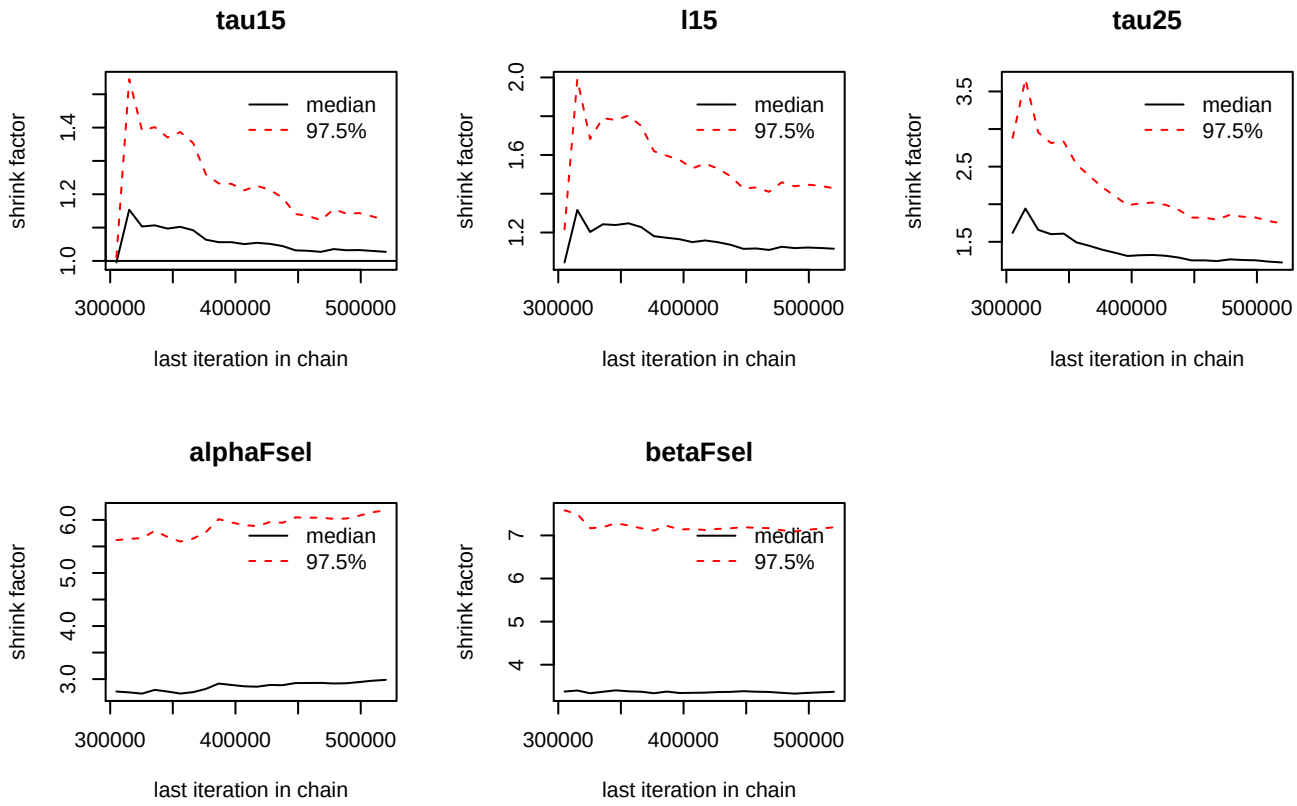
K_{bh}



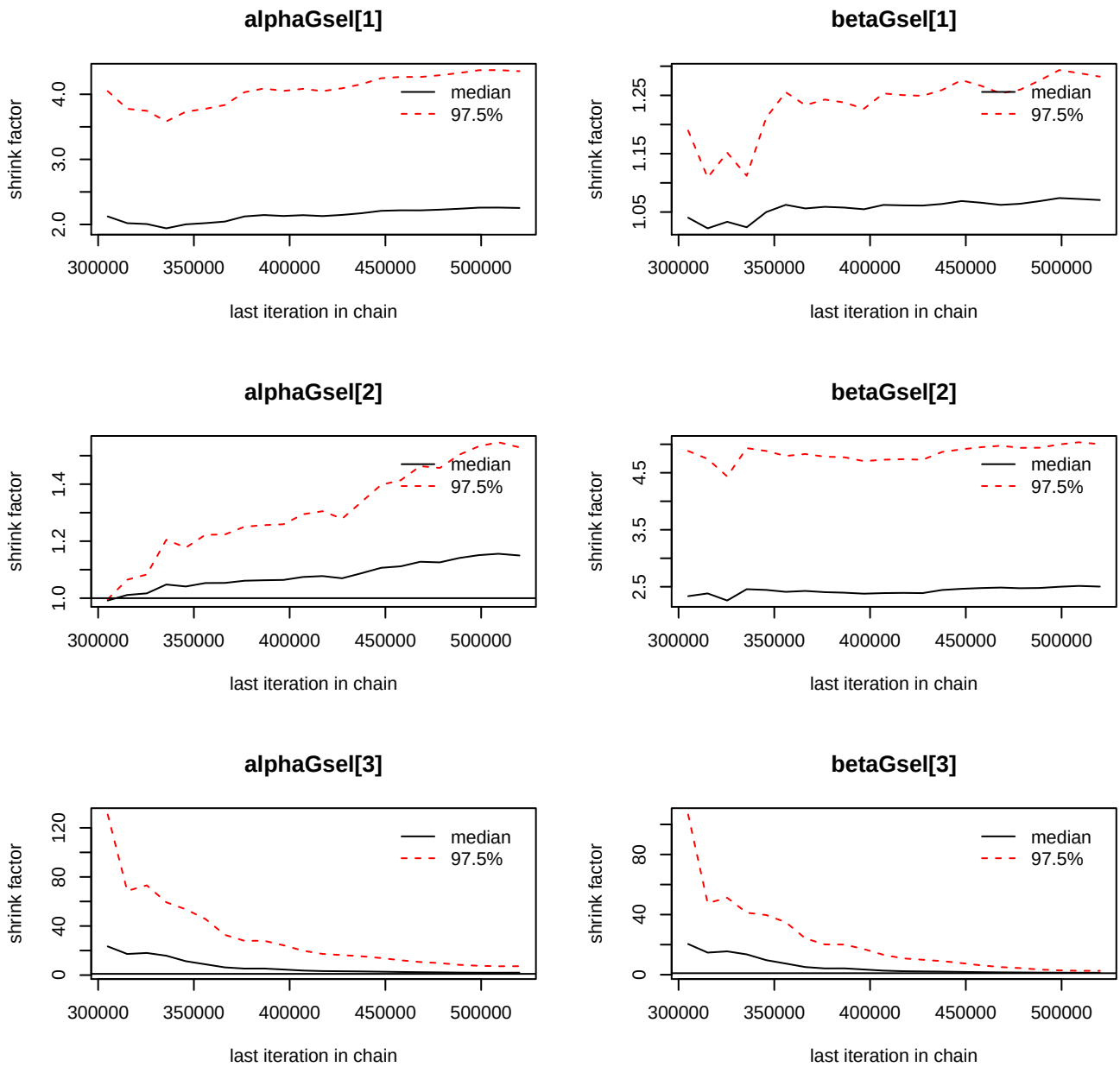
Gelman Plots for Double normal parameters. Fleets 1, 2 and 3



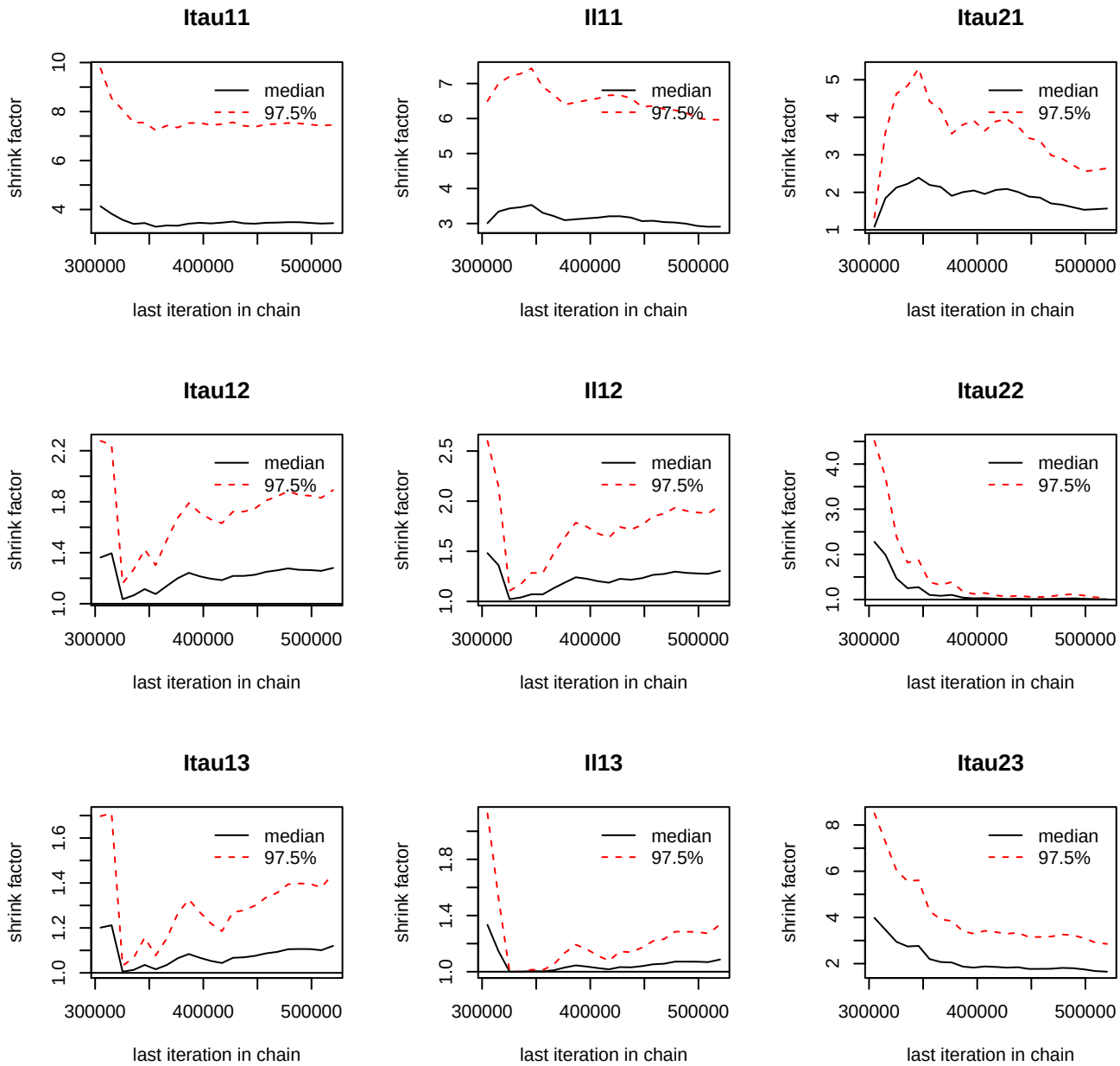
Gelman Plots for Double normal (5) and logistic (4) fleet parameters



