A study of the Surplus Production Model

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June 28, 2007

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Part 1

Introduction

The ultimate goal of fisheries assessment is to estimate exploitation quotas which maximize the production and minimize the impact on fish population. Unfortunately, modeling and estimating this kind of population is a complex task and cannot include everything that may have an influence on them such as unusual environment perturbations or species competition. However, some basic factors such as catches can be considered in modeling. A simple way to model fish stock was developed by Russell (1931). Let B_t be the stock biomass at time t,

$$B_{t+1} = B_t + (R + G) - (F + M), \tag{1.1}$$

where R is the weight of the new individuals in the population (recruits), G is the total growth of the individuals already in the population, F is the weight of the catches and M is the weight of the fish that die from natural causes. Note that in a more general model, these four parameters may change in time and hence be indexed by t. The main interest of the fisheries sciences is to determine whether a certain catch level is sustainable or not.

Our main objective is to investigate the Surplus Production Model (SPM), one of the many methods of stock assessment available in the litterature. We will examine various aspects of the SPM such as the possible sources of error (the difference between the model and the reality) and their effect on exploitation parameter estimates, like the maximum sustainable yield (MSY).

1.1 The Surplus Production Model

The SPM is one of the simplest analytical methods that can be used to assess fish stock. Its simplicity arises from the fact that it is parsimonious (many parameters of the model are pooled) and that it requires only a minimum amount of data. Actually, SPM needs only a series of catches and abundance index. The SPM models only the stock dynamics and does not take into account the age structure of the stock population, as some other models, such as VPA, do. The SPM is used to study how a fish population is responding to harvesting. Because SPMs are often used with few years of observations (usually 20 to 30), a good estimation is hard to obtain if catch data are too stable. This means that a good dataset should indicate various catch intensities relatively to the stock population size (which is unfortunately unknown before the analysis). Such a variability helps the model in its evaluation of the stock response to high and low catch levels (is the population able to recover rapidly or slowly?). For example, if a population is very large and harvesting is very low relatively to stock size during all the periods of interest, there will not be enough contrast in the perturbations made to the population to estimate the SPM parameters. As will be described later, it is important to have good data because at least four parameters need to be estimated in the SPM.

Actually, there are several mathematical forms for the SPM, but if we relate to the Russell's formulation of stock dynamic, the SPM can generally be written as

$$B_{t+1} = B_t + f(B_t) - C_t, t = 0, 1, \ldots, \tag{1.2}$$

where B_t is the stock biomass at the beginning of year t, $f(B_t)$ is the production function of the biomass in year t, and C_t is the catches in year t. $f(B_t)$ is a function which describes the population dynamic; it can be seen as the agglomeration of the R, G and M parameters in equation (1.1). The name *production function* comes from the idea that a population reacts to harvesting by *producing* new biomass. As we will describe later, the production function is usually parameterized by at least two parameters. Of course, stock biomass is impossible to measure, so we need a second equation to relate the population biomass to an abundance index,

$$I_t = qB_t, \tag{1.3}$$

where I_t is the abundance index and q is a scaling parameter. Catch-Per-Unit-of-Effort (CPUE) are often used as abundance index. The CPUE is measured by fisheries scientists using surveys. The *Unit of Effort* is referring to a standardized way to measure the effort made to catch the fish. It may take into account the number of boats as well as the type of boats used or the number of hooks. Not every series of CPUE refer to the same definition of *Unit of Effort*. However, within a dataset for a specific species, it has to be the same standardization. When a CPUE series is used, q may refer to the fish catchability.

The production function in (1.2), $f(B_t)$, may take different forms. The most popular are perhaps

$$f(B_t) = rB_t\left(1-\frac{B_t}{K}\right), \text{ Schaefer (1954);} \tag{1.4}$$

$$f(B_t) = \frac{r}{p}B_t\left(1-\left\{\frac{B_t}{K}\right\}^p\right), \text{ modified by Pella and Tomlinson (1969).} \tag{1.5}$$

In these two formulations, the r parameter stands for the growth rate of the population, K for the virgin biommass size and p is an asymmetry parameter. Note that Schaefer's formulation is the same as Pella and Tomlinson with $p = 1$ and it will be the model used from now on.

There are many ways to define B_1. In this manuscript, we will use $B_1 = K$, unless a specific mention is made. This assumption means that population is unexploited before the first year of the series. Although this is rarely a true assumption, it is often seen in scientific publications. Also, because our studies of the SPM model are based on simulations, it does not have much impact and simplifies greatly our calculations.

The production function is probably the best way to understand the origin of the name *Surplus Production* for this model. Basically, the population's production is the population's growth (if there is no harvesting), or in terms of the biomass, $B_{t+1} - B_t$. Thus, if our interest is to calculate MSY, we need to know what stock biomass provides the largest production. By maximizing (1.4) in terms of B_t, this population size is $B_{msy} = K/2$ (see figure 1.1). The maximum sustainable yield (the maximum catch that would leave the stock size intact) is then $MSY = rK/4$. Note that if the stock size is already bellow B_{msy}, allowing a catch as large a MSY over the years will lead fish stock to collapse.

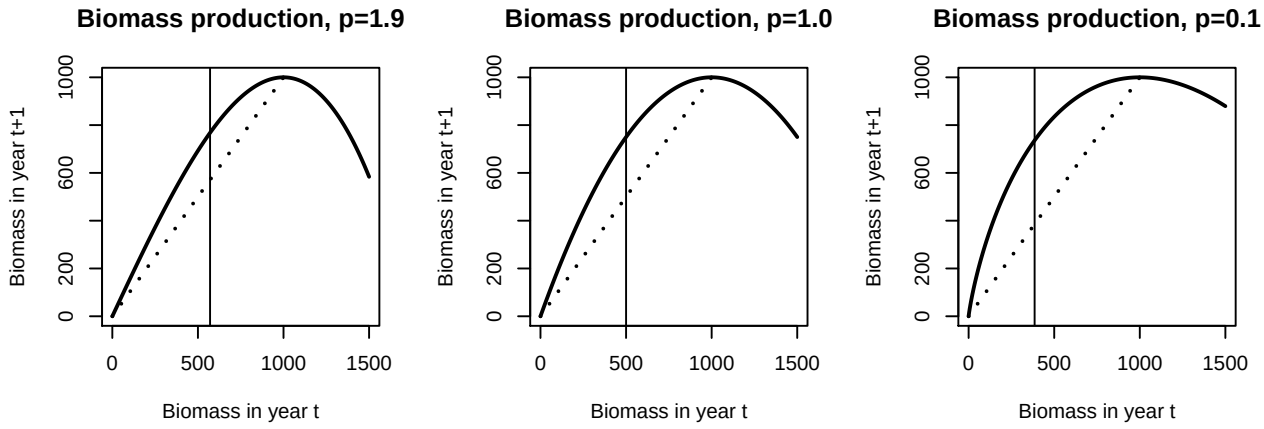


Figure 1.1: These three plots compare different scenarios for p values in equation (1.5). The vertical line is the B_{msy}. The oblique doted line represents a model where $B_{t+1} = B_t$. Note that the middle panel represents the model used for all of the following analysis

1.1.1 In practice

When using the SPM, observed data cannot be fit perfectly. For this reason, hypotheses have to be made on the source of discordance between the model and the observations. In the following, we will study three of these sources :

1. the observation error;
2. the process error;
3. the censored catches, i.e. when only a lower bound is observed for catches C_t in a year.

In this document, parts 2 and 3 will treat observation and process error, respectively, and part 4 will treat censored catches. These three parts are indeed the three reports made within the framework of my work in collaboration with the Department of Fisheries and Oceans (DFO) of Canada .

Observation error

Observation error occurs when the abundance index is not observed exactly. We will make the assumption that these error terms (e^{ε_t}) are independent and log-normally distributed with $\mu = 0$ so that (1.3) becomes

$$I_t = qB_t e^{\varepsilon_t}, \tag{1.6}$$

where $\varepsilon_t \sim \mathbf{N}(0, \tau^2)$. If there is only observation error in the SPM, it means that the populations dynamics from (1.2) and (1.4) are assumed to be exact.

Process error

Process error occurs when the dynamic equation (1.2) is not exactly modeling the reality. We will also make the assumption that process error is log-normally distributed with $\mu = 0$, so that (1.2) becomes

$$B_{t+1} = \{B_t - f(B_t) - C_t\} e^{\varepsilon'_{t+1}}, \tag{1.7}$$

where $\varepsilon'_{t+1} \sim \mathbf{N}(0, \sigma^2)$.

Censored catches

Censoring is a concept often observed in survival analysis and must not be confused with truncation. When dealing with censored data, we have a set of observation intervals $\{(x_{1L}, x_{1U}), (x_{2L}, x_{2U}), \ldots, (x_{nL}, x_{nU})\}$[1]in which the exact observations $\{x_1, x_2, \ldots, x_n\}$ lie. This often occurs because we cannot observe exactly the random variable of interest. In the case of the SPM, we will assume that the true catches lie in (Ct, ∞), where C_t are the observed/reported catches at time t.

It is important to make the distinction between censored and truncated data. Truncation happens when a random variable can only be observed in an observation window (Y_L, Y_U). An occurrence of this random variable that is not in this observation window will not be observed and no information will be available (as if it did not exist). Under censoring however, we have at least partial information on every occurrence of the random variable.

[1] x_{iL} or x_{iU} (but not both) may be respectively $-\infty$ or ∞. This occurs when we have only an upper or lower bound for the observation.

1.2 Inference

This section is presenting how we can make statistical inference about the SPM parameters for a population. We will describe two approaches to inference : maximum likelihood and Bayesian.

1.2.1 Maximum Likelihood Estimation

In a frequentist point of view, the parameters of a model (here the SPM) are considered as fixed but unknown constants. One of the key methods used in frequentist inference is based on the likelihood principle, which states that information in a sample is contained in the likelihood function. To define this function, let us say that we have a sample of observations $x_1, x_2, \ldots, x_n$. Then, the likelihood function is the joint probability of observing [2] $X_1{=}x_1, X_2{=}x_2, \ldots, X_n{=}x_n$ conditionally on the parameter(s) θ,

$$L(\theta|x) = P(X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n|\theta).$$

Thus, if we suppose that the X_i are independent and identically distributed with probability density function (pdf) $f(x;\theta)$, the likelihood function may be written as

$$L(\theta|x) = \prod_{i=1}^{n} f(x_i;\theta).$$

To obtain a point estimate $\hat{\theta}$, we need to maximize the likelihood function in term of θ so that we have $L(\hat{\theta}|x) \geq L(\theta|x)$ for every θ in Θ.[3] These estimates are known as the maximum likelihood estimates (MLE), and can be thought of as the value of θ that makes the observed data most probable. Note that the maximization process is often done on the log-likelihood function $l(\theta|x) = \ln\{L(\theta|x)\}$, and this often cannot be done analytically.

When using the MLE method for finding parameter estimates in a SPM, we need to make some assumptions. In our work we investigated three cases :

- SPM with observation error only (MLEO);

[2] Here X_i refers to random a variable and x_i stands for its observed value.

[3] Θ is the space of all possible values for θ.

- SPM with process error only (MLEP);
- SPM with both types of errors (MLEPO).

MLEO

When we consider the SPM with observation error only, its formulation becomes

$$\begin{aligned} B_1 &= K; && (1.8)\\ B_{t+1} &= B_t + rB_t\left(1-\frac{B_t}{K}\right) - C_t, t = 1,2,\ldots,N; && (1.9)\\ I_t &= qB_t e^{\varepsilon_t}, t = 1,2,\ldots,N; && (1.10) \end{aligned}$$

where $\varepsilon_t \overset{iid}{\sim} N(0,\tau^2)$.

From this, we can see that, given r and K, the series of biomasses is known for all years in the data, and we denote these biomasses $B_t(r,K)$ to highlight this fact. Thus, considering these two parameters as fixed, we can write the likelihood function as

$$L(q,\tau^2,r,K|\mathbf{I_t},\mathbf{C_t}) = \prod_{t=1}^{N}\frac{1}{\sqrt{2\pi\tau^2}I_t}\exp\left(\frac{-[\log I_t - \log\{qB_t(r,K)\}]^2}{2\tau^2}\right). \quad (1.11)$$

Maximizing this function in terms of q and τ^2 for fixed values of r and K may be done explicitly, with MLEs given by

$$\hat{q}(r,K) = \exp\left[\frac{\sum_t \log\{I_t/B_t(r,K)\}}{N}\right] \text{ and } \hat{\tau}^2(r,K) = \frac{\sum_t[\log I_t - \log\{\hat{q}(r,K)B_t(r,K)\}]^2}{N}.$$

When substituting these values for q and τ^2 in (1.11), the likelihood function still has to be maximized in terms of the parameters r and K, which cannot be done analytically. In such a case, we can use a numerical optimization method such as the Nelder-Mead algorithm (Nelder & Mead 1965).

MLEP

When we consider the SPM with process error only, its formulation becomes :

$$\begin{aligned} B_1 &= Ke^{\varepsilon'_1}; && (1.12)\\ B_{t+1} &= \left\{B_t + rB_t\left(1-\frac{B_t}{K}\right) - C_t;\right\} e^{\varepsilon'_t}, t = 1,2,\ldots,N; && (1.13)\\ I_t &= qB_t, t = 1,2,\ldots,N, && (1.14) \end{aligned}$$

where $\varepsilon'_t \overset{iid}{\sim} N(0, \sigma^2)$.

To write down the likelihood function under this SPM specification, we use the fact that (1.3) contains no error term, so that $B_t = I_t/q$, and then substitute this expression into equations (1.12) and (1.13) to obtain

$$\begin{aligned} I_1 &= qK\varepsilon_1, \\ I_{t+1} &= \left\{ I_t(1+r) - \frac{r}{qK} I_t^2 - qC_t \right\} \varepsilon_{t+1}, t = 1, 2, \ldots, N. \end{aligned}$$

The likelihood function becomes

$$L(r, K, q, \sigma^2 | \mathbf{I_t}, \mathbf{C_t}) = \prod_{t=1}^{N} \frac{1}{\sqrt{2\pi\sigma^2} I_t} \exp\left[\frac{-\{\log I_t - \log I_t^*(r, K, q)\}^2}{2\sigma^2} \right], \tag{1.15}$$

where $I_t^*(r, K, q) = I_t(1+r) - \frac{r}{qK} I_t^2 - qC_t$. In this case, for fixed values of r, K and q, the likelihood function may be explicitly maximized in terms of σ^2, with

$$\hat{\sigma}^2(r, K, q) = \frac{\sum_t \{\log I_t - \log I_t^*(r, K, q)\}^2}{N}.$$

Again, after substituting $\hat{\sigma}^2(r, K, q)$ for σ^2 in (1.15), maximization of (1.15) with respect to the other three parameters must be done numerically.

MLEPO

When we consider the SPM with observation and process errors, its formulation becomes

$$\begin{aligned} B_1 &= Ke^{\varepsilon'_1}; & (1.16) \\ B_{t+1} &= \left\{ B_t + rB_t \left(1 - \frac{B_t}{K} \right) - C_t; \right\} e^{\varepsilon'_t}; & (1.17) \\ I_t &= qB_t e^{\varepsilon_t}, & (1.18) \end{aligned}$$

where $\varepsilon_t \overset{iid}{\sim} N(0, \tau^2)$, $\varepsilon'_t \overset{iid}{\sim} N(0, \sigma^2)$ and ε_t and ε'_t are independent.

In this case, we cannot express the B_t as a deterministic function of the observations or the SPM parameters. For this reason, the maximization of the likelihood is more difficult. At this moment, we have not used this model with a frequentist method. However, investigating whether algorithms such as the Monte Carlo EM-algorithm or the Gibbs sampler (Robert and Casella, 2004) may be implemented in order to estimate the parameters of a SPM with both process and observation errors by maximum likelihood.

1.2.2 Bayes Estimators

Unlike maximum likelihood estimators, the Bayesian estimators do not rely only on the sample. Actually Bayesian analysis is a method use to combine the information contained in the data and some external intuition, or *expertise* which will be called uncertainty. Basically, Bayesian analysis relies on Bayes' rule which states that for two events A and B

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)},$$

where $P(A|B)$ refers to the probability of the event A to happen knowing that event B occurred and $P(A)$ is the marginal probability of the event A to occur. This rules applies also to probability density functions, so if X and Y are two random variables with joint density f_{XY}, then

$$f_{X|Y} = \frac{f_{Y|X} f_X}{f_Y},$$

where $f_{X|Y}$ is the conditional pdf of X knowing Y and f_X the marginal pdf of X.