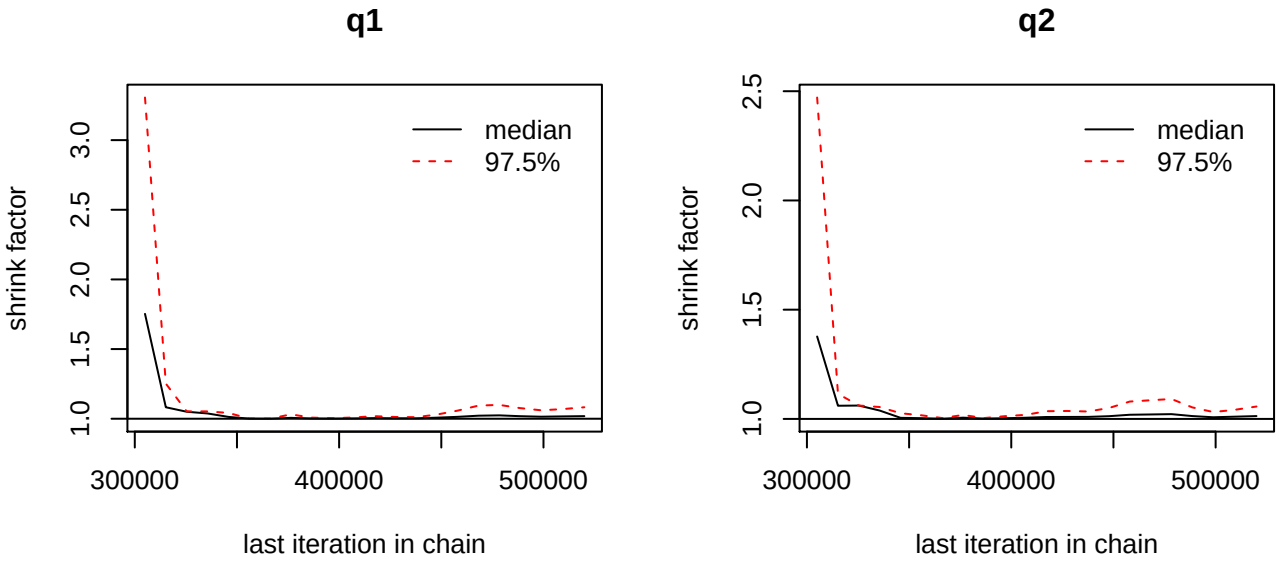
Gelman plots for Discard probability parameters