When applying Bayesian analysis to a model, the Bayesian analysis differs drastically from the maximum likelihood in the fact that model parameters are now considered as random variables (in maximum likelihood estimation, the parameters are considered as fixed but unknown values). This lets us presume a certain amount of uncertainty to the model parameters, prior to the analysis, and combine it to our data to calculate our estimates. Let $f(x|\theta)$ be a model of interest. Then to use Bayesian analysis we need prior distributions, $\pi(\theta)$, for all your parameters (θ). These priors have to reflect our uncertainty in the parameters before observing the data; Then we calculate the posterior distribution of the parameter, $\pi(\theta|x)$, by using Bayes' rule, i.e.,

$$\pi(\theta|x) = \frac{f(x|\theta)\pi(\theta)}{f(x)}, \tag{1.19}$$

where $f(x)$ is the marginal distribution of the data. Usually, we set the mean of the posterior distribution (1.19) as the Bayes estimates of the parameters. The marginal distribution of the data $f(x)$ can be obtained by integrating the joint distribution of the data and parameter, $f(x|\theta)\pi(\theta)$, relatively to θ. However, because $f(x)$ is not a function of θ, in some cases it is easier to find the constant α that makes the function $\alpha f(x|\theta)\pi(\theta)$ a probability density function (i.e. continuous on the domain and integrating to 1). In some more complicated cases, it is

not possible to calculate this constant because of the complex form of $f(x|\theta)\pi(\theta)$. To avoid this calculation, algorithms such as Gibbs sampler may be used to sample from the posterior densities.

When Bayesian analysis is applied to the SPM, we are in the kind of situation where computational methods like the Gibbs sampler are needed. First, let us recall our goal : we need to calculate the posterior mean of the SPM parameters, which is the mean of

$$\pi(\theta|x) = \pi(r, K, q, \sigma^2, \tau^2, B_1 \dots B_N | I_1 \dots I_N),$$

see equation (1.19). As the maximum likelihood method, the Bayesian analysis depends on the sources of error included in the model. In this particular Bayesian analysis study of the SPM, we have investigated only the case with both process and observation errors (see equations 1.17, 1.18 and 1.18). In this case, the density

$$f(x|\theta) = f(I_1 \dots I_N | r, K, q, \sigma^2, \tau^2, B_1 \dots B_N)$$

can be defined recursively using conditional probability proprieties:

$$f(I_1 \dots I_N|\theta) = f(I_N|I_{N-1}, \theta) \times f(I_{N-1}|I_{N-2}, \theta) \times \dots \times f(I_2|I_1, \theta) \times f(I_1|\theta).$$

The prior distribution can be define using the same recursive scheme :

$$\pi(\theta) = \pi(r, K, q, \sigma^2, \tau^2, B_1 \dots B_N)$$

$$\begin{aligned} \pi(\theta) &= \pi(B_N|B_{N-1}, r, K, q, \sigma^2, \tau^2) \times \pi(B_{N-1}|B_{N-2}, r, K, q, \sigma^2, \tau^2) \times \dots \\ &\quad \times \pi(B_1|r, K, q, \sigma^2, \tau^2) \times \pi(r)\pi(K)\pi(q)\pi(\sigma^2)\pi(\tau^2) \end{aligned}$$

Note that in the Bayesian analysis of the SPM, the B_t's are now considered as parameters of the models, like r, K, ..., contrary to MLE analysis where we can't maximize the likelihood function in terms of random variables.

Now, because of the complex formulation of $f(x|\theta)\pi(\theta)$, the marginal distribution $f(I_1 \dots I_N)$ cannot be calculated analytically. For this reason, the Gibbs sampler is used to sample from the explicitly unknown distribution $\pi(\theta|x)$. The parameter estimations will then be obtained from the sample means of the r, K, q, σ^2 and τ^2 generated by the Gibbs sampler.

Part 2

Application of the MLEO and MLEP

2.1 Introduction

The Surplus Production Model (SPM) is a widely used fish stock population assessment model. To apply SPM, all that is required is a series of abundance indices (CPUEs are often used), and the series of catches related to the years to be assessed. In our previous work (Lemay et al, 2006), we looked at the reliability of Bayesian estimators in a SPM context and also investigated the application of the Hammond an Trenkel (2005) method for mis-reported (censored) catches. Though Bayesian methods may be easily adapted to include many sources of errors in the data, the results in Lemay et al (2006) suggest that a frequentist (non Bayesian) approach to SPM fitting may be interesting to investigate because it is not subject to prior distribution specification that can have unduly affect the inferences. Indeed, the simulation study reported in Lemay et al (2006) showed that some parameters in the SPM are difficult to identify from the data alone and that inferences about these parameters are highly dependent on the prior distributions used in the Bayesian inferences. Therefore, our ultimate objective is to study the use of frequentist censored method(s) applied to SPM. To achieve this goal, we must first examine how maximum likelihood may be utilized with SPM when catches are considered as exact (i.e., non censored, without misreporting). Because in practice a frequentist approach to SPM fitting often only assumes observation error, we investigate if considering one or both types between observation and process errors really matters when it comes to parameter estimation. Actually, because process error and observation error may be hard to distinguish, a model with only one type of error might exhibit good properties when it comes to estimating, for example, the maximum sustainable yield (MSY) of a fish population, even if both types of error are present. A study of this problem had been done by Polacheck et al (1993), but it was based only on three series of data. Since we want to test a wider variety of population biomass, we designed a much broader simulation study; this design will be described in Section 2.3.1.

This manuscript is divided as follows. We introduce the SPM and briefly explain how to estimate its parameters by maximum likelihood in Section 2.2. We describe the design of the simulation study and give a detailed account and interpretation of the simulation results in Section 2.3. We give our main conclusions and discuss ideas for further research in Section 2.4.

2.2 Preliminaries

2.2.1 Surplus Production Model

The model we investigate is the Scheafer annual SPM :

$$B_{t+1} = B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t, \tag{2.1}$$

where B_t represents the biomass (e.g. 1,000 tons) in year t, r is the intrinsic population growth rate parameter, K is the virgin population biomass (or the biomass when the population is in equilibrium) and C_t represents the catches in year t (1,000 tons).

Stock biomass usually cannot be measured directly to estimate the r and K parameters in (4.1) and additional information is required to estimate these parameters. Often, a CPUE time series is used, but a research survey biomass index is also commonly used. We need a second equation to include the information provided by the survey index,

$$I_t = q_s B_t, \tag{2.2}$$

where I_t is the survey index at time t and q_s represents the fish catchability in the survey. The parameters to estimate are r, K and q_s. Note that equation (2.3) implies that we are assuming that the biomass in the first year of data is the virgin biomass, i.e., there were no fisheries before this first year. This hypothesis might not be verified, but it will simplify the optimization process needed by the maximum likelihood estimation by removing one parameter (B_1) in the log-likelihood functions.

In our study, we considered a SPM with two kinds of errors : process error (related to equation (4.1)) and observation error (related to the equation (4.2)); we assumed a log-normal distribution for both process and observation error. Including both types of errors, the model becomes

$$\begin{aligned} B_1 &= K\varepsilon_1 && (2.3)\\ B_{t+1} &= \left\{B_t + rB_t(1 - \frac{B_t}{K}) - C_t\right\}\varepsilon_{t+1}; && (2.4)\\ I_t &= q_s B_t \varepsilon_t^*, && (2.5) \end{aligned}$$

where $\log(\varepsilon_t) \sim \mathbf{N}(0, \sigma^2)$ and $\log(\varepsilon_t^*) \sim \mathbf{N}(0, \tau^2)$, and where all ε_t^* and ε_t are assumed independent.

2.2.2 Maximum Likelihood Estimation

The maximum likelihood method consists of estimating the parameters of a model by choosing, as the parameter estimates, the value of the parameters that makes the observed data most probable. Mathematically, suppose that we observe data $x_1, \ldots, x_n$ and that under the model, the joint probability/density of the data is $f(x_1, \ldots, x_n; \theta)$, where θ denotes the unknown parameters to be estimated. Then the maximum likelihood estimator of θ is the value $\hat{\theta}$ such that $f(x_1, \ldots, x_n; \hat{\theta}) \geq f(x_1, \ldots, x_n; \theta)$ for any value of θ, i.e., the value of θ that maximizes $f(x_1, \ldots, x_n; \theta)$.

In the case of the SPM, we observe a sample of observations of the form (I_1, C_1), ..., (I_N, C_N) and on the basis of this sample, we want to estimate the parameters q_s, r and K, as well as the error variances τ^2 and σ^2.

Maximum likelihood estimators for a SPM with observation errors only (MLEO)

When accounting for observation error only, the SPM may be written as

$$B_1 = K \tag{2.6}$$

$$B_{t+1} = B_t + rB_t(1 - \frac{B_t}{K}) - C_t; \tag{2.7}$$

$$I_t = q_s B_t \varepsilon_t^*. \tag{2.8}$$

From this, we can see that, given r and K, the series of biomasses is known for all years in the data, and we denote these biomasses $B_t(r, K)$ to highlight this fact. Thus, considering these two parameters as fixed, we can write the likelihood function as

$$L(q_s, \tau^2, r, K | \mathbf{I_t}, \mathbf{C_t}) = \prod_{t=1}^{N} \frac{1}{\sqrt{2\pi\tau^2} I_t} \exp\left(\frac{-[\log I_t - \log\{q_s B_t(r, K)\}]^2}{2\tau^2} \right).$$

Maximizing this function in terms of q_s and τ^2 may be done explicitely, with MLEs given by

$$\hat{q}_s(r, K) = \exp\left[\frac{\sum_t \log\{I_t / B_t(r, K)\}}{N} \right] \text{ and } \hat{\tau}^2(r, K) = \frac{\sum_t [\log I_t - \log\{\hat{q}_s(r, K) B_t(r, K)\}]^2}{N}.$$

But the likelihood function still has to be maximized in terms of the parameters r and K, which cannot be done analytically. In such a case, we can use a numerical optimization method; for all results reported in this manuscript, we performed the numerical optimization using the

Nelder-Mead algorithm (Nelder and Mead, 1965) implemented in the `optim( )` function of the package R.

Maximum likelihood estimators for a SPM with process errors only (MLEP)

When accounting for process error only, the SPM may be written as

$$B_1 = K\varepsilon_1 \tag{2.9}$$

$$B_{t+1} = \left\{B_t + rB_t(1 - \frac{B_t}{K}) - C_t\right\}\varepsilon_{t+1}; \tag{2.10}$$

$$I_t = q_s B_t. \tag{2.11}$$

To write down the likelihood function under this SPM specification, we use the fact that equation (2.11) contains no error term, so that $B_t = I_t/q_s$, and then substitute this expression into equations (2.9) and (2.10) to obtain

$$\begin{aligned} I_1 &= q_s K\varepsilon_1 \\ I_{t+1} &= \left\{I_t(1+r) - \frac{r}{q_s K}I_t^2 - q_s C_t\right\}\varepsilon_{t+1}. \end{aligned}$$

The likelihood function becomes

$$L(r, K, q_s, \sigma^2|\mathbf{I_t}, \mathbf{C_t}) = \prod_{t=1}^{N} \frac{1}{\sqrt{2\pi\sigma^2}I_t} \exp\left[\frac{-\{\log I_t - \log I_t^*(r, K, q_s)\}^2}{2\sigma^2}\right],$$

where $I_t^*(r, K, q_s) = I_t(1+r) - \frac{r}{q_s K}I_t^2 - q_s C_t$. In this case, the likelihood function may be explicitly maximized in terms of σ^2,

$$\hat{\sigma}^2(r, K, q_s) = \frac{\sum_t \{\log I_t - \log I_t^*(r, K, q_s)\}^2}{N},$$

but maximization with respect to the other three parameters must be done numerically.

Maximum likelihood estimators for a SPM with process and observation errors (MLEPO)

When both types of errors are present, we cannot express B_t as a deterministic function of the observed data or the model parameters. In this case, the likelihood function can only be written in terms of a high dimensional integral with respect to the error terms. Nonetheless,

methods to find maximum likelihood estimators that do not require calculation of this likelihood function do exist. We are currently investigating whether algorithms such as the Monte Carlo EM-algorithm or the Gibbs sampler (Robert and Casella, 2004) can be implemented in order to estimate the parameters of a SPM with both process and observation errors by maximum likelihood.

2.3 Simulation study

The purpose of this simulation study is to assess the performance of the maximum likelihood estimators of the SPM parameters under various simulation and model fitting scenarios. Our specific objectives are to

1. study the properties of the maximum likelihood estimators when fitting a SPM with observation error only (MLEO) to data generated from (i) a SPM with observation error only; (ii) a SPM with process error only; (iii) a SPM with both process and observation error;

2. study the properties of the maximum likelihood estimators when fitting a SPM with process error only (MLEP) to data generated from (i) a SPM with observation error only; (ii) a SPM with process error only; (iii) a SPM with both process and observation error.

We have designed a simulation study that has allowed us to study the impact of all the important model parameters (r, K, τ^2 and σ^2). The details of the study design are given in Section 2.3.1. The results are summarized in Section 2.3.2 and these results are analyzed in Section 2.3.3.

2.3.1 Simulation Design

In order to study the effect of each of the parameter of interest, we used a complete factorial design for both MLEO and MLEP. We included three factors in our design :

The combination of (r, K) parameters: We simulated at two levels of this factor, $(r, K) = (0.16,\ 4000)$ (giving an almost linearly decreasing biomass series) and $(r, K) = (0.4,\ 3500)$ (giving a convex biomass series, i.e., a two-way trip).

The observation error τ^2: We simulated at three levels of this factor, $\tau^2 = 0$ (no observation error), $\tau^2 = 0.04$ (mild observation error), $\tau^2 = 0.09$ (strong observation error).

The process error σ^2: We simulated at three levels of this factor, $\sigma^2 = 0$ (no process error), $\sigma^2 = 0.04$ (mild process error), $\sigma^2 = 0.09$ (strong process error).

Our design thus has $2 \times 3 \times 3 = 18$ "treatment" levels, and for each treatment level, we simulate 1,000 series of CPUEs to which we fit 1,000 SPMs. The series of catches was fixed for all 18,000 datasets; we used the series of catches related to Northern Namibian hake during years 1965 to 1988 (Polacheck et al, 1993). We also held the value of q_s fixed at $q_s = 0.2$ for each of the 18 treatments, as this parameter is a scale parameter linking the indices and biomasses and thus has no impact on the population dynamics. The levels of the parameters used for each of the 18 treatments are summarized in Table 2.1.

Table 2.1: This table shows the 18 combinations of SPM parameter values used in the simulation study. Note that for every simulation, $q_s = 0.2$ and the catch series is that on Namibian hake given by Polacheck et al (1993).

Treatment	(r, K)	τ^2 (obs. err. variance)	σ^2 (proc. err. variance)
1	$(r = 0.16, K = 4000)$	0	0
2	$(r = 0.16, K = 4000)$	0	0.04
3	$(r = 0.16, K = 4000)$	0	0.09
4	$(r = 0.16, K = 4000)$	0.04	0
5	$(r = 0.16, K = 4000)$	0.04	0.04
6	$(r = 0.16, K = 4000)$	0.04	0.09
7	$(r = 0.16, K = 4000)$	0.09	0
8	$(r = 0.16, K = 4000)$	0.09	0.04
9	$(r = 0.16, K = 4000)$	0.09	0.09
10	$(r = 0.40, K = 3500)$	0	0
11	$(r = 0.40, K = 3500)$	0	0.04
12	$(r = 0.40, K = 3500)$	0	0.09
13	$(r = 0.40, K = 3500)$	0.04	0
14	$(r = 0.40, K = 3500)$	0.04	0.04
15	$(r = 0.40, K = 3500)$	0.04	0.09
16	$(r = 0.40, K = 3500)$	0.09	0
17	$(r = 0.40, K = 3500)$	0.09	0.04
18	$(r = 0.40, K = 3500)$	0.09	0.09

The simulation of each series of CPUE indices was done according to this algorithm:

1. Given the r, K and σ^2 parameter values, simulate a series of biomasses using equation (4.4);

2. Given the biomass series, q_s and τ^2, simulate the CPUE indices using equation (4.3).

During the first step, we had to be careful not to simulate negative biomasses, which could happen when process error was present ($\sigma^2 \neq 0$), because the catch series was fixed and did not depend on the simulated biomass series. To account for this, we adjusted our simulations in the presence of process error in this way :

- Given the biomass and catches in year t, if biomass in year $t+1$ is lower than 400, resimulate the biomass for year $t+1$;
- If, after 5 attempts, a biomass greater than 400 is not simulated, resimulate the whole series of biomasses.

Of course, this adjustment should influence the estimation results, as we are then not exactly simulating from the SPM model. For instance, the process error variance should be underestimated as extreme values of the errors will be rejected and resimulated. Note that Punt (2003) also used the Namibian hake catches in his simulation study, but in his simulations he held the biomasses at times 1 and N fixed to avoid negative biomasses. We elected not to use a similar correction, as we feel that this would remove too much of the variability in the model and hence make the estimators a lot less volatile than they really should be under the SPM.

2.3.2 Results

This sections gives a detailed account of the outcome of the simulations. For both MLEO and MLEP, we present graphics and tables summarizing the results obtained under all 18 treatment levels; we defer the analysis and interpretation of these results to Section 2.3.3.

Because maximum likelihood estimation is computed using an iterative numerical algorithms, an assessment of the convergence of this algorithm is given. To be sure that maximum likelihood estimates were not dependent on the starting point of the algorithms, we ran the optimization process using the same 4 different starting values in each of the 18,000 simulations and we kept the best estimation in terms of the likelihood function evaluation. Because it was not possible to monitor the progress of all 18,000 simulations and make adjustments to the iterative scheme "manually", we compiled results **only** for datasets giving "valid" final results:

- K estimate needs to be smaller than 8,000;

- r estimate needs to be between 0 and 1;
- q_s estimate needs to be between 0 and 1;
- the numerical optimization algorithm must have converged according to the software.

For each of MLEO and MLEP, the presentation of the results is done in this order. First, we give the proportion of valid samples for each treatment. Then for all treatment levels except 1 and 10 (these treatments have neither observation nor process error), we give plots of density estimates of the distribution of

- the maximum likelihood estimators of r, K, q_s and τ^2 or σ^2;
- the "prediction error", defined as $\hat{B}_{N+1}/B_{N+1}$, the ratio of the estimated biomass at time $N+1$ to the simulated biomass at time $N+1$;
- the maximum sustainable yield, MSY$= rK/4$.

Tables presenting the mean values of the maximum likelihood estimators as well as their bias, variance and root mean squared error are also given.

Results for the MLEO method

Because this method is accounting only for observation error, we expect it to perform much better with datasets simulated without process error. We thus expect to get more valid samples and better parameter estimates for treatment levels 1,4,7,10,13 and 16. Indeed, Figure 2.1 shows that for these treatments, the proportion of valid samples is always above 80% and stands much higher than the proportion of valid samples under treatments with process error.

Figure 2.1: This plots presents the proportion of valid estimations out of 1000 replicates when using the MLEO method. The validity of an estimation is detailed in the beginning of this section.

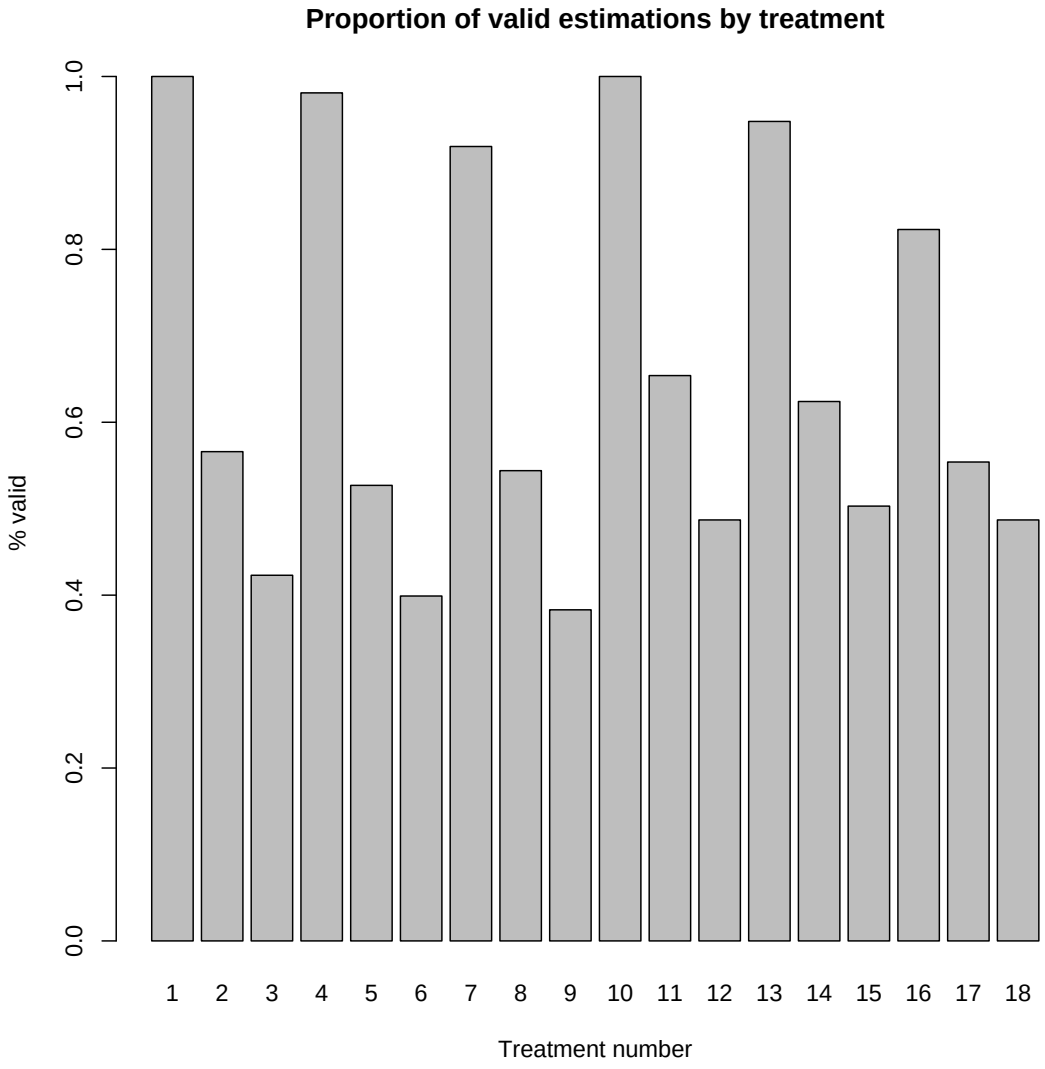


Figure 2.2: These plots represents the kernel density estimation of the parameters estimates for the treatment 2 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is small (0.04)

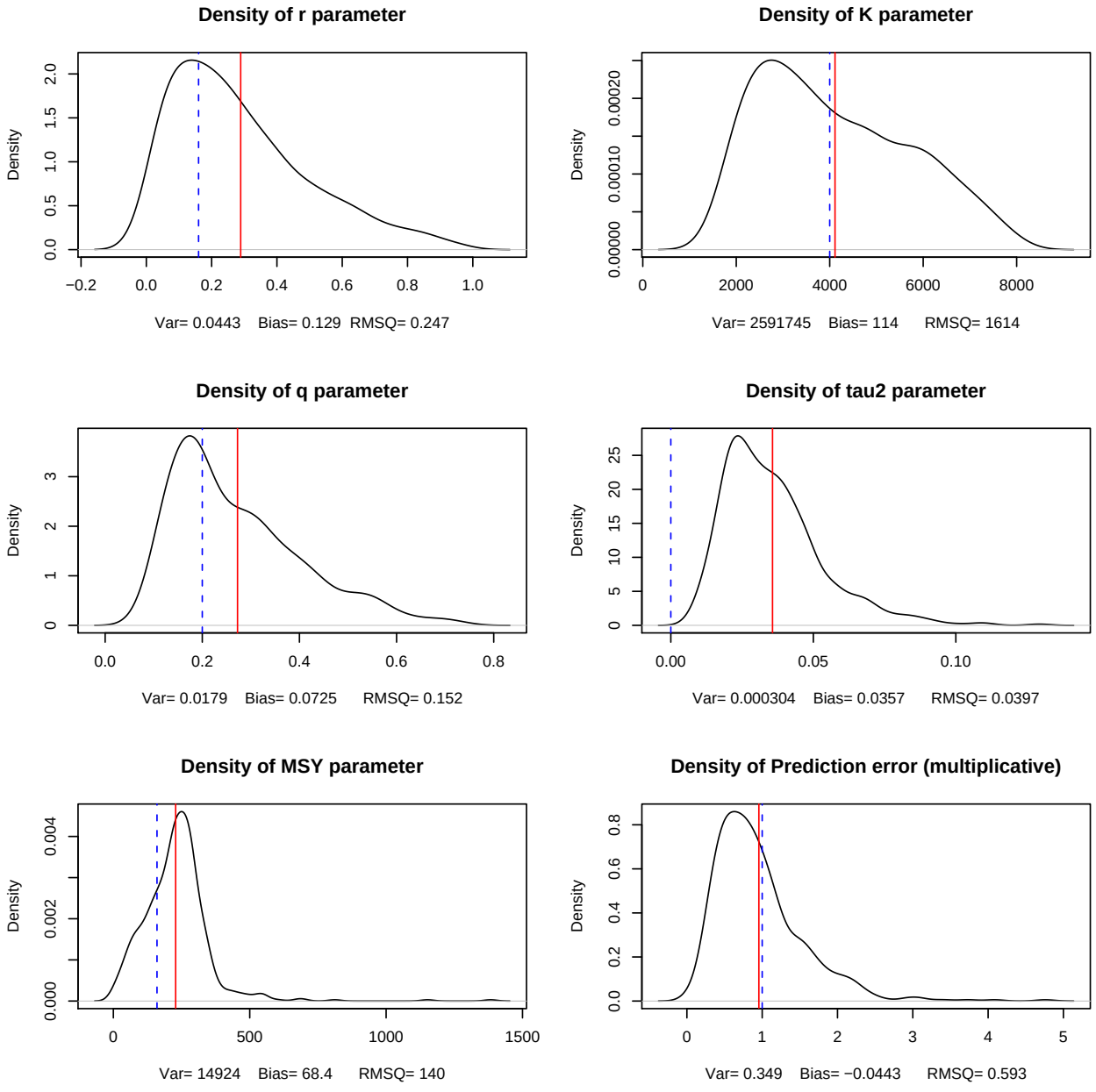


Figure 2.3: These plots represents the kernel density estimation of the parameters estimates for the treatment 3 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is high(0.09)

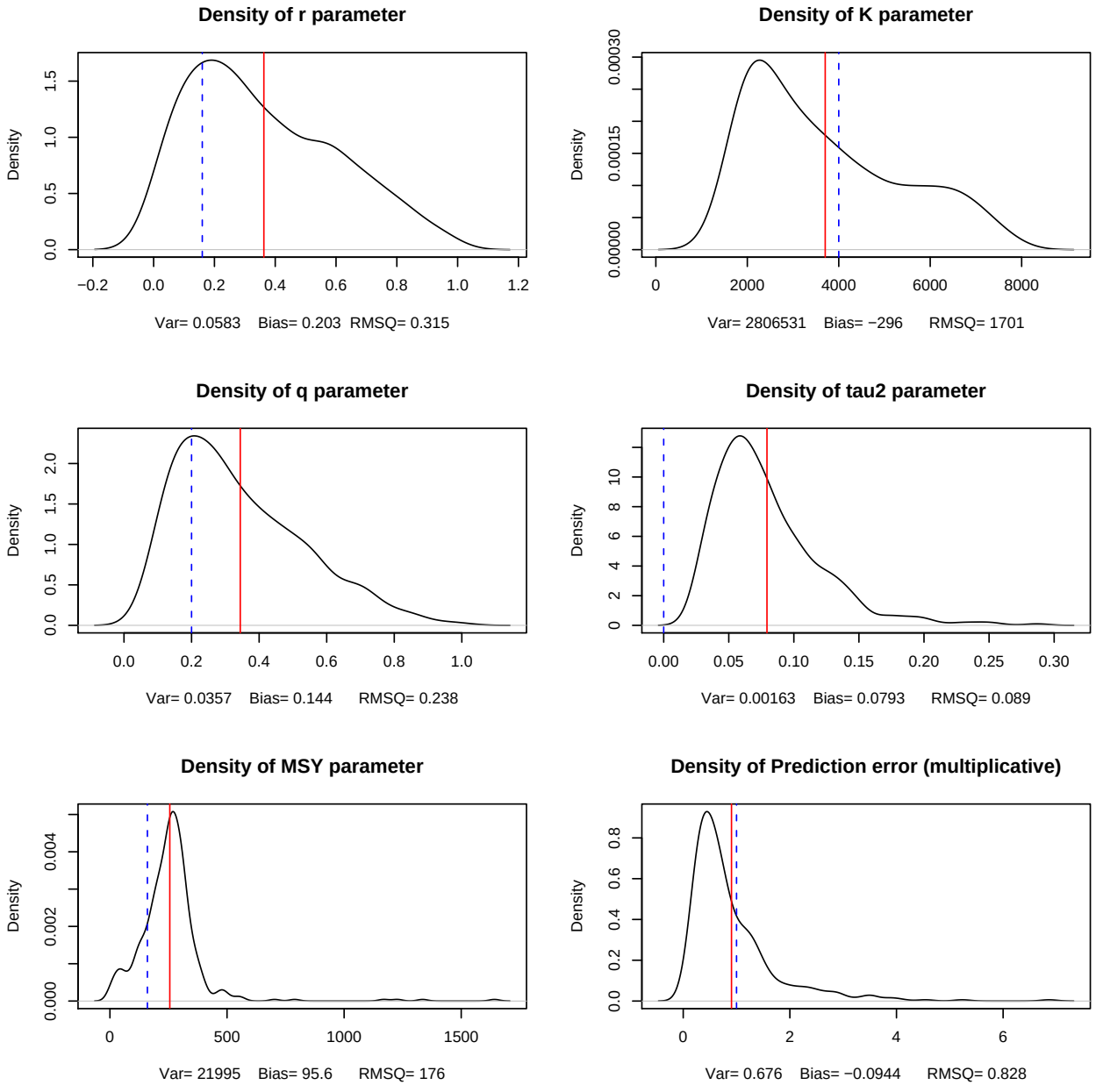


Figure 2.4: These plots represents the kernel density estimation of the parameters estimates for the treatment 4 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no process error and observation error variance is small (0.04)