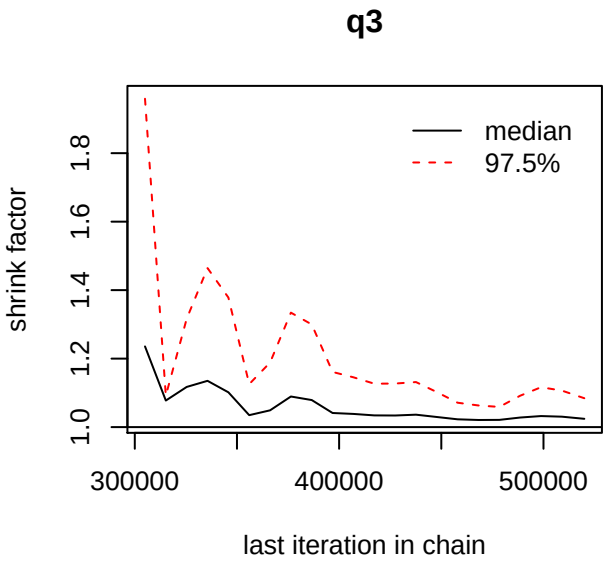


Double normal survey parameters − Gelman Plots

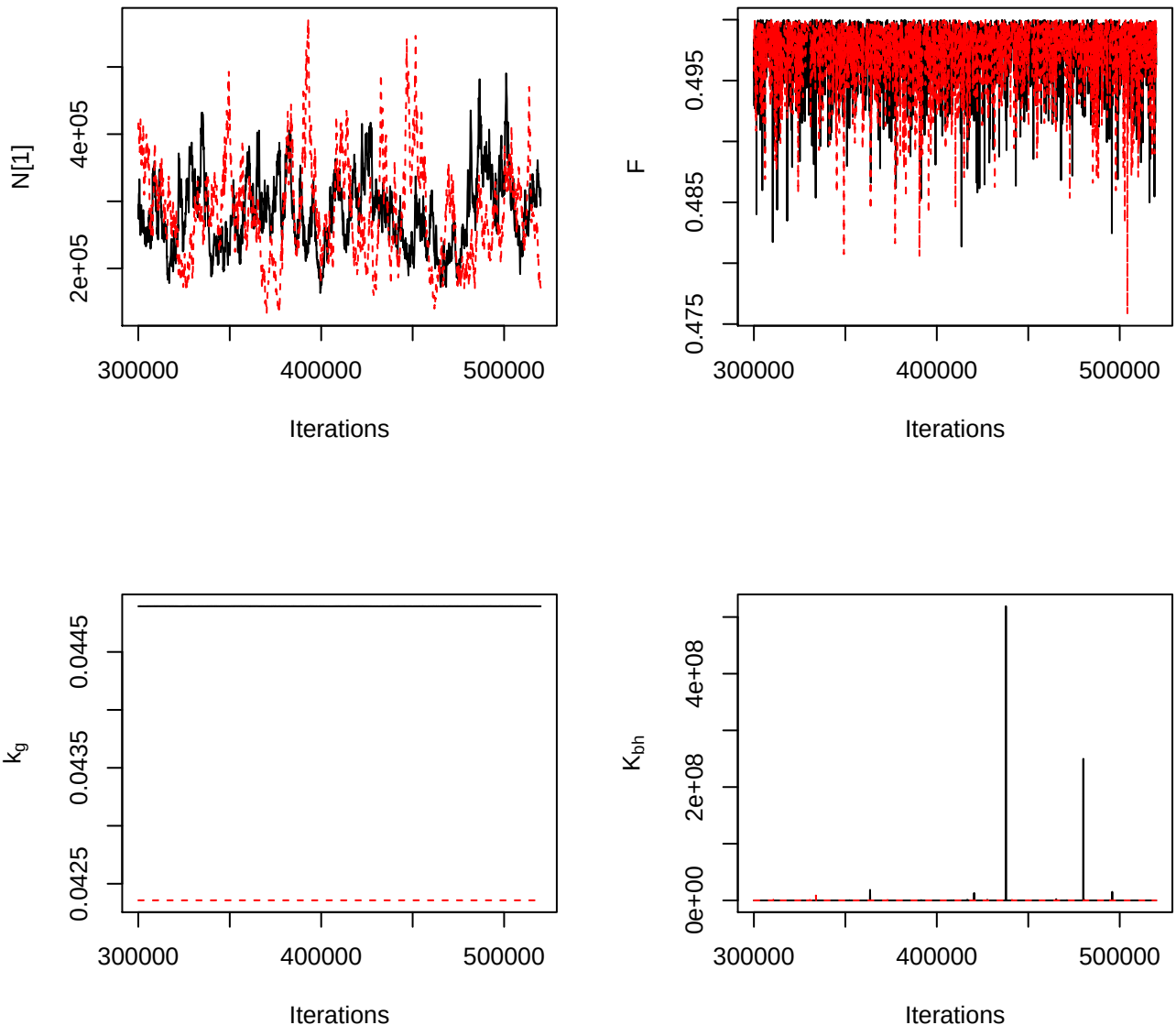


Suervey Catchability Gelman PLots

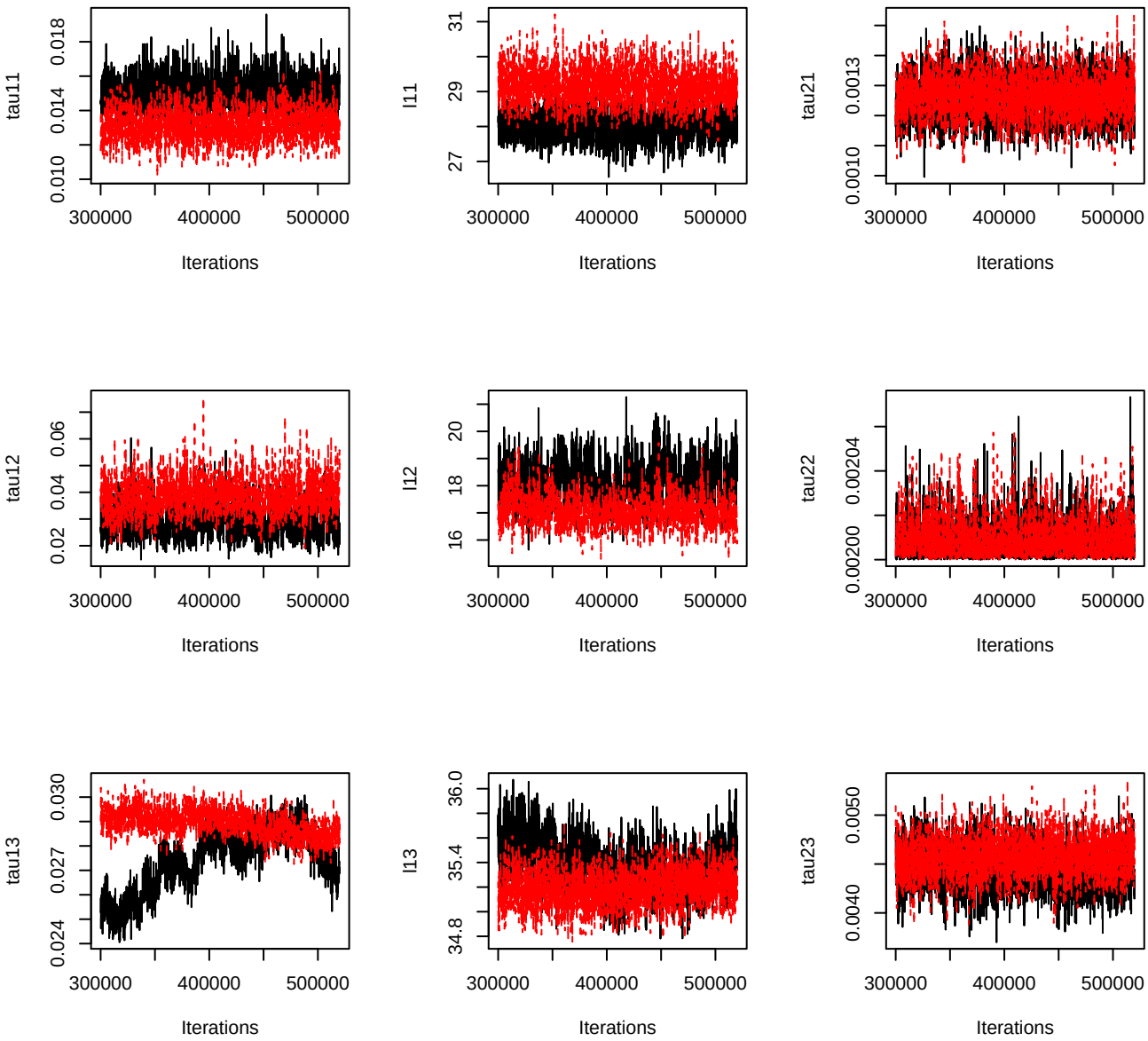




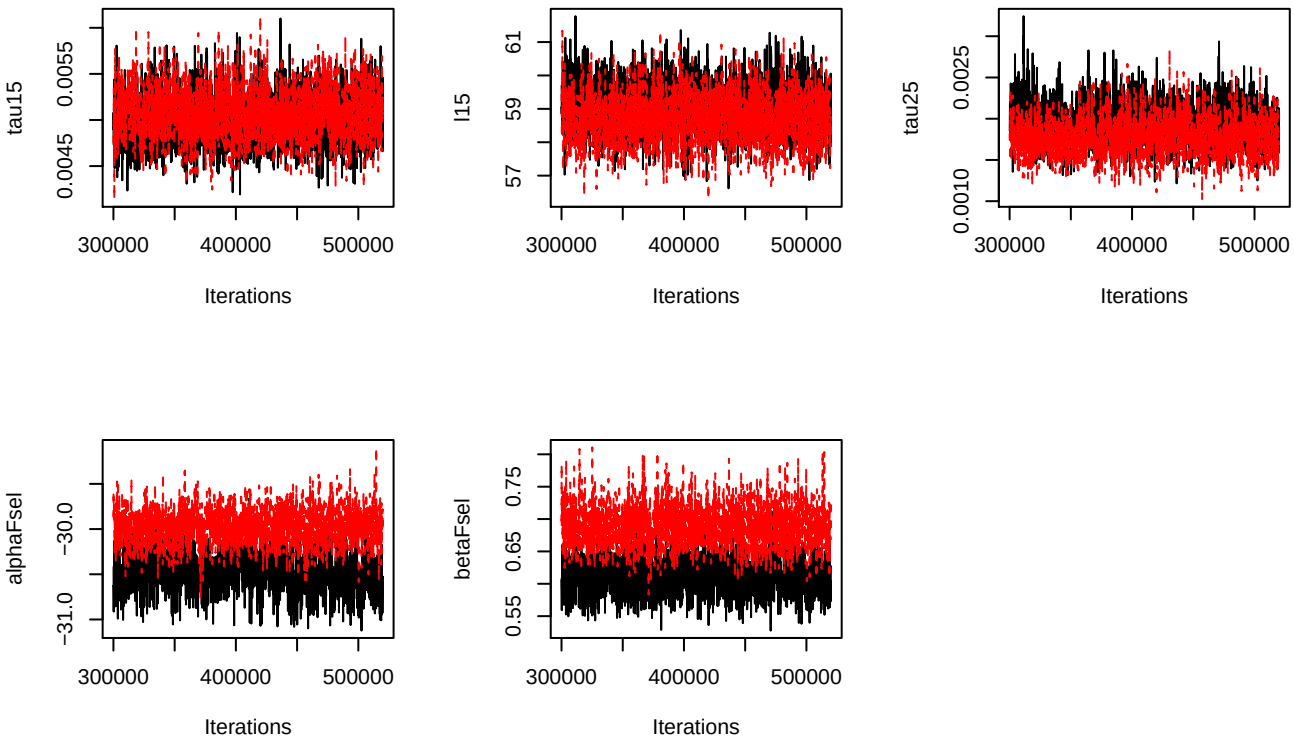
TRACES for general parameters



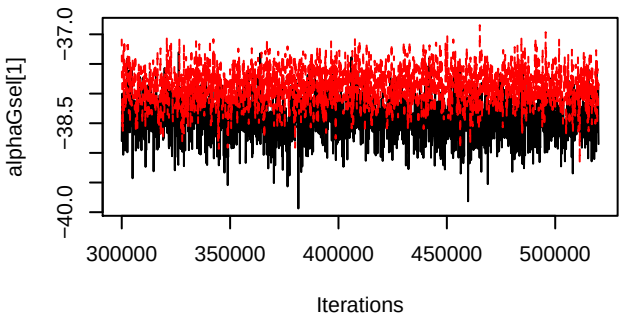
Double normal parameters. Fleets 1, 2 and 3

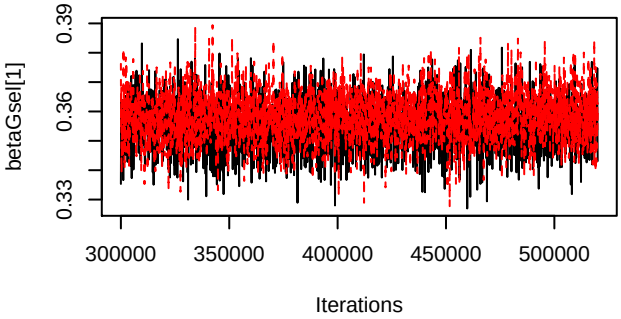


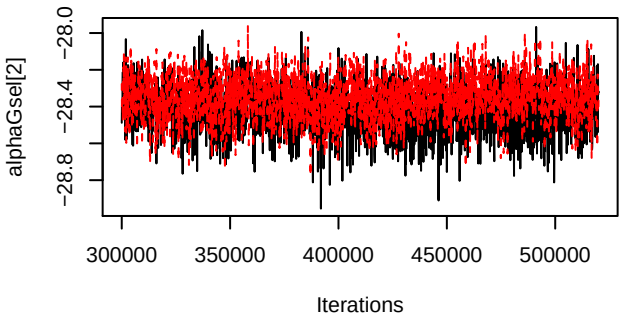
Double normal (5) and logistic (4) fllet parameters