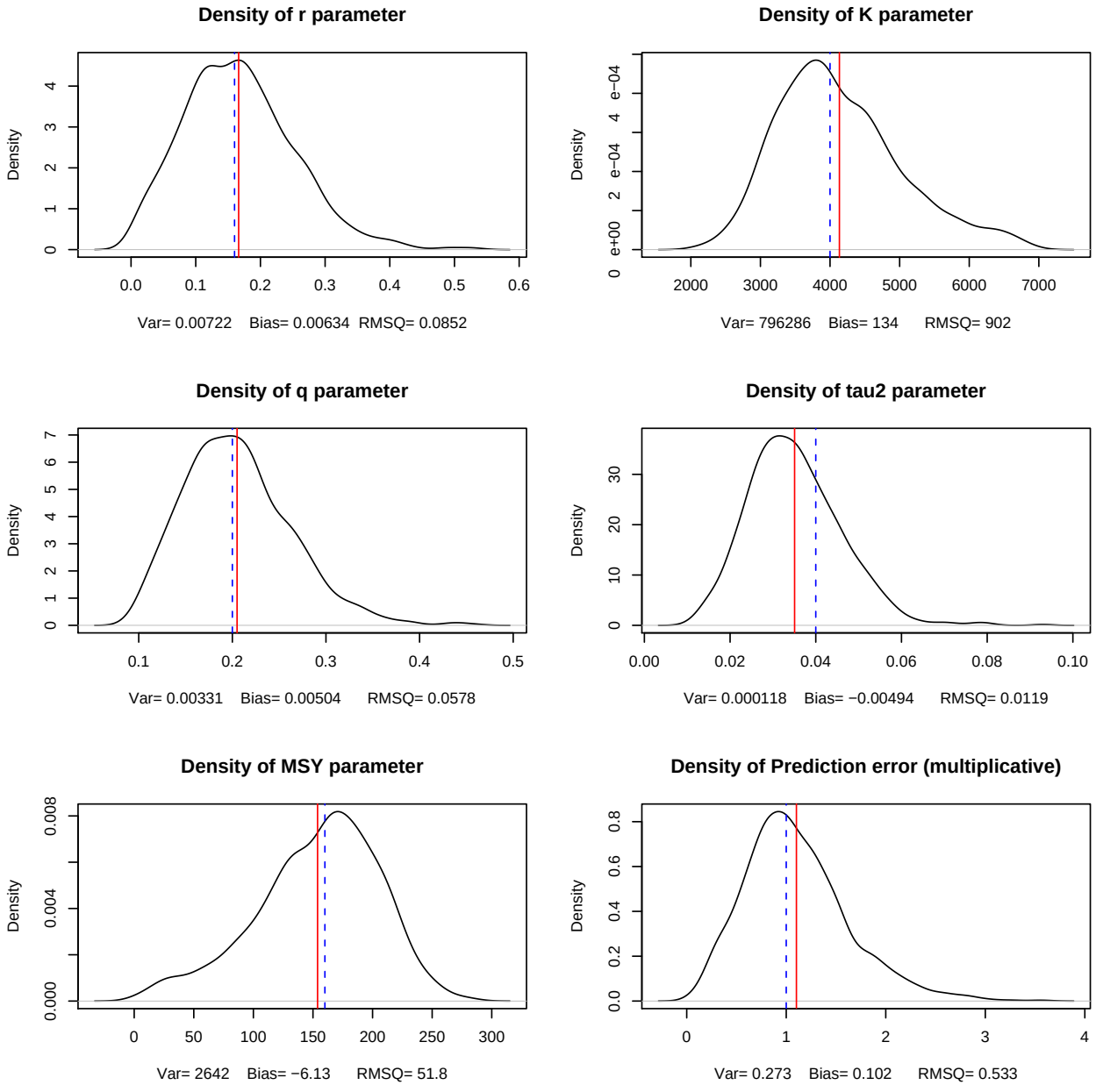


Figure 2.5: These plots represents the kernel density estimation of the parameters estimates for the treatment 5 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance is small (0.04)

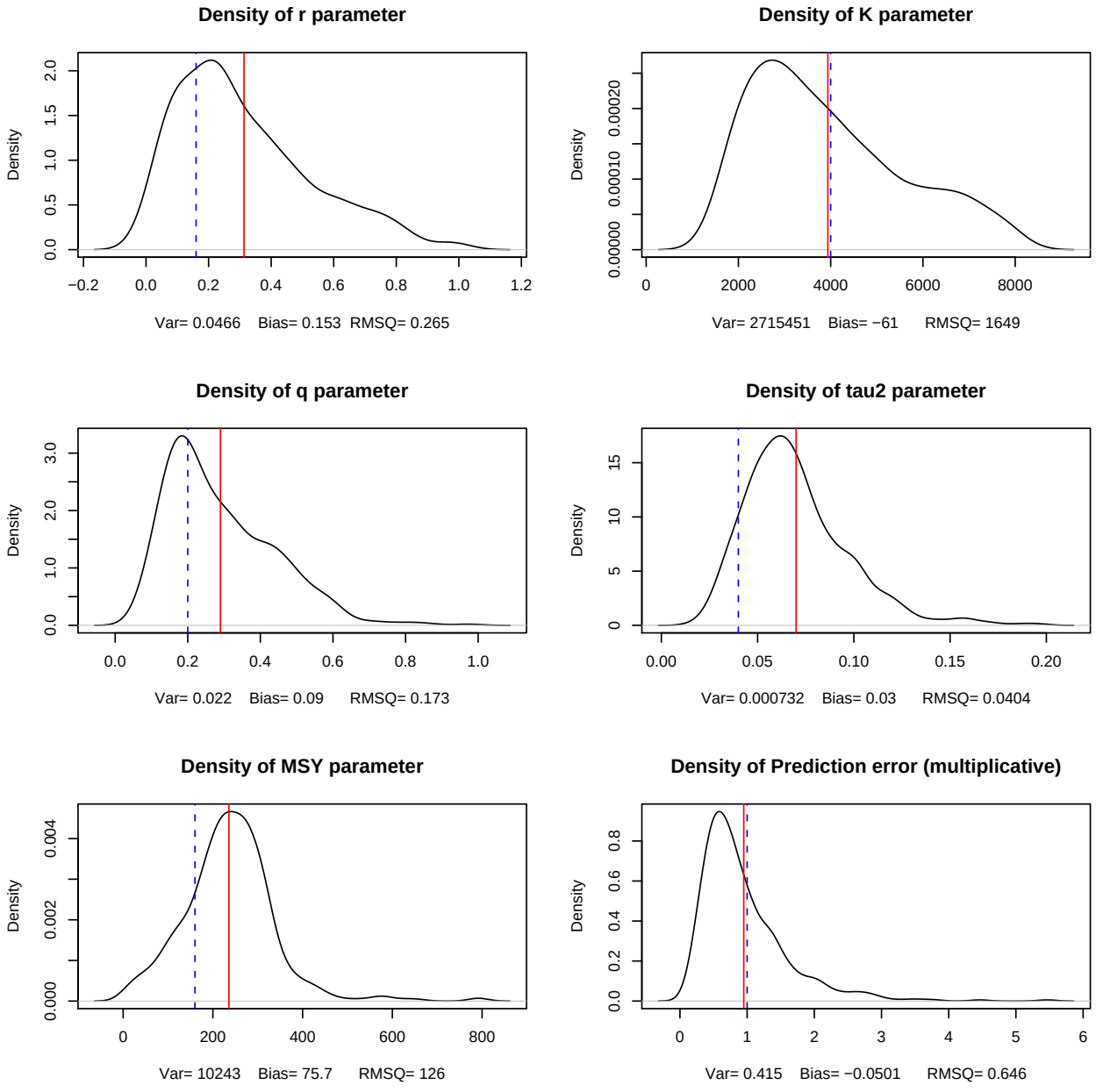


Figure 2.6: These plots represents the kernel density estimation of the parameters estimates for the treatment 6 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance had is high (0.09)

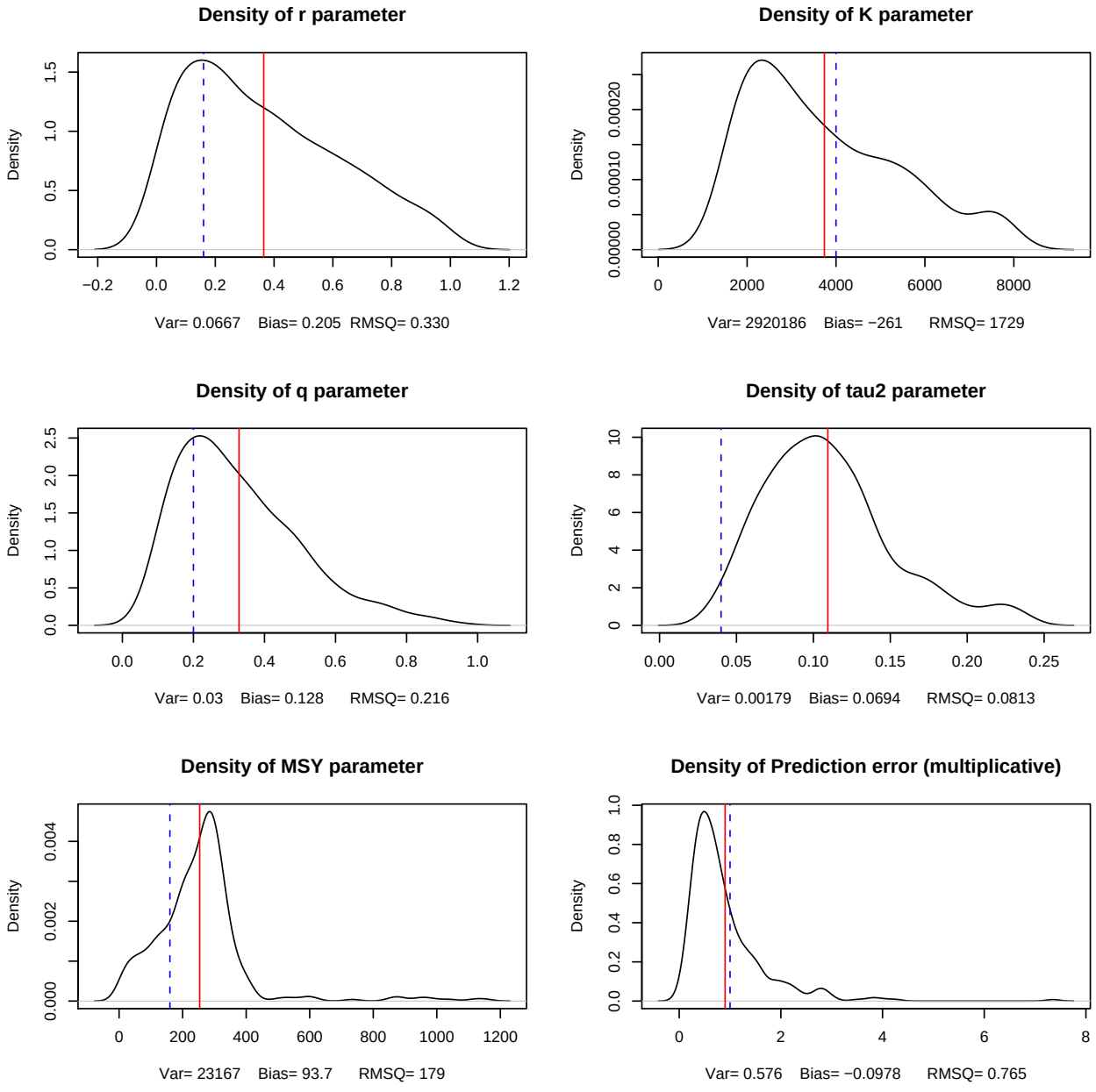


Figure 2.7: These plots represents the kernel density estimation of the parameters estimates for the treatment 7 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and there is no process error

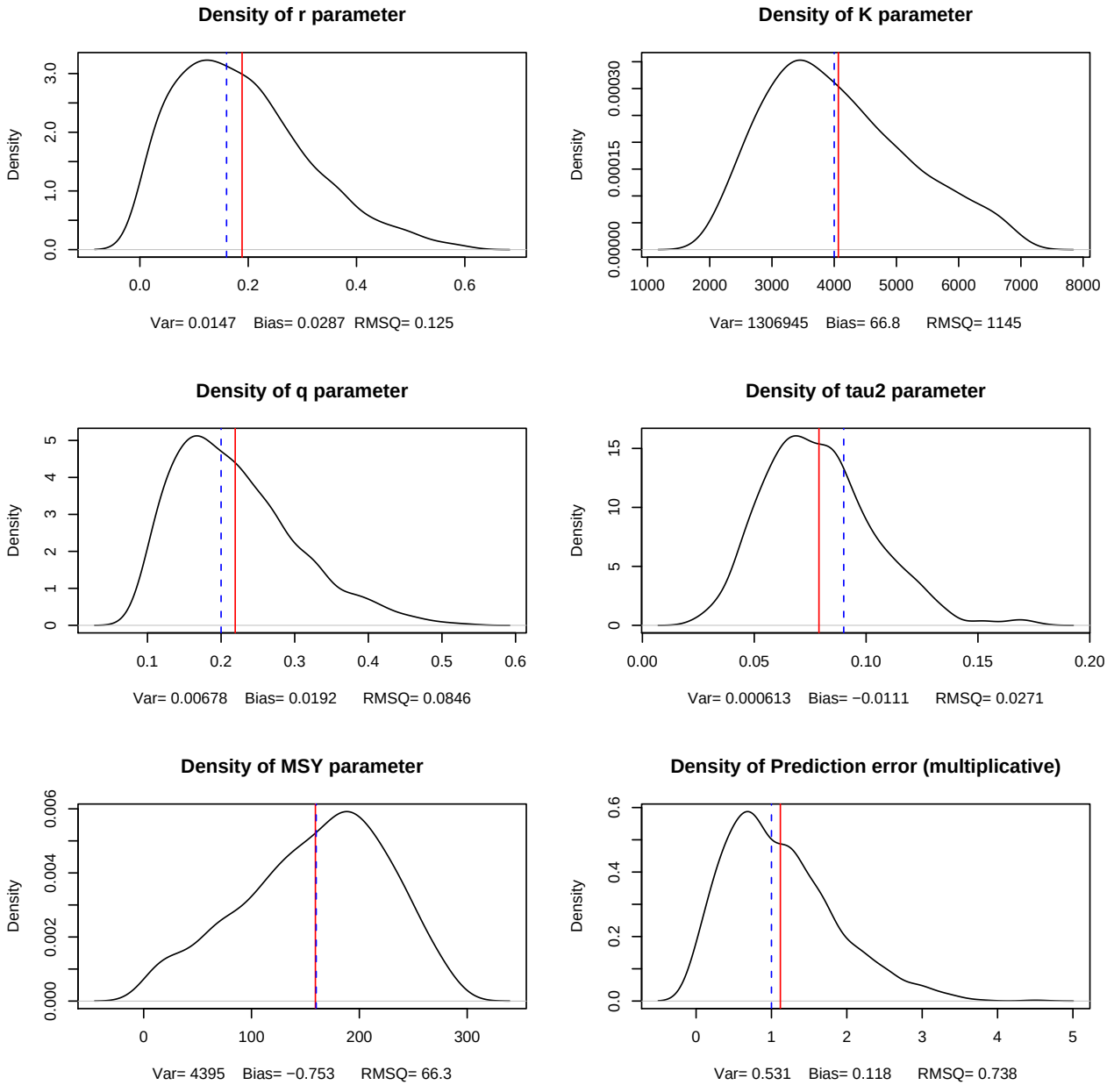


Figure 2.8: These plots represents the kernel density estimation of the parameters estimates for the treatment 8 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is small (0.04)

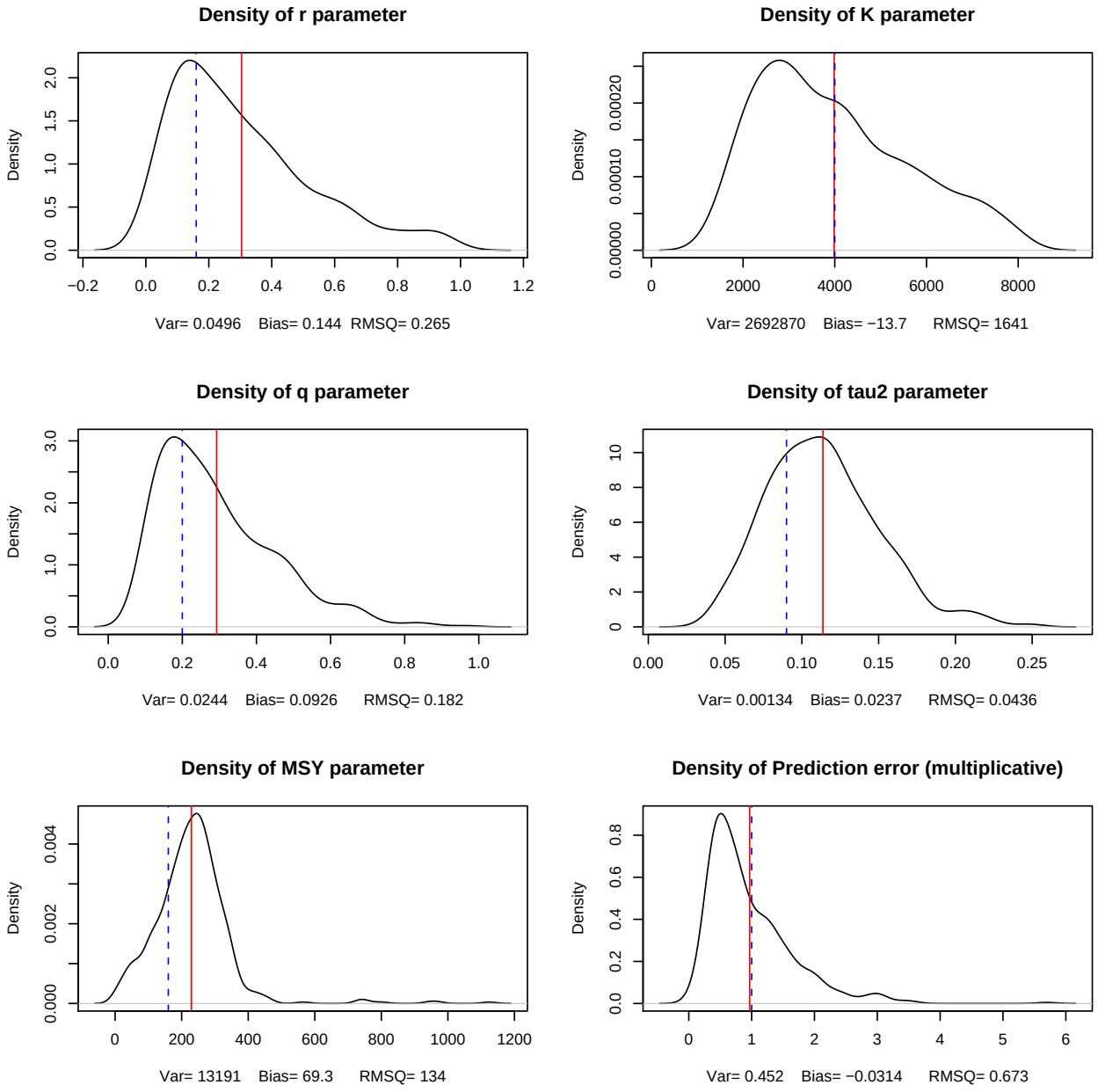


Figure 2.9: These plots represents the kernel density estimation of the parameters estimates for the treatment 9 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is high (0.09)