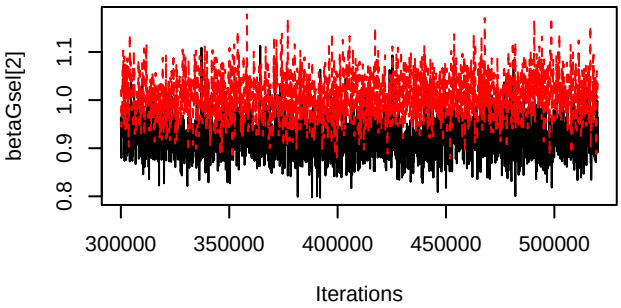


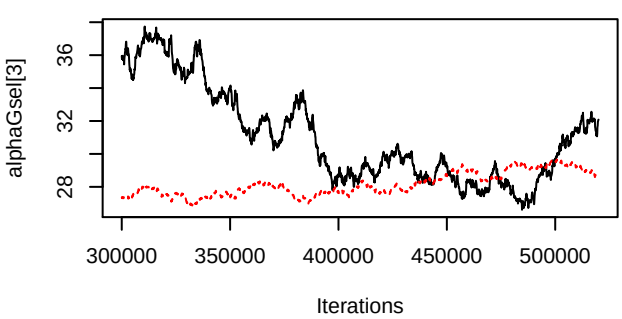
Discard probability for 3 trawl fleets

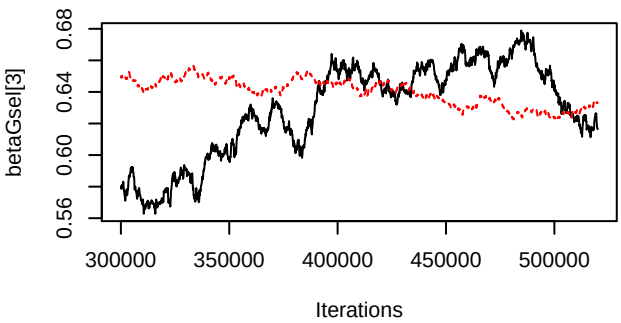




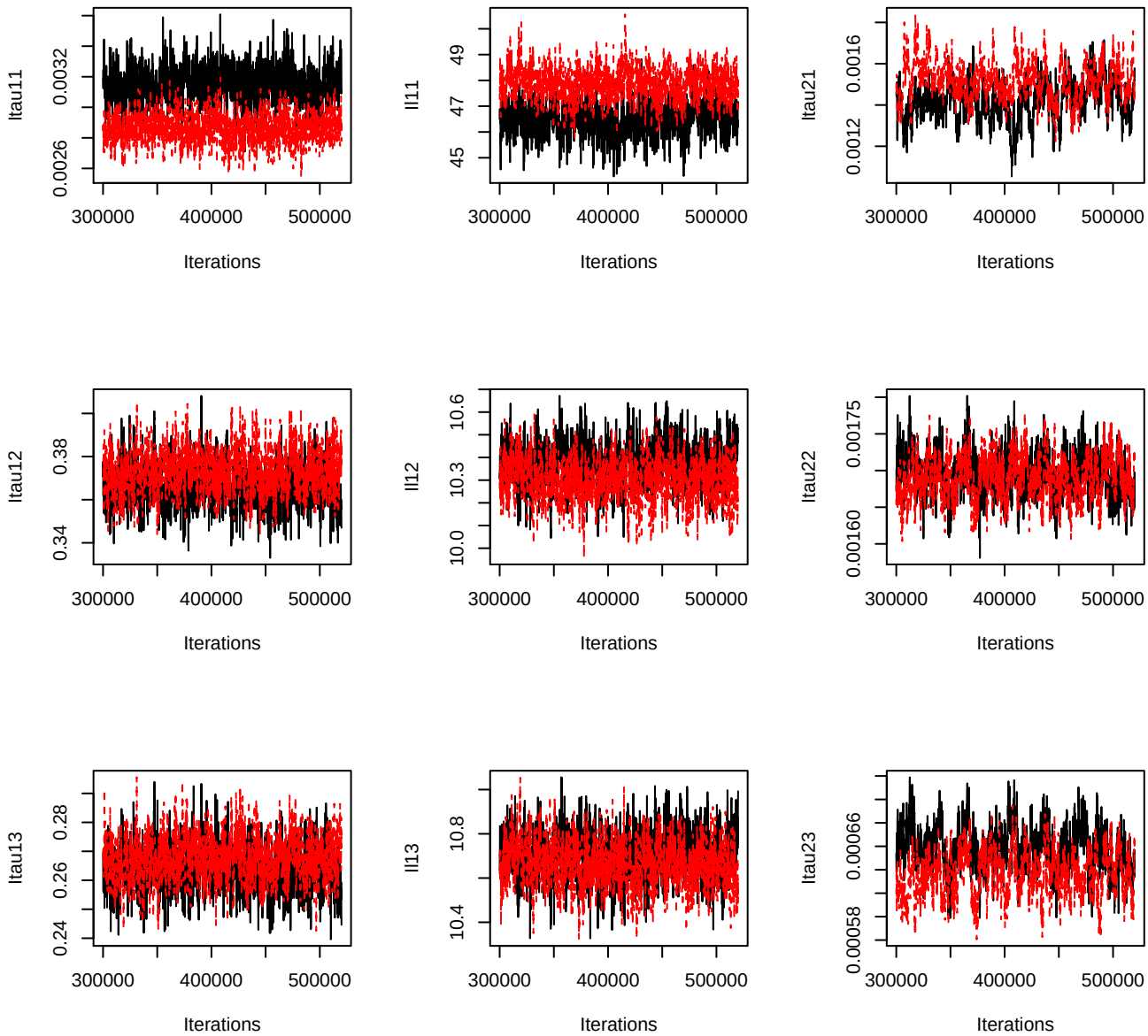




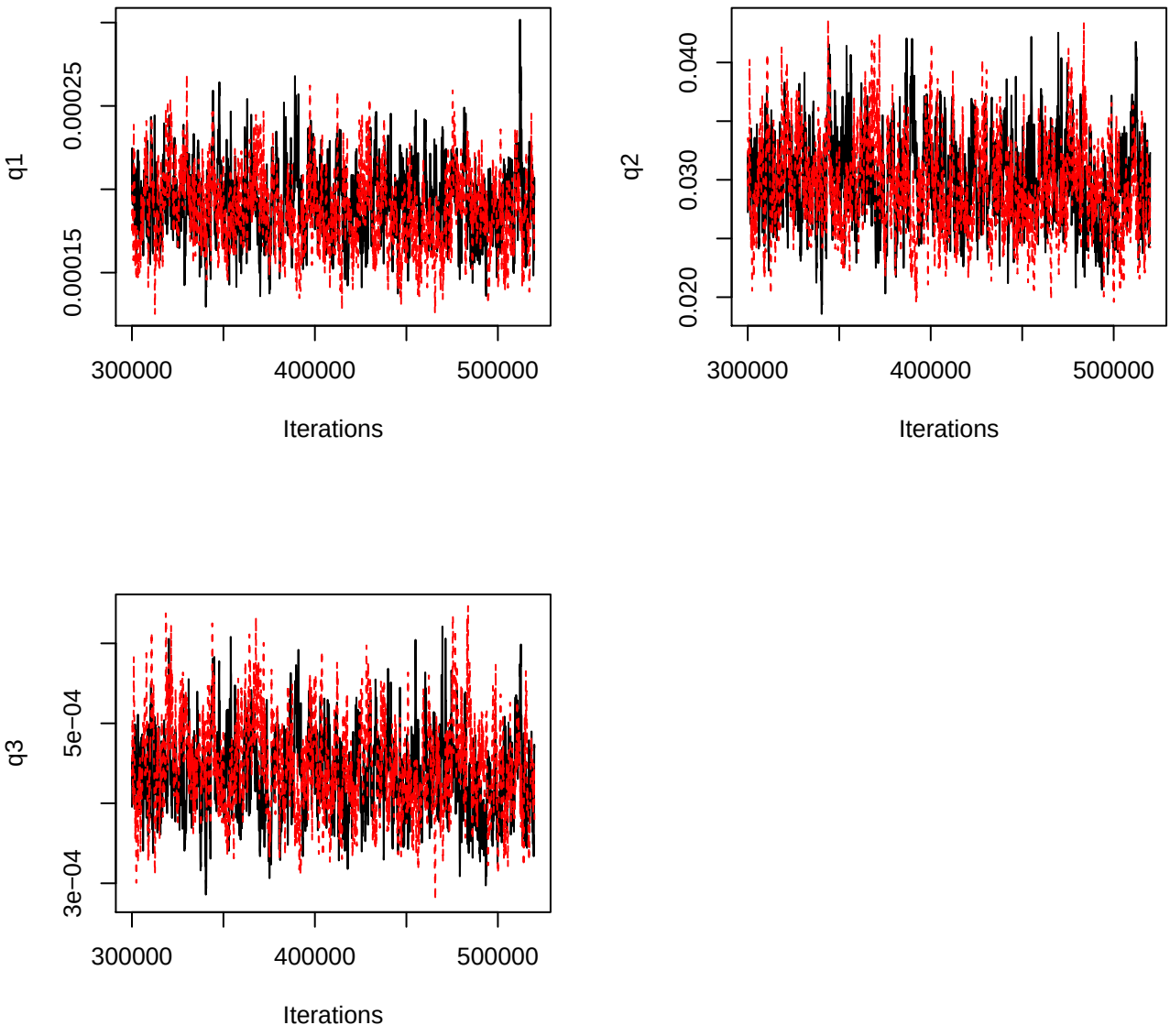




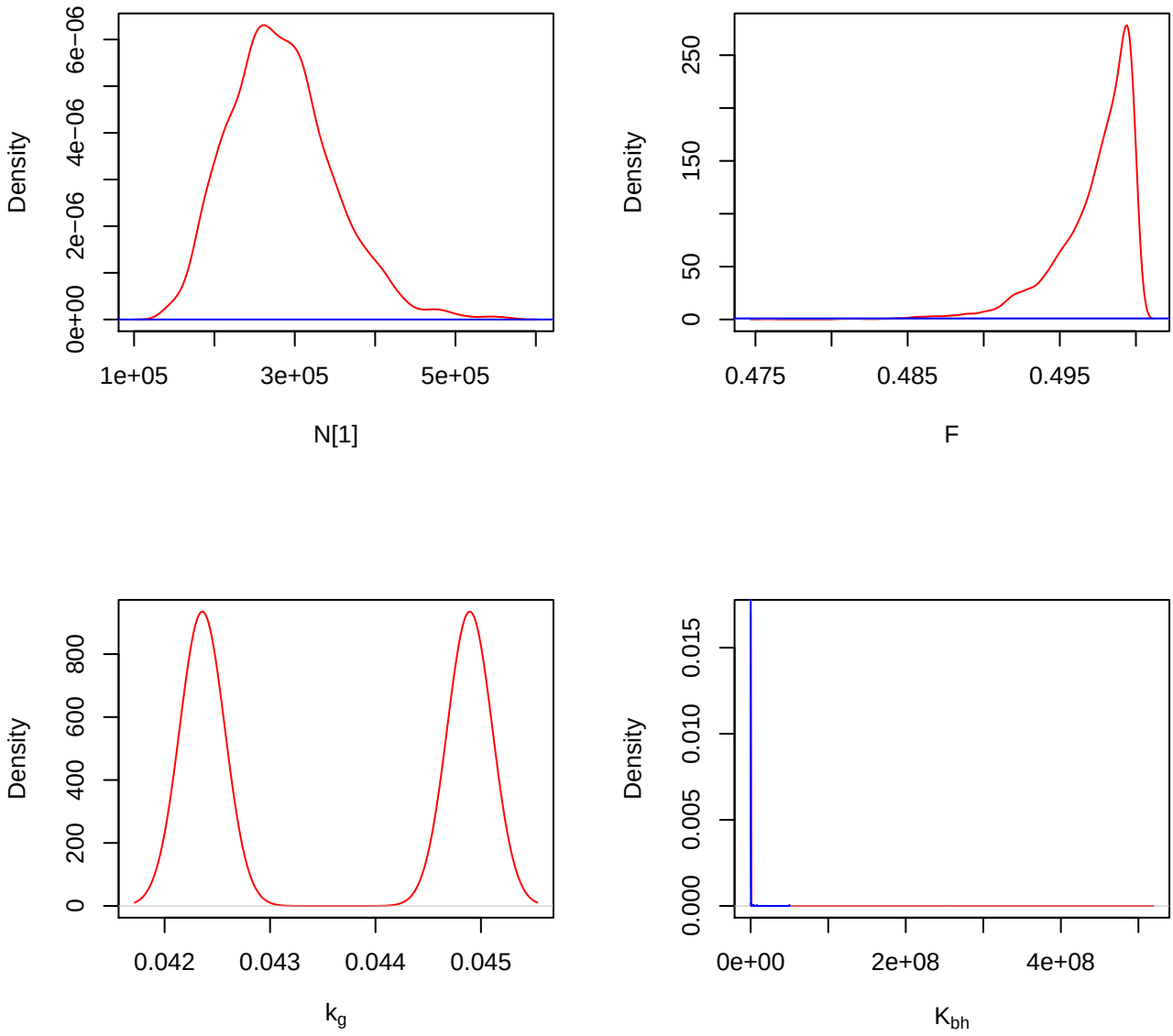