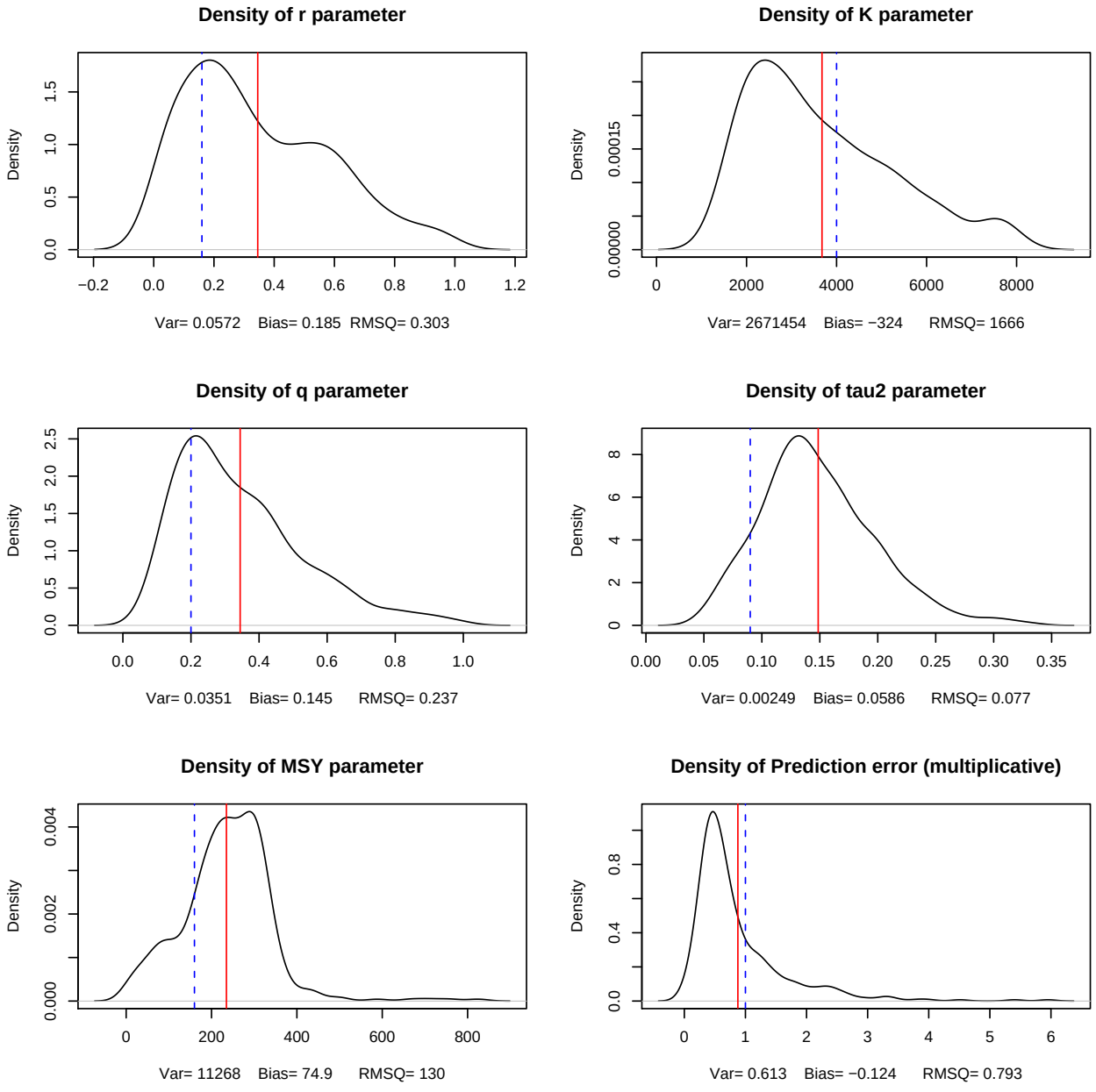


Figure 2.10: These plots represents the kernel density estimation of the parameters estimates for the treatment 11 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is small (0.04)

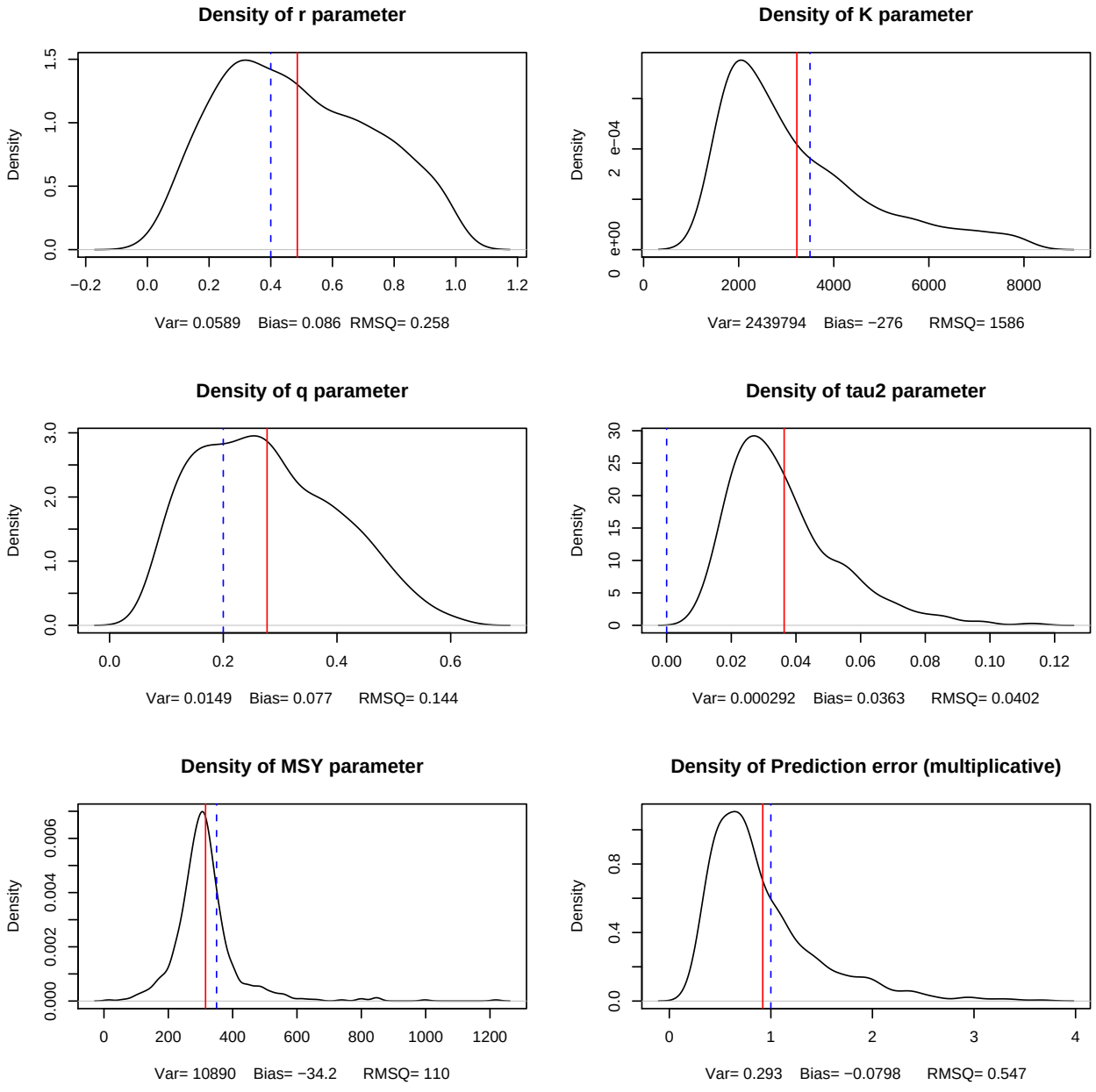


Figure 2.11: These plots represents the kernel density estimation of the parameters estimates for the treatment 12 using MLEO method. In this case there is no observation error and process error variance is high(0.09)

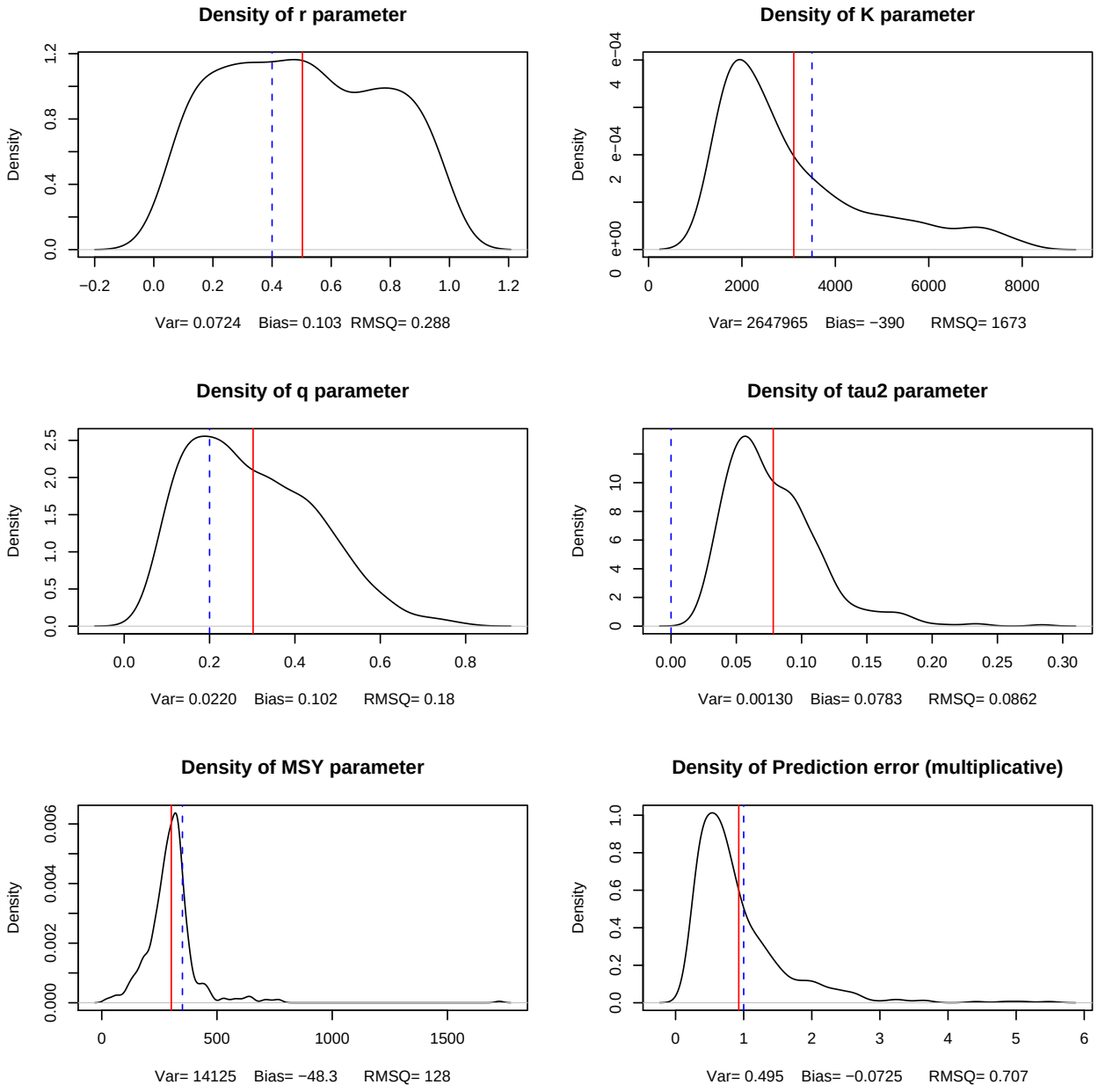


Figure 2.12: These plots represents the kernel density estimation of the parameters estimates for the treatment 13 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no process error and observation error variance is small (0.04)

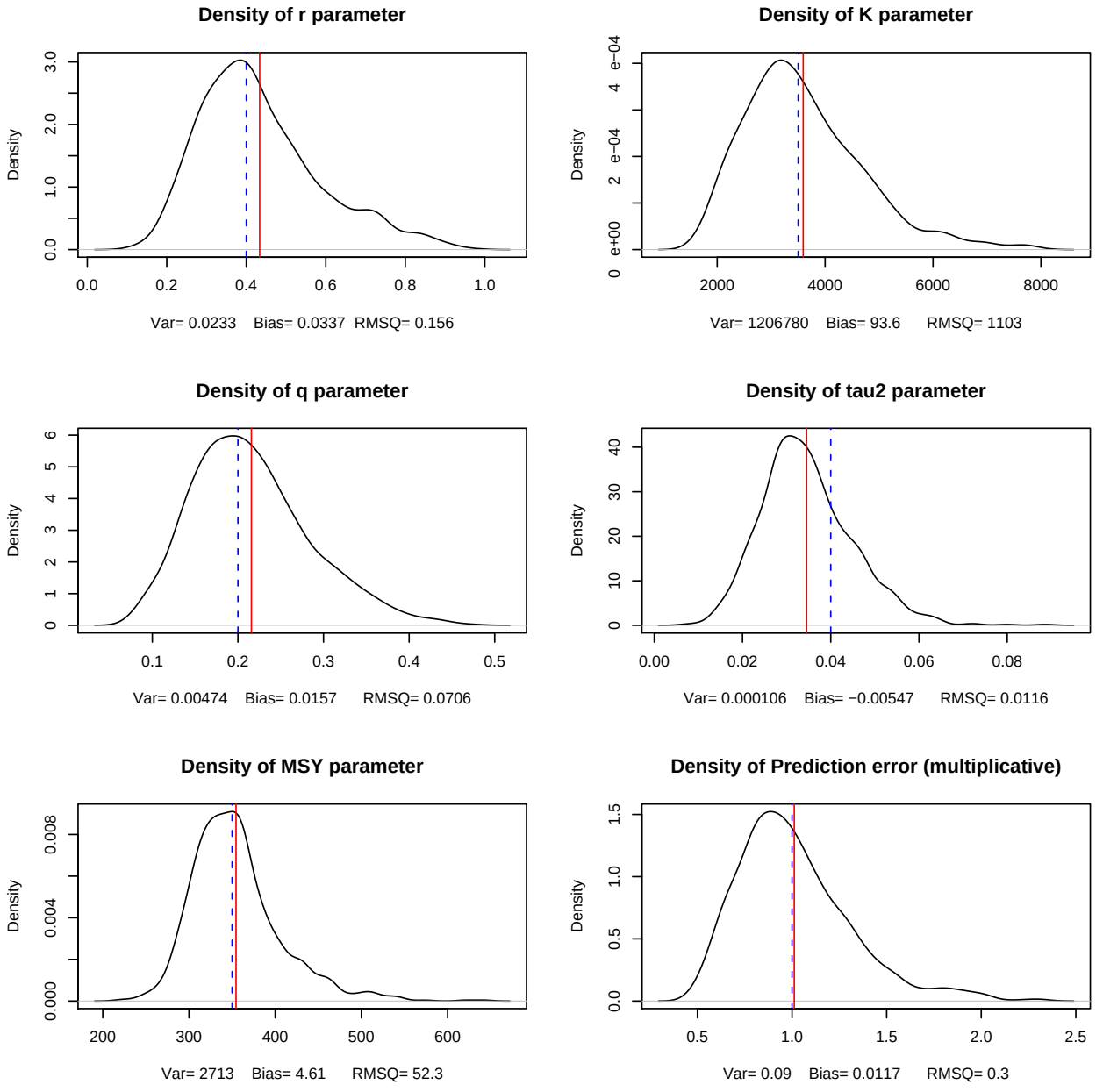


Figure 2.13: These plots represents the kernel density estimation of the parameters estimates for the treatment 14 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance is small (0.04)