Double normal survey parameters



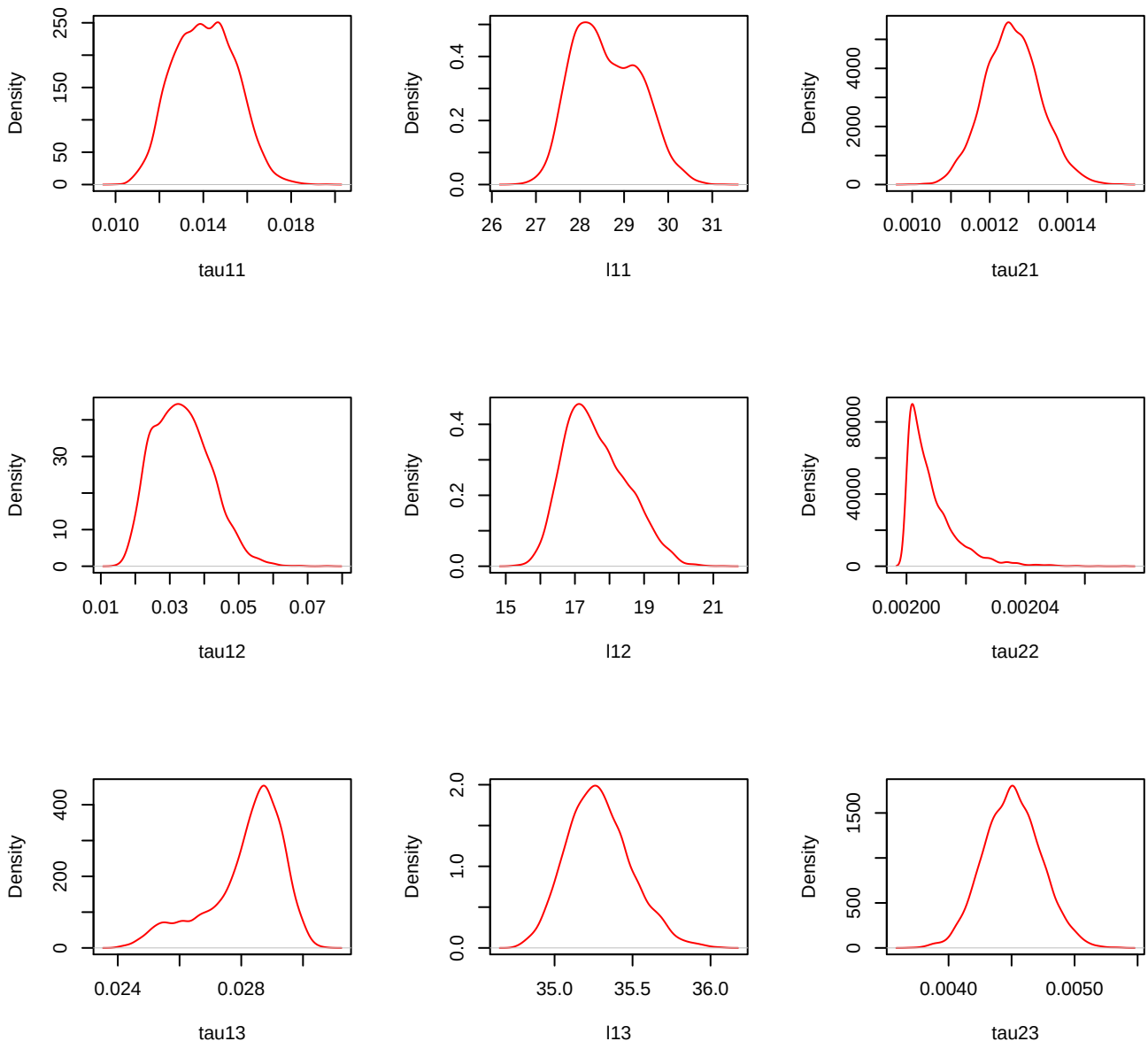
Survey Catchability (scaled to initial abundance)



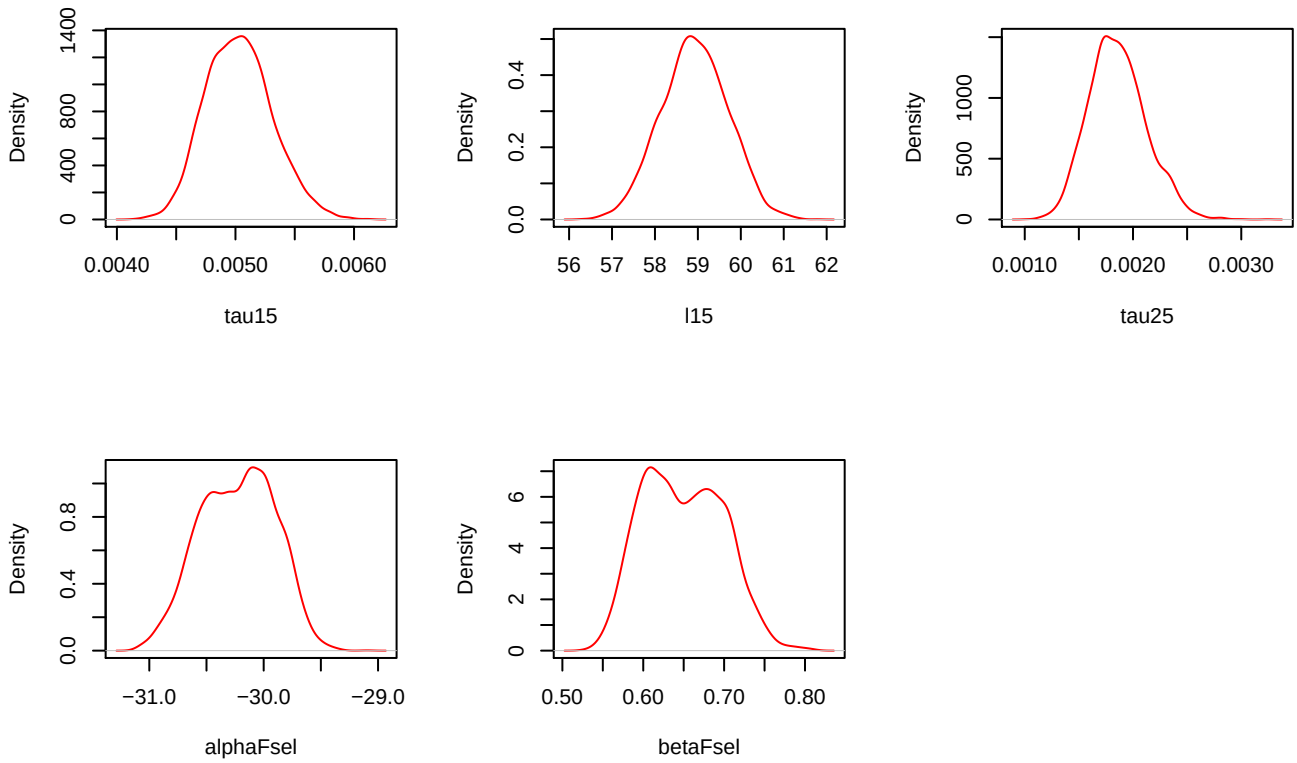
Density for general parameters. Priors (blue) and Posteriors (red)



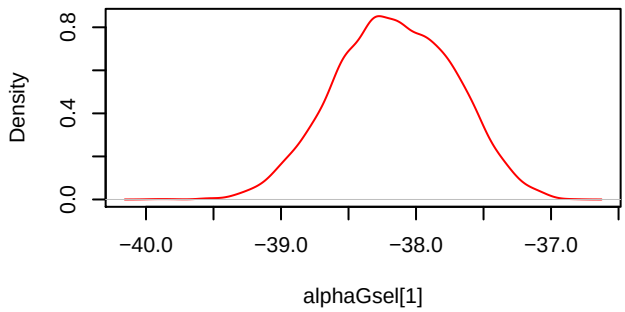
Double normal Selection. Fleets 1, 2 and 3

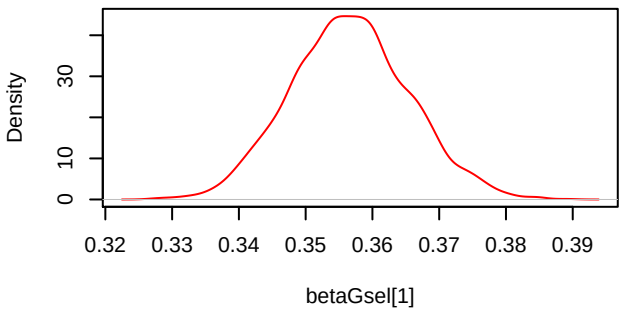


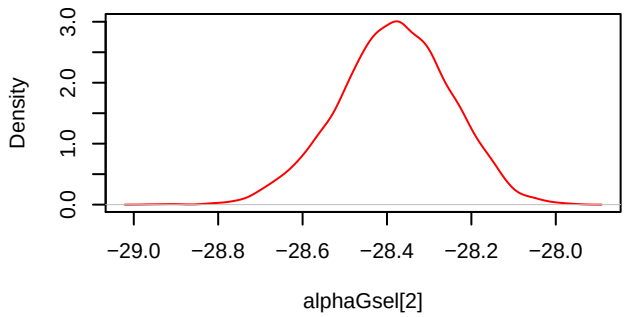
Double normal (5) and logistic (4) fleet parameters

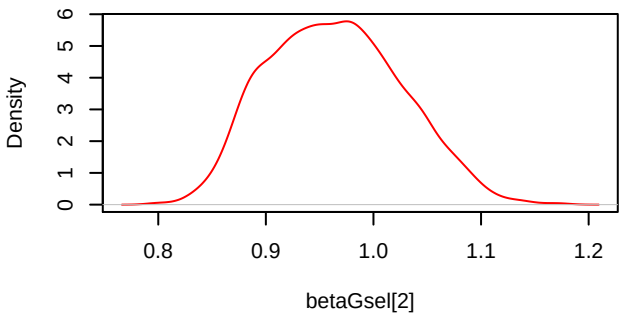


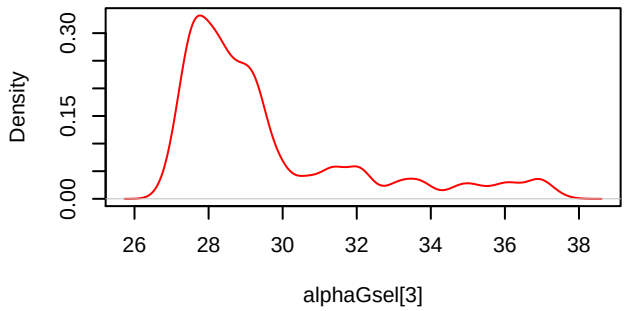
Discard probability for 3 trawl fleets

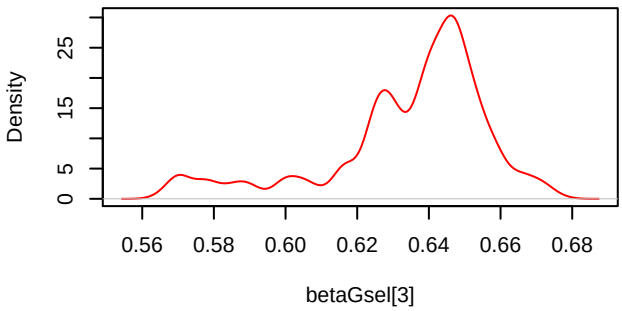




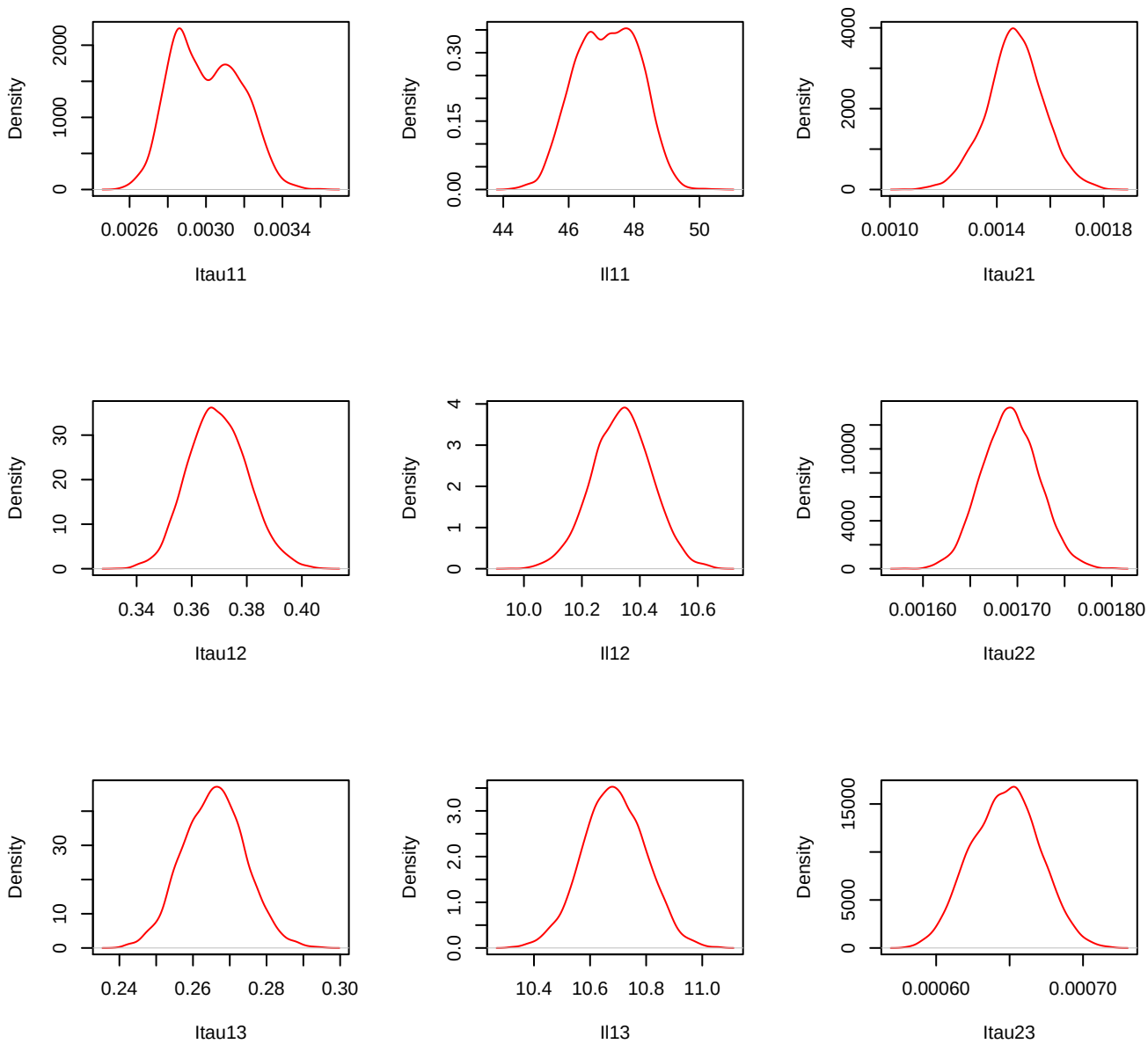




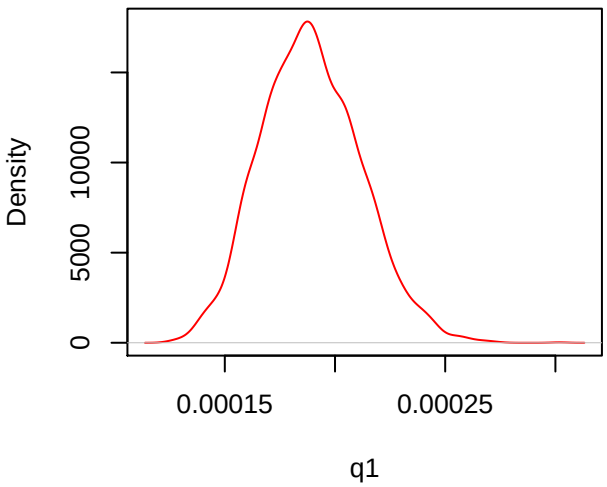


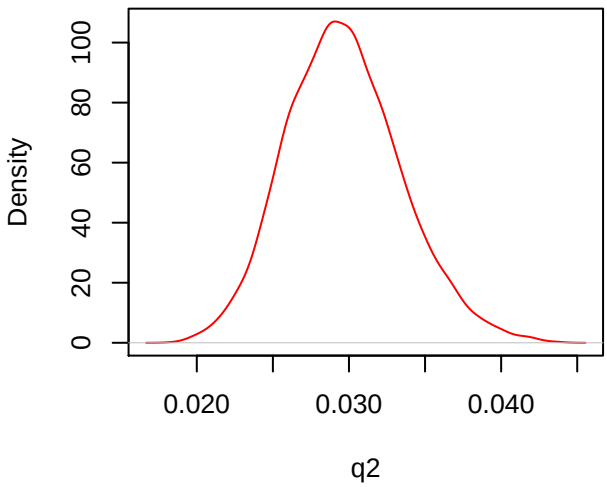


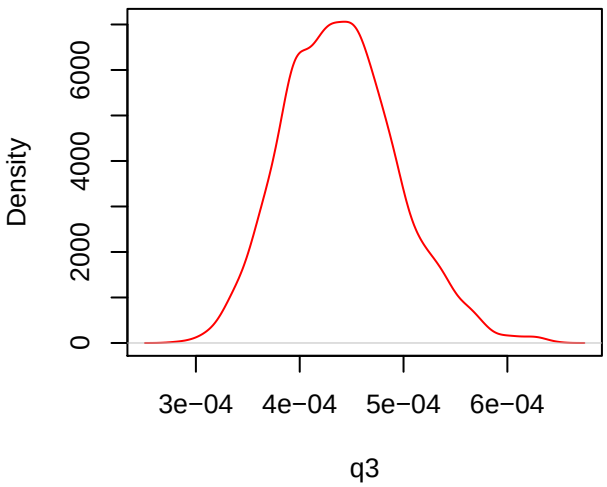
Double normal survey parameters



Suervey Catchability (scaled to initial abundance)