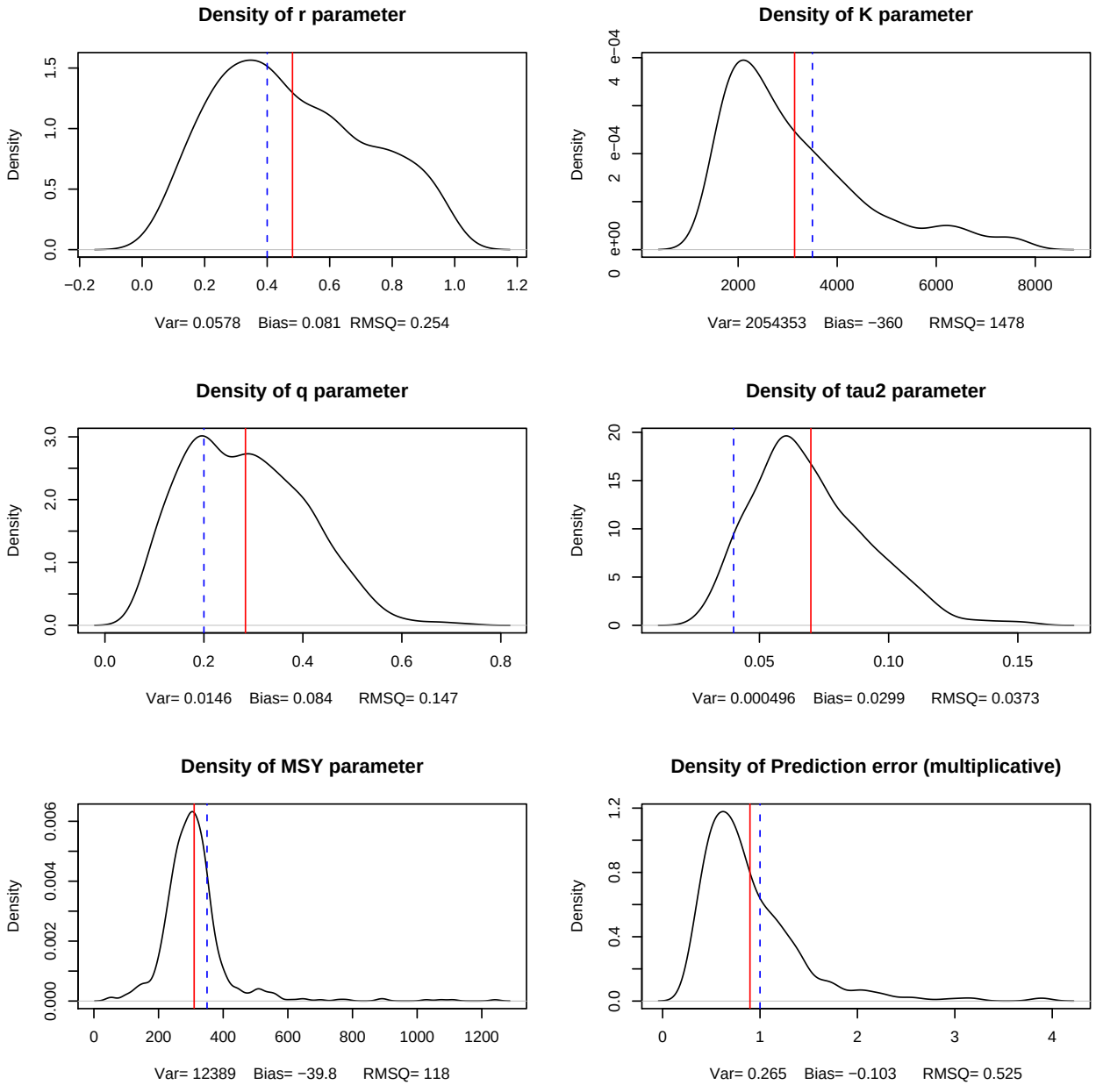


Figure 2.14: These plots represents the kernel density estimation of the parameters estimates for the treatment 15 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance had is high (0.09)

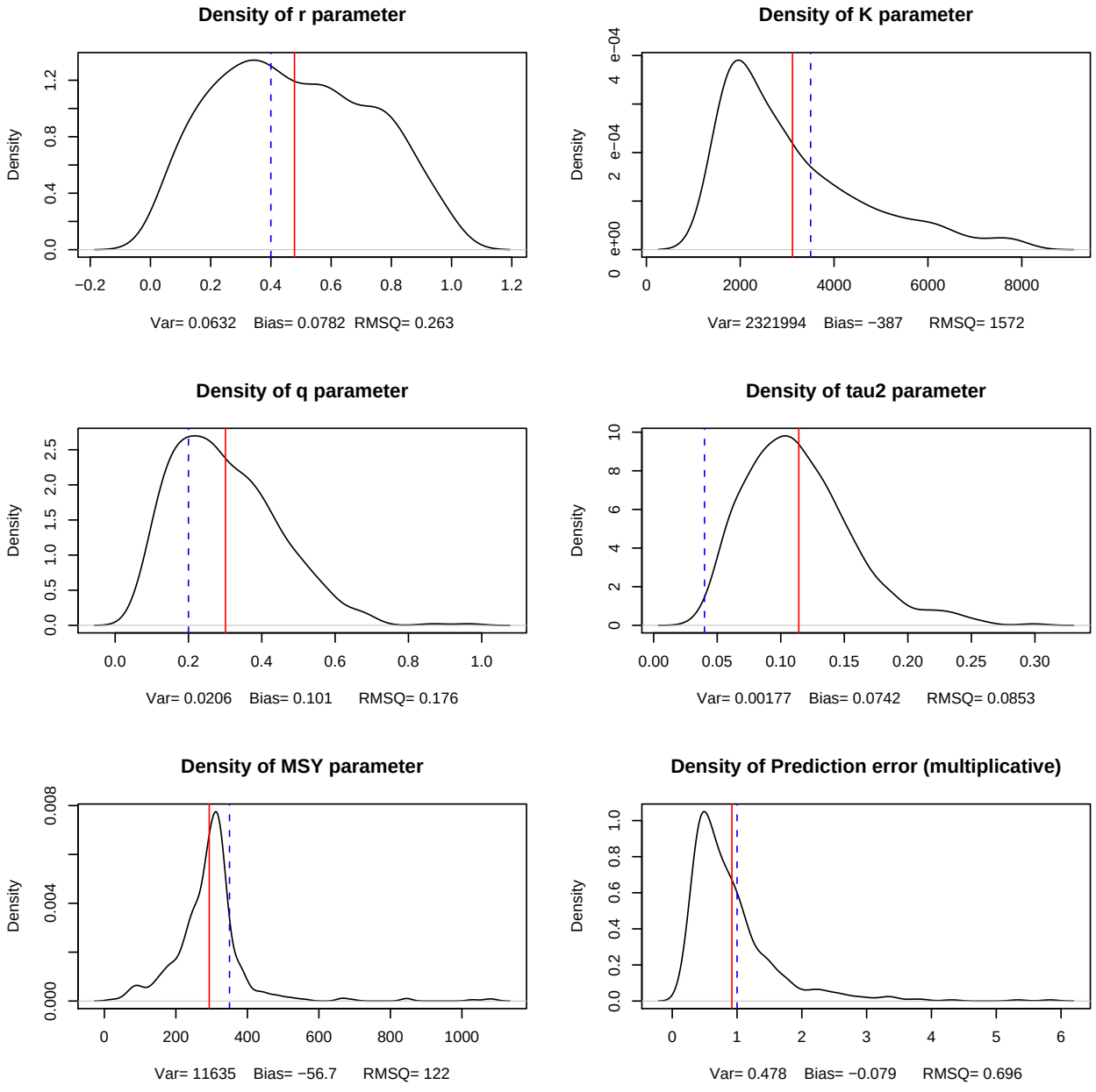


Figure 2.15: These plots represents the kernel density estimation of the parameters estimates for the treatment 16 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and there is no process error

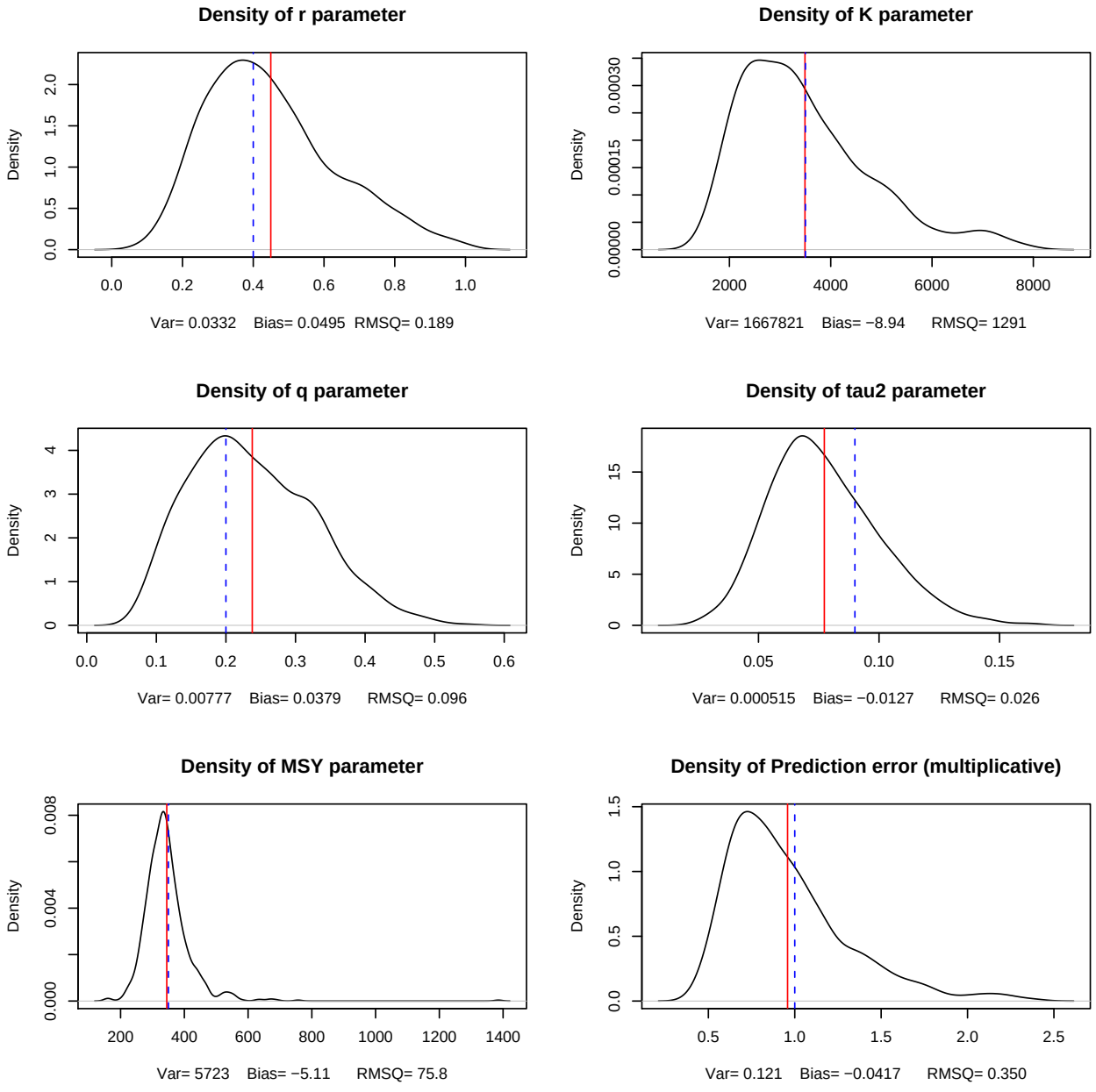


Figure 2.16: These plots represents the kernel density estimation of the parameters estimates for the treatment 17 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is small (0.04)

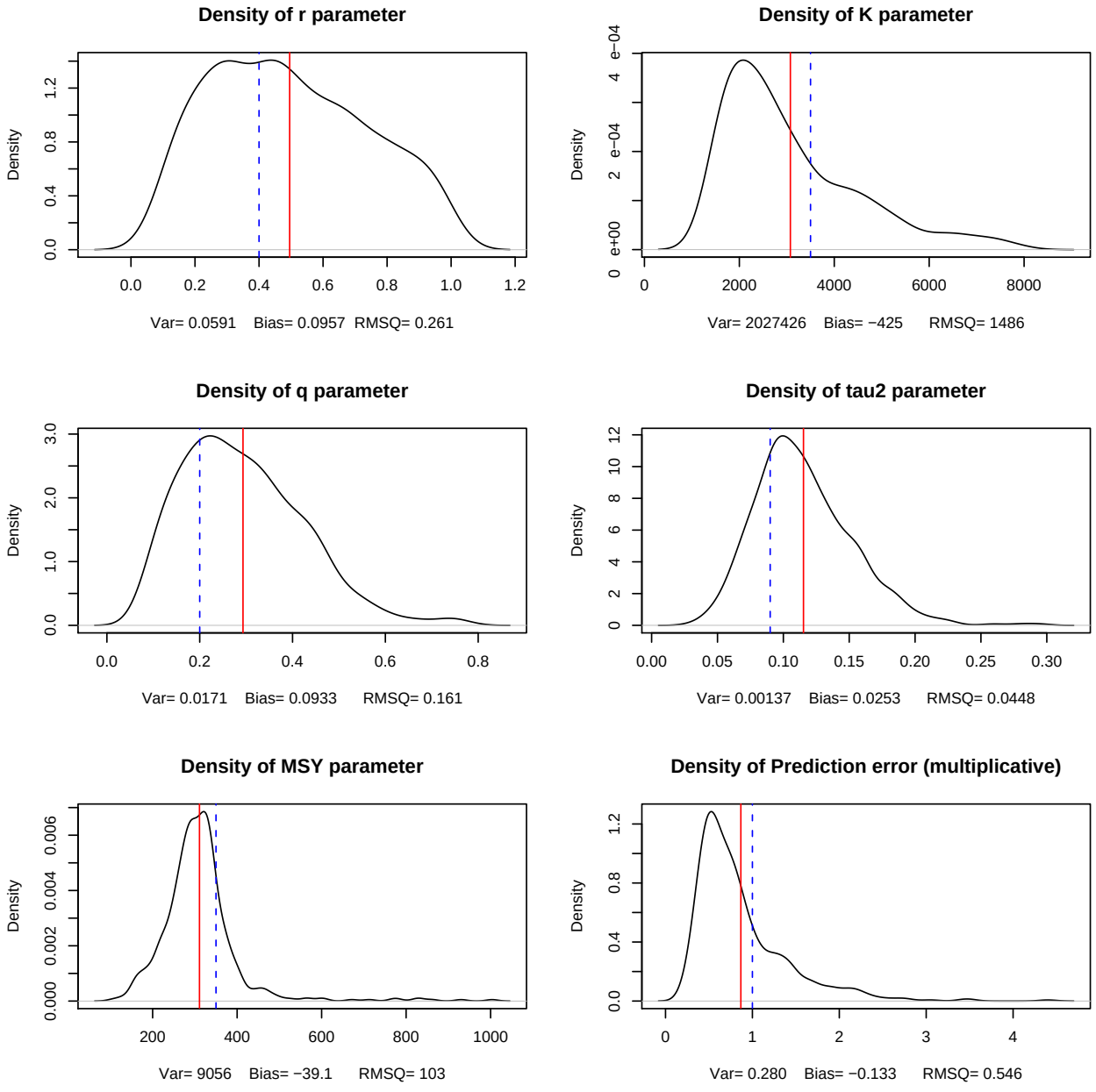


Figure 2.17: These plots represents the kernel density estimation of the parameters estimates for the treatment 18 using MLEO method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is high (0.09)