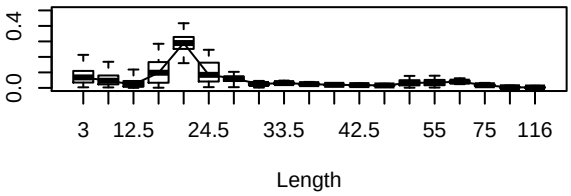




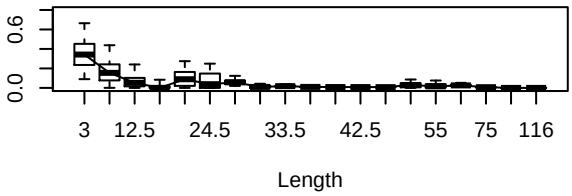


APPENDIX II− Modelled Length Frequency by quarter

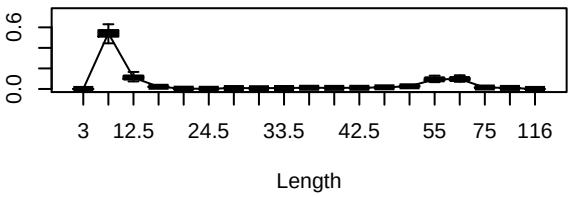
Φ_1



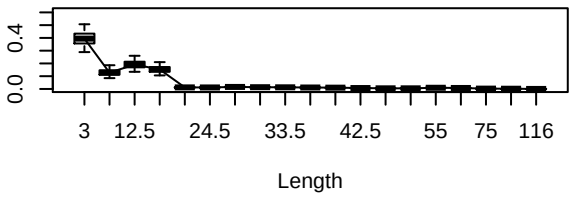
Φ_2



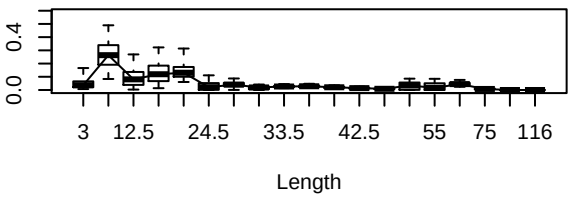
Φ_3



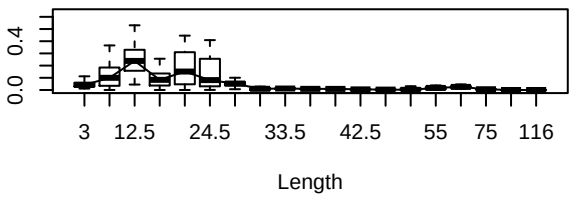
Φ_4



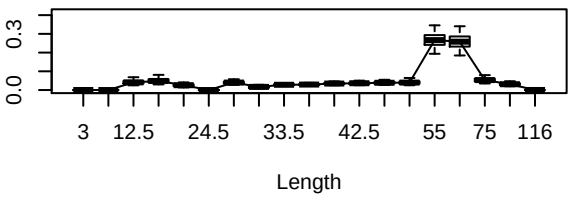
Φ_5



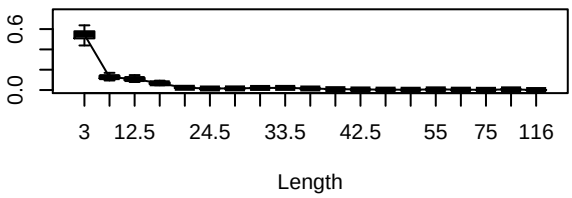
Φ_6

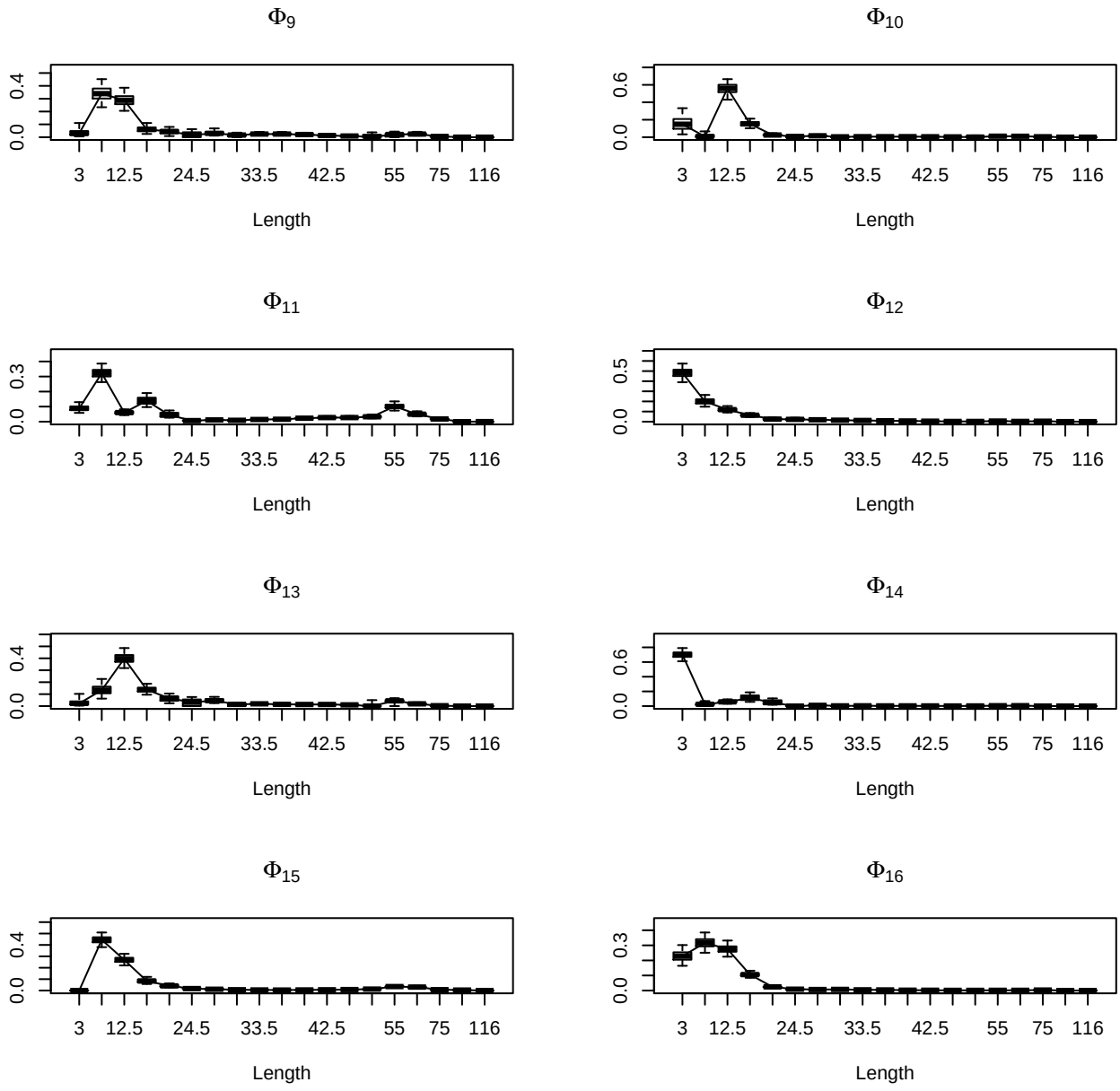


Φ_7



Φ_8




Φ_9
0.0
0.4
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{10}
0.0
0.6
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{11}
0.0
0.3
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{12}
0.0
0.5
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{13}
0.0
0.4
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{14}
0.0
0.6
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{15}
0.0
0.4
3
12.5
24.5
33.5
42.5
55
75
116
Length
Φ_{16}
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0.3
3
12.5
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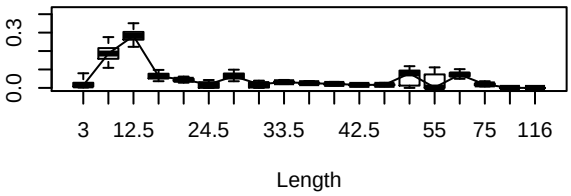
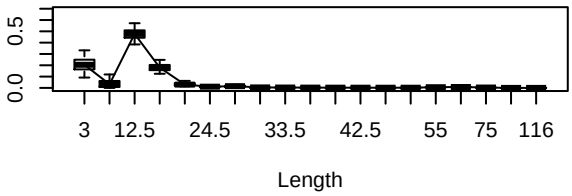
116
Length

Φ_{17}



Φ_{18}



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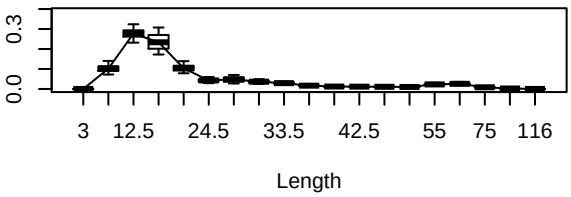

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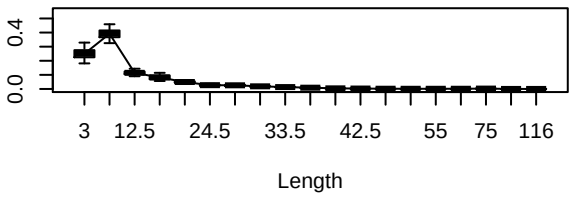

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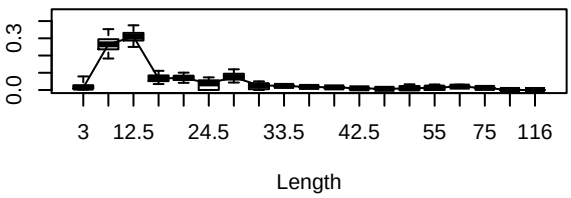

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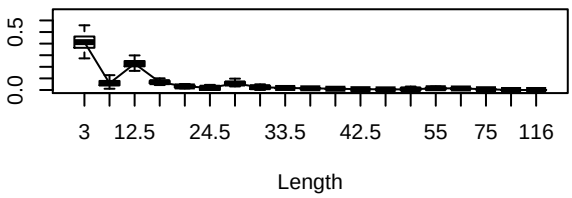

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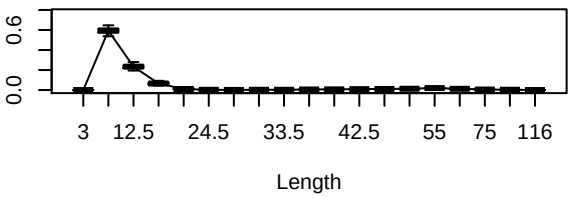

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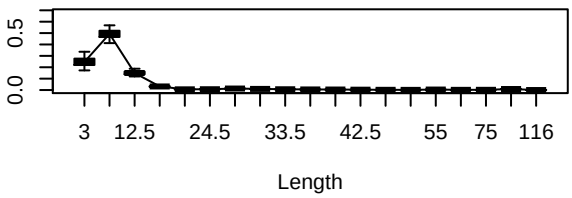

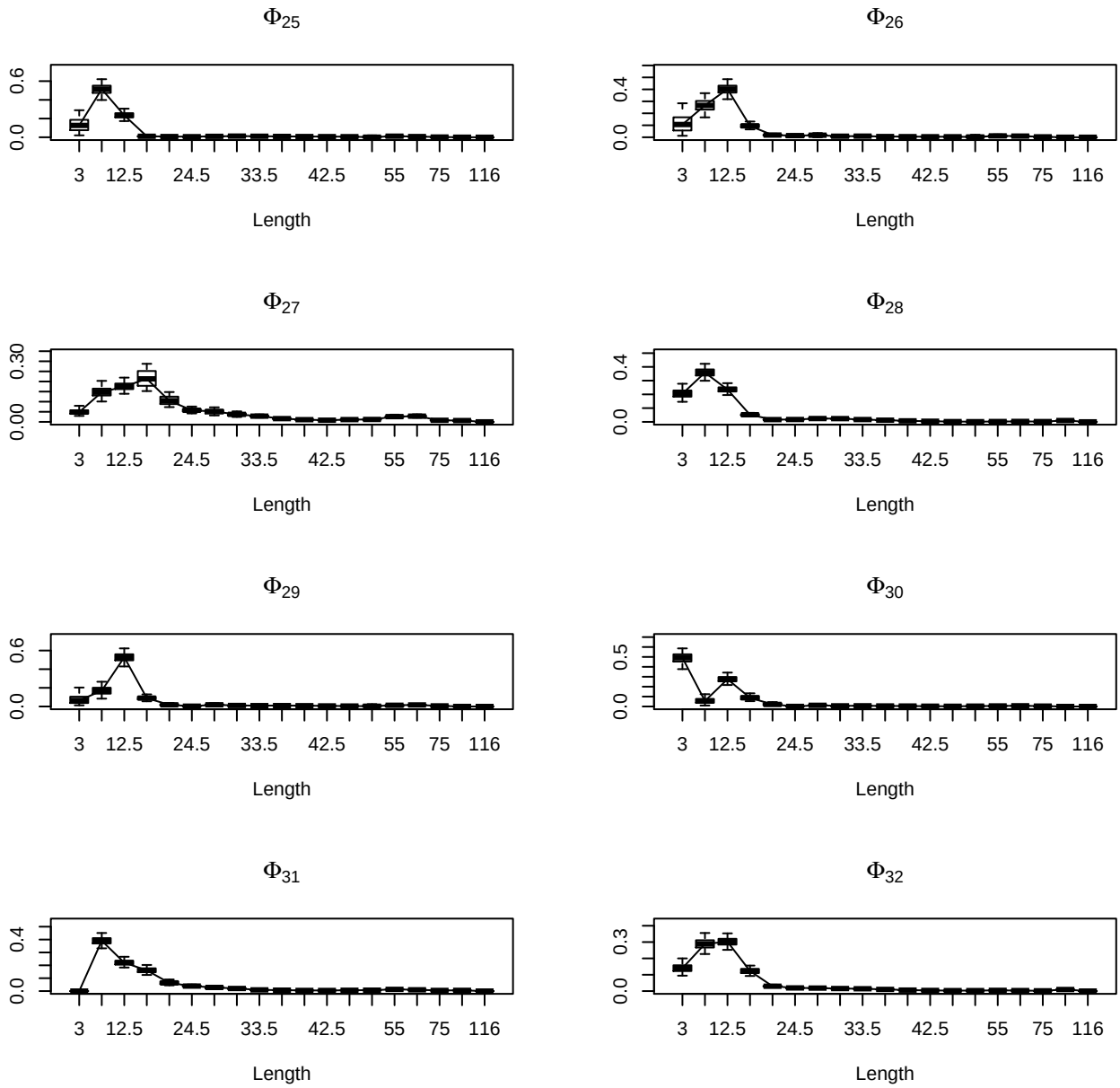
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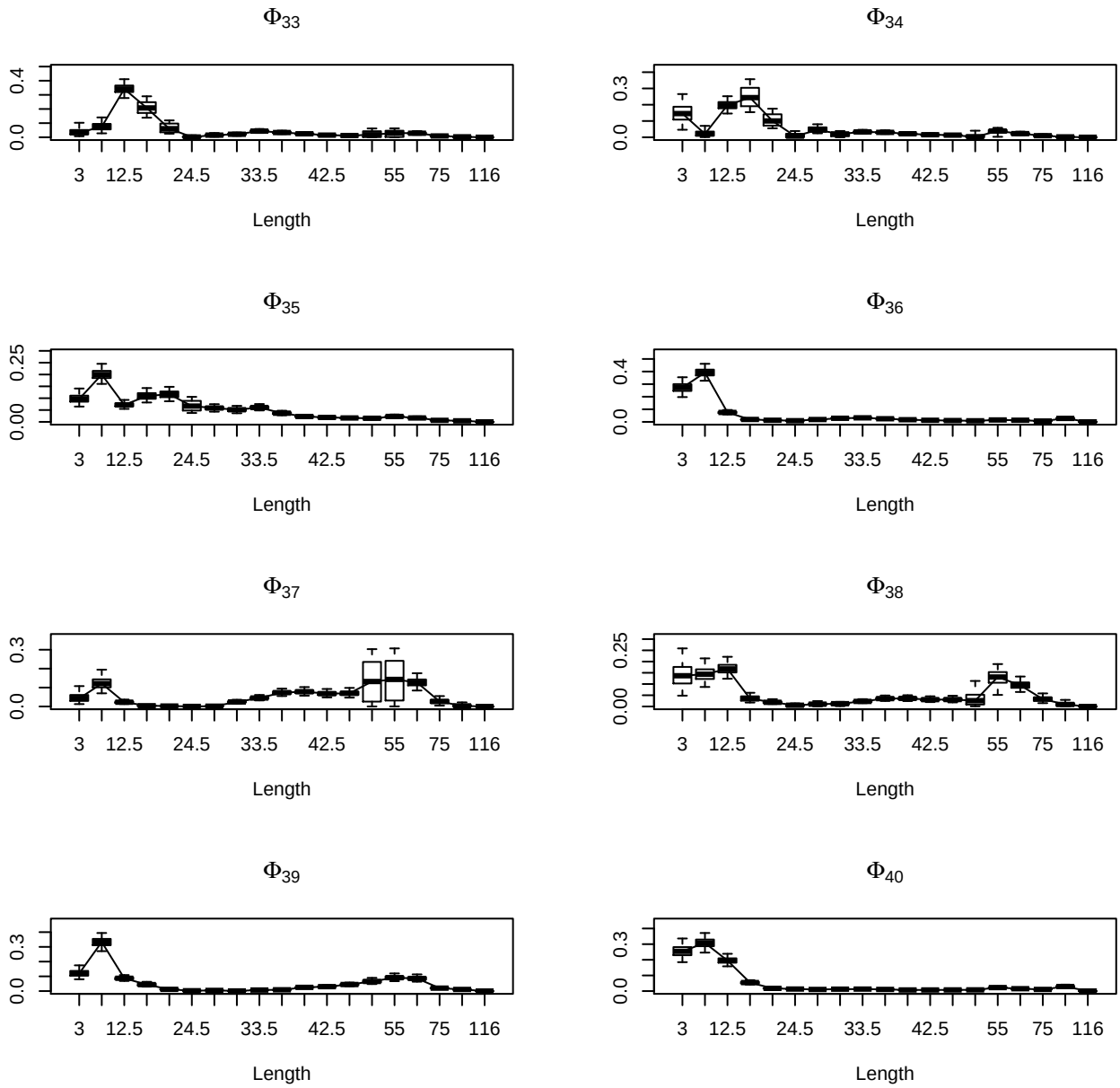
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