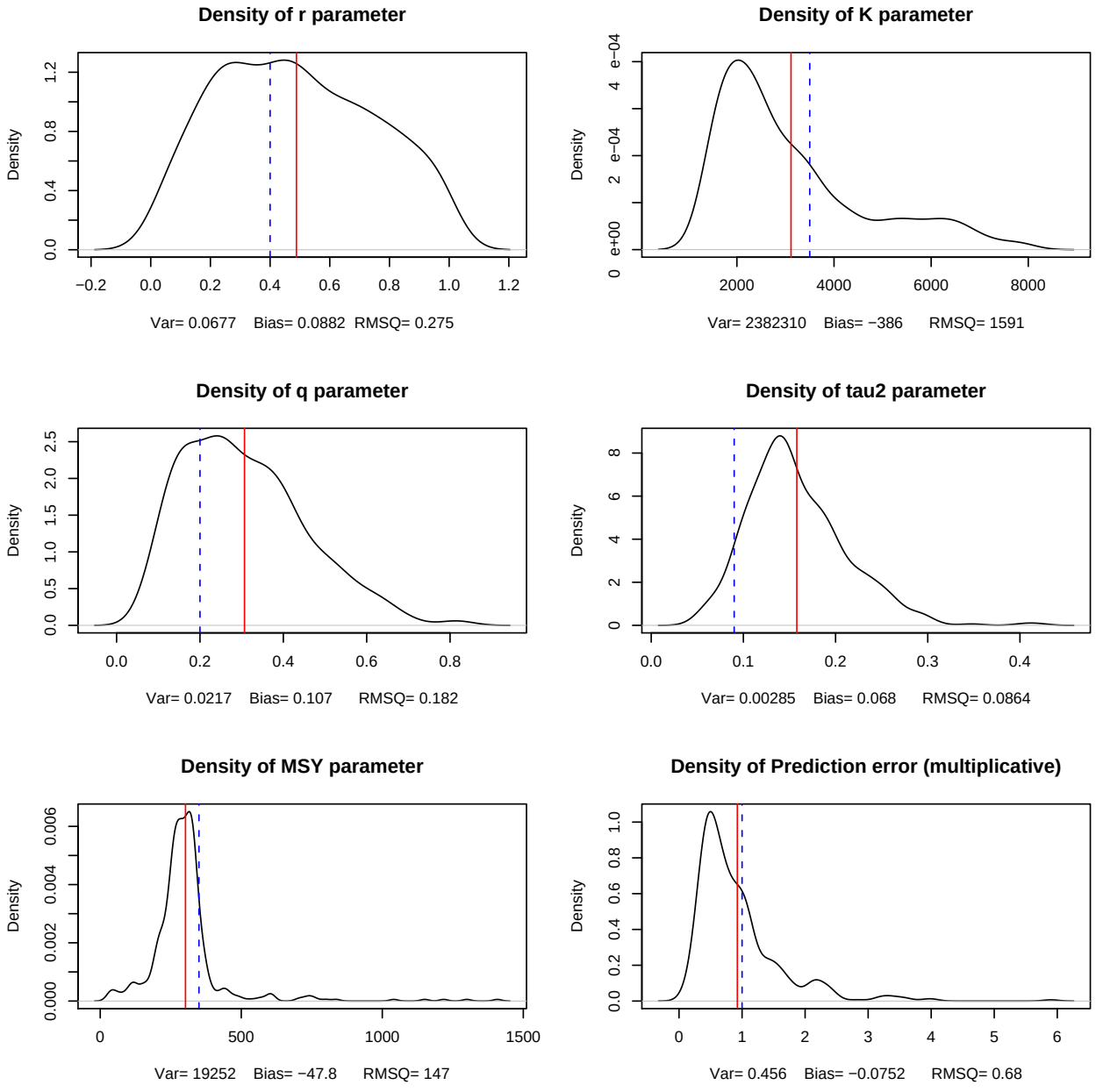


Figure 2.18: Correlation between r and K estimates using the MLEO method. The dependency is pretty impressive

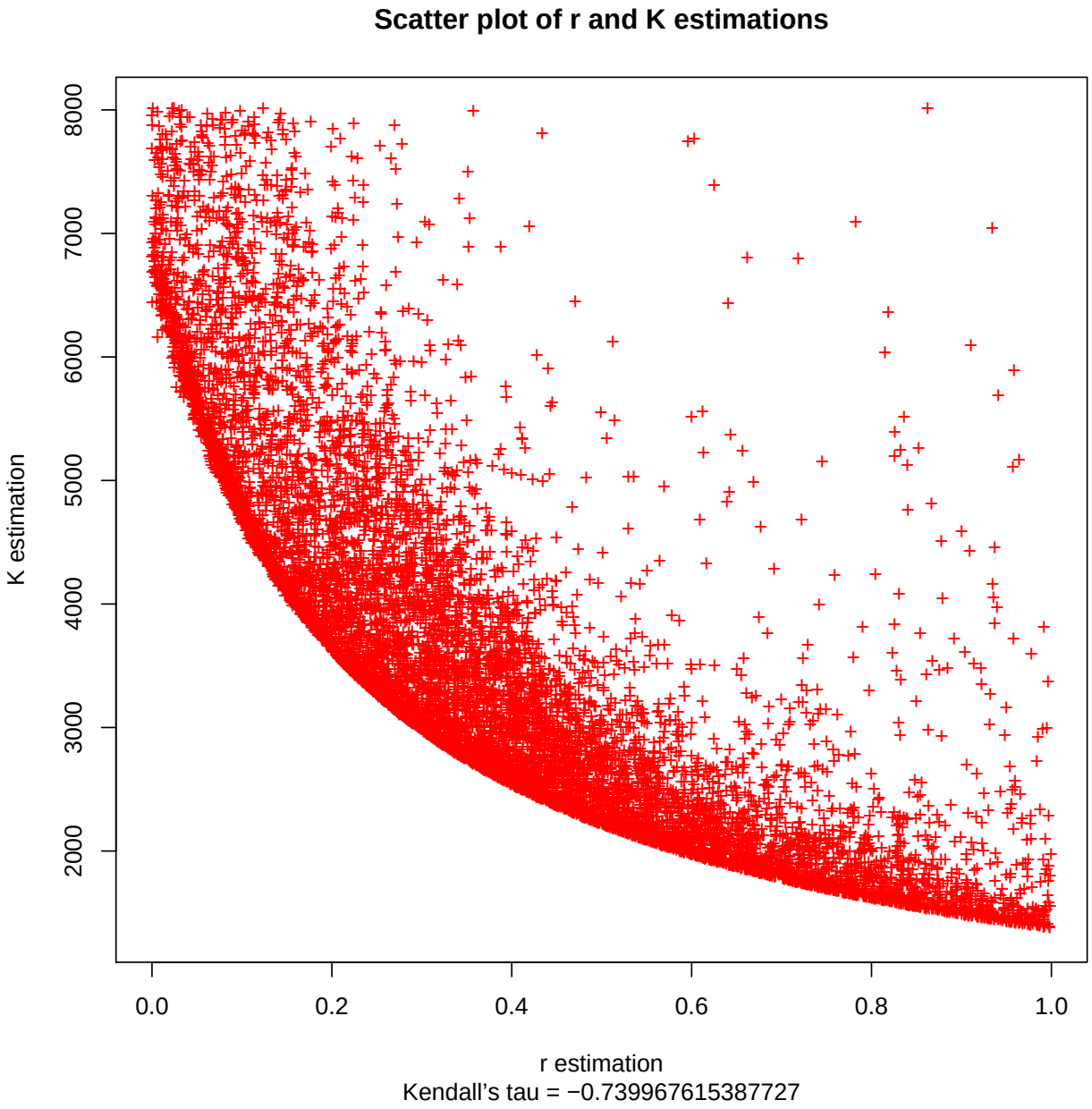


Table 2.2: Estimates means for the MLEO methods

treatment	r	K	q	sigma2	Prediction error
2	0.29	4113.53	0.27	0.04	0.96
3	0.36	3703.85	0.34	0.08	0.91
4	0.17	4134.48	0.21	0.04	1.10
5	0.31	3939.05	0.29	0.07	0.95
6	0.36	3738.76	0.33	0.11	0.90
7	0.19	4066.85	0.22	0.08	1.12
8	0.30	3986.27	0.29	0.11	0.97
9	0.35	3676.40	0.34	0.15	0.88
11	0.49	3223.64	0.28	0.04	0.92
12	0.50	3110.38	0.30	0.08	0.93
13	0.43	3593.64	0.22	0.03	1.01
14	0.48	3140.09	0.28	0.07	0.90
15	0.48	3112.70	0.30	0.11	0.92
16	0.45	3491.06	0.24	0.08	0.96
17	0.50	3075.04	0.29	0.12	0.87
18	0.49	3114.41	0.31	0.16	0.92

Table 2.3: Estimates variance for the MLEO methods

treatment	r	K	q	sigma2	Prediction error
2	0.0443	2591744.6095	0.0179	0.0003	0.3493
3	0.0583	2806530.5922	0.0357	0.0016	0.6765
4	0.0072	796285.7613	0.0033	0.0001	0.2733
5	0.0466	2715450.5854	0.0220	0.0007	0.4152
6	0.0667	2920186.2495	0.0300	0.0018	0.5760
7	0.0147	1306945.4846	0.0068	0.0006	0.5309
8	0.0496	2692869.9543	0.0244	0.0013	0.4520
9	0.0572	2671454.3744	0.0351	0.0025	0.6130
11	0.0589	2439794.1369	0.0149	0.0003	0.2933
12	0.0724	2647964.7690	0.0220	0.0013	0.4952
13	0.0233	1206780.4138	0.0047	0.0001	0.0900
14	0.0578	2054352.5647	0.0146	0.0005	0.2649
15	0.0632	2321994.2625	0.0206	0.0018	0.4778
16	0.0332	1667821.3749	0.0078	0.0005	0.1211
17	0.0591	2027425.7936	0.0171	0.0014	0.2803
18	0.0677	2382310.3002	0.0217	0.0029	0.4559

Table 2.4: Estimates bias for the MLEO methods

treatment	r	K	q	sigma2	Prediction error
2	0.129	113.531	0.073	0.036	0.956
3	0.203	-296.145	0.144	0.079	0.906
4	0.006	134.481	0.005	-0.005	0.082
5	0.153	-60.948	0.090	0.030	0.950
6	0.205	-261.242	0.128	0.069	0.902
7	0.029	66.848	0.019	-0.011	0.072
8	0.144	-13.731	0.093	0.024	0.969
9	0.185	-323.603	0.145	0.059	0.876
11	0.086	-276.364	0.077	0.036	0.920
12	0.103	-389.615	0.102	0.078	0.928
13	0.034	93.641	0.016	-0.005	-0.008
14	0.081	-359.913	0.084	0.030	0.897
15	0.078	-387.303	0.101	0.074	0.921
16	0.050	-8.938	0.038	-0.013	-0.088
17	0.096	-424.962	0.093	0.025	0.867
18	0.088	-385.591	0.107	0.068	0.925

Table 2.5: Estimates root mean square error for the MLEO methods

treatment	r	K	q	sigma2	Prediction error
2	0.25	1613.89	0.15	0.04	1.12
3	0.32	1701.24	0.24	0.09	1.22
4	0.09	902.43	0.06	0.01	0.53
5	0.26	1648.99	0.17	0.04	1.15
6	0.33	1728.71	0.22	0.08	1.18
7	0.12	1145.17	0.08	0.03	0.73
8	0.27	1641.05	0.18	0.04	1.18
9	0.30	1666.19	0.24	0.08	1.18
10	0.40	3500.00	0.20	0.00	1.00
11	0.26	1586.24	0.14	0.04	1.07
12	0.29	1673.25	0.18	0.09	1.16
13	0.16	1102.52	0.07	0.01	0.30
14	0.25	1477.80	0.15	0.04	1.03
15	0.26	1572.26	0.18	0.09	1.15
16	0.19	1291.47	0.10	0.03	0.36
17	0.26	1485.94	0.16	0.04	1.02
18	0.27	1590.91	0.18	0.09	1.15

Results for the MLEP method

Because this method is accounting only for process error, datasets simulated without observation error are expected to be more efficient. For this reason, we expected more datasets to be valid in the treatments $1, 2, 3, 10, 11 and 12$ (see figure (2.19)).

Figure 2.19: This plots presents the proportion of valid estimations out of 1000 replicates when using the MLEP method. The validity of an estimation is detailed in the beginning of this section.

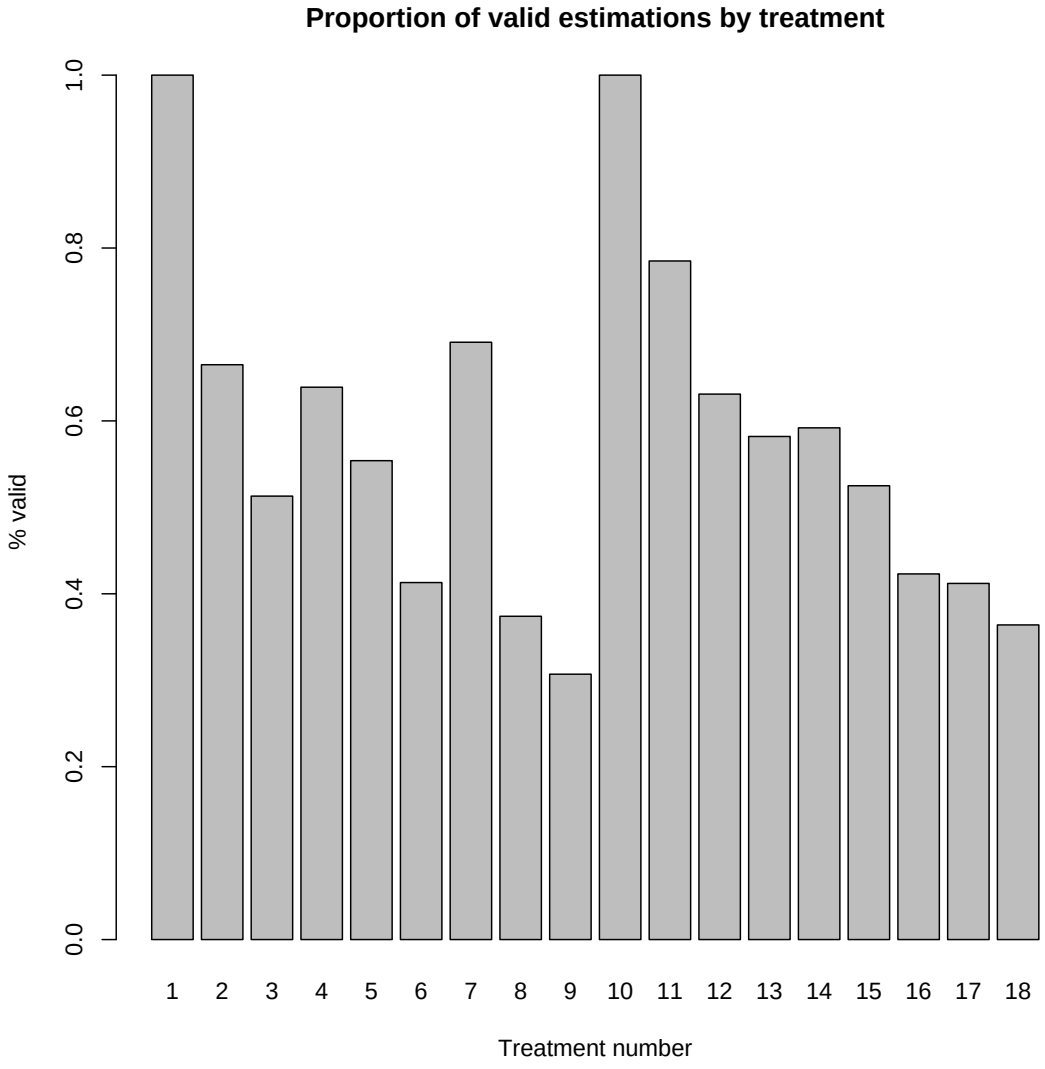


Figure 2.20: These plots represents the kernel density estimation of the parameters estimates for the treatment 2 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is small (0.04)

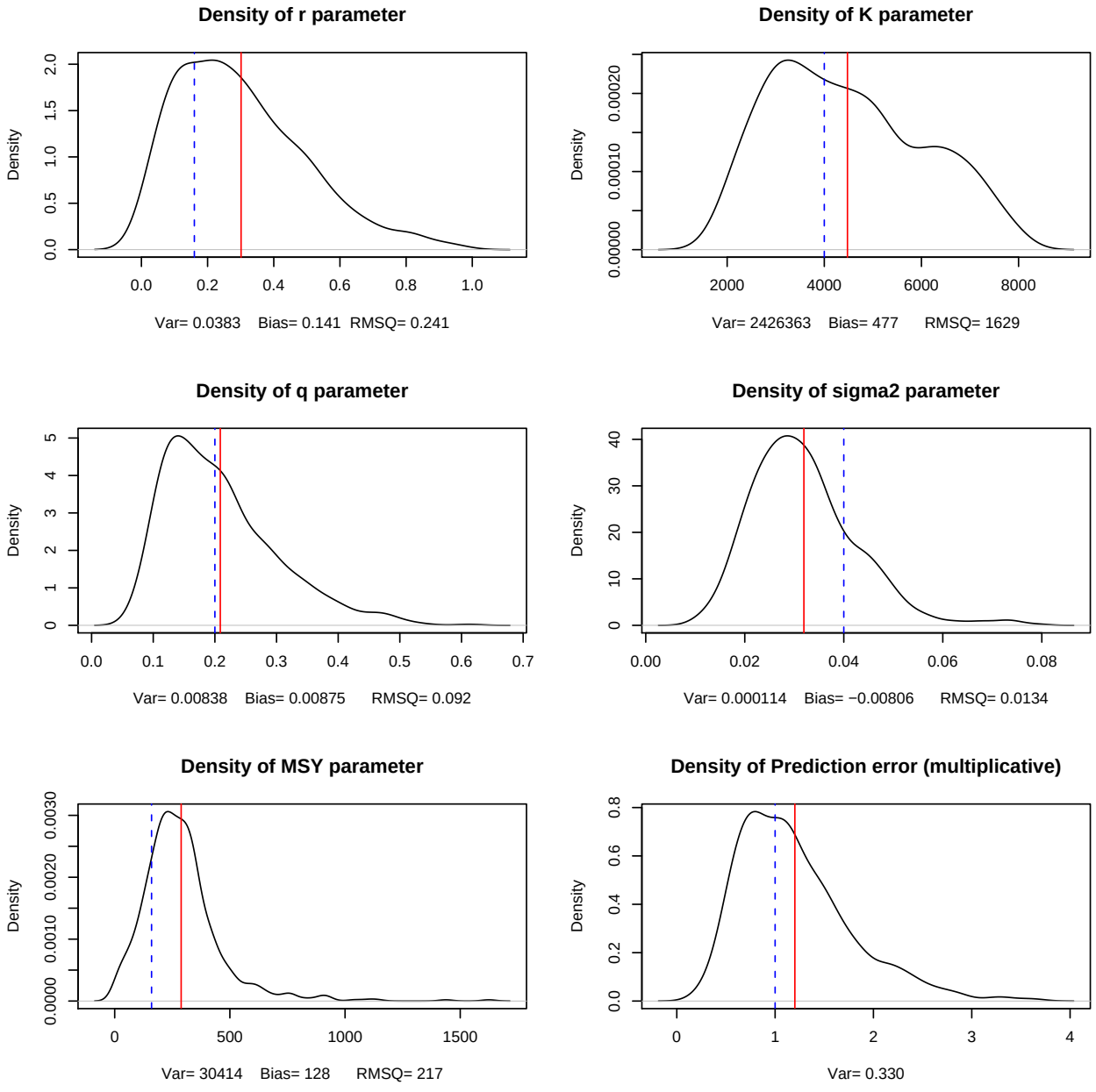


Figure 2.21: These plots represents the kernel density estimation of the parameters estimates for the treatment 3 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is high(0.09)

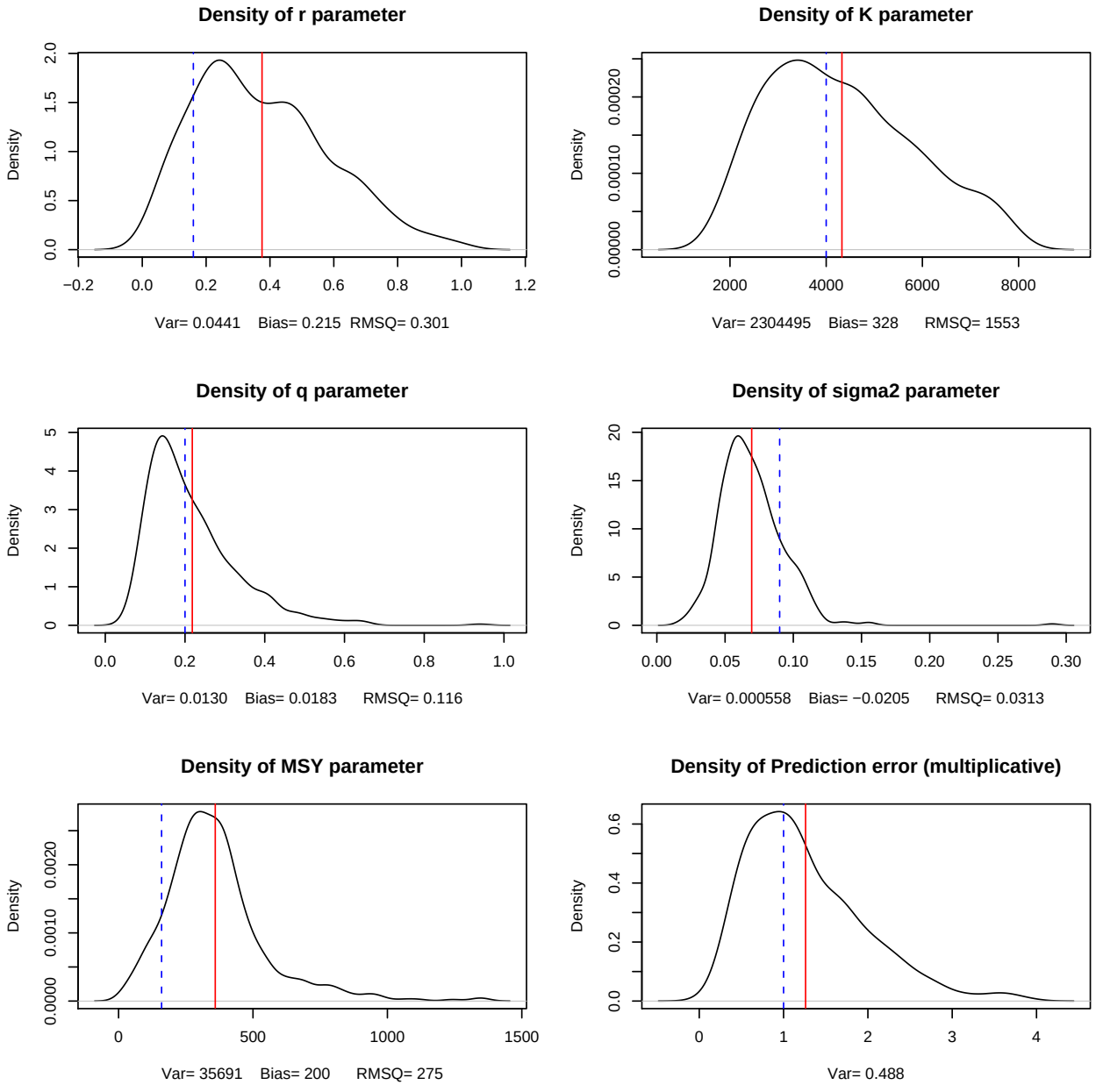


Figure 2.22: These plots represents the kernel density estimation of the parameters estimates for the treatment 4 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no process error and observation error variance is small (0.04)

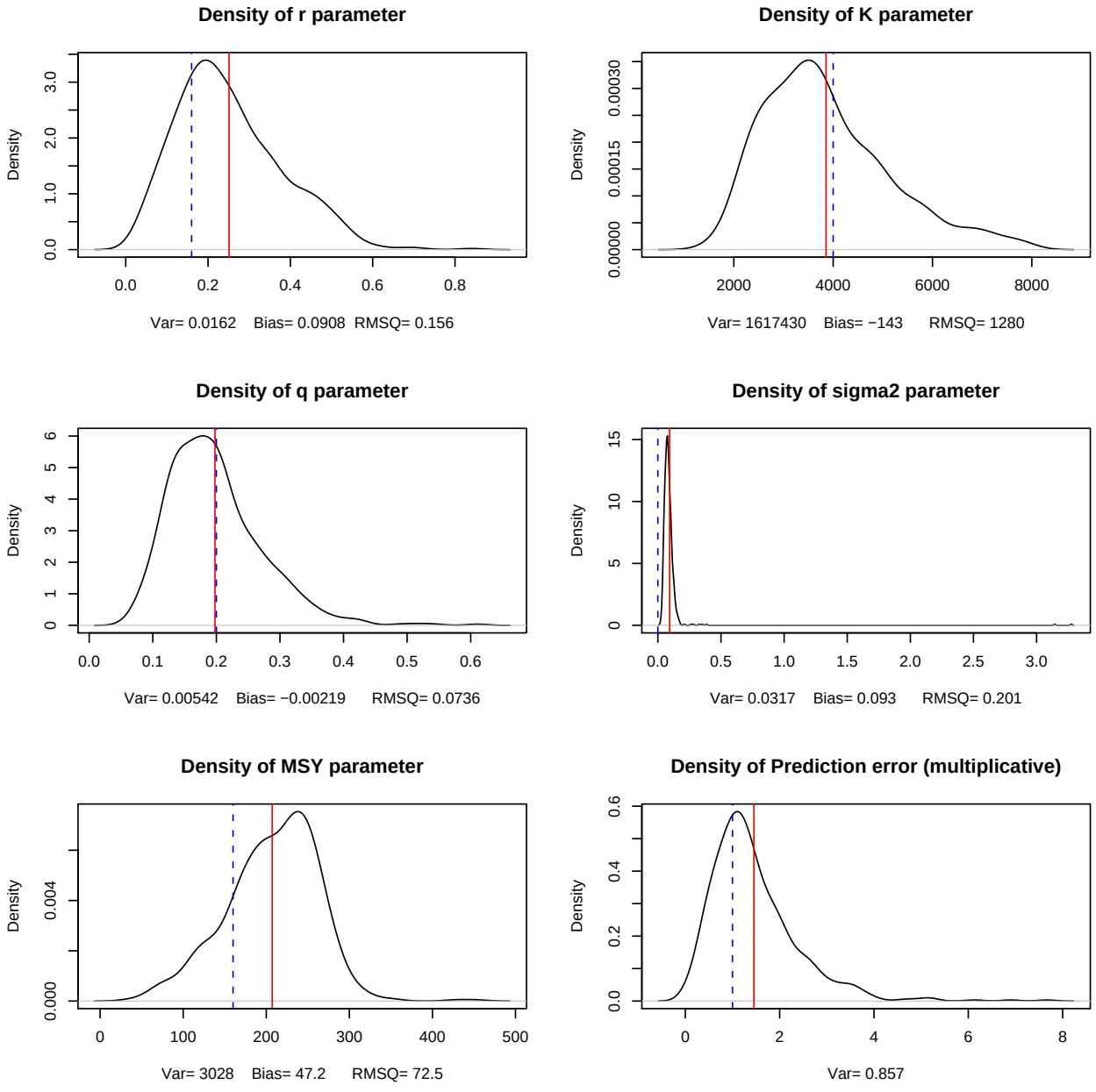


Figure 2.23: These plots represents the kernel density estimation of the parameters estimates for the treatment 5 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance is small (0.04)

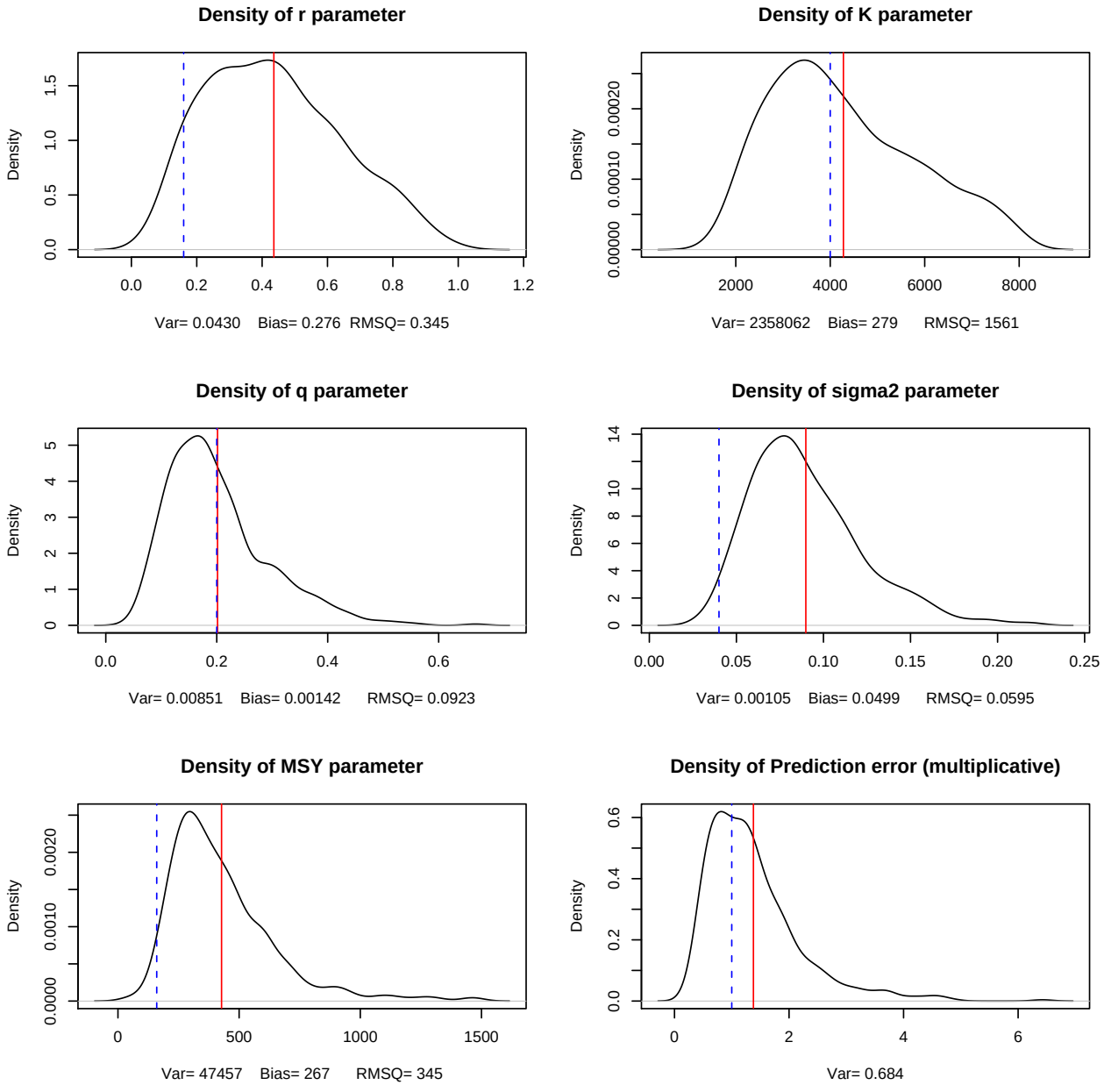


Figure 2.24: These plots represents the kernel density estimation of the parameters estimates for the treatment 6 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance had is high (0.09)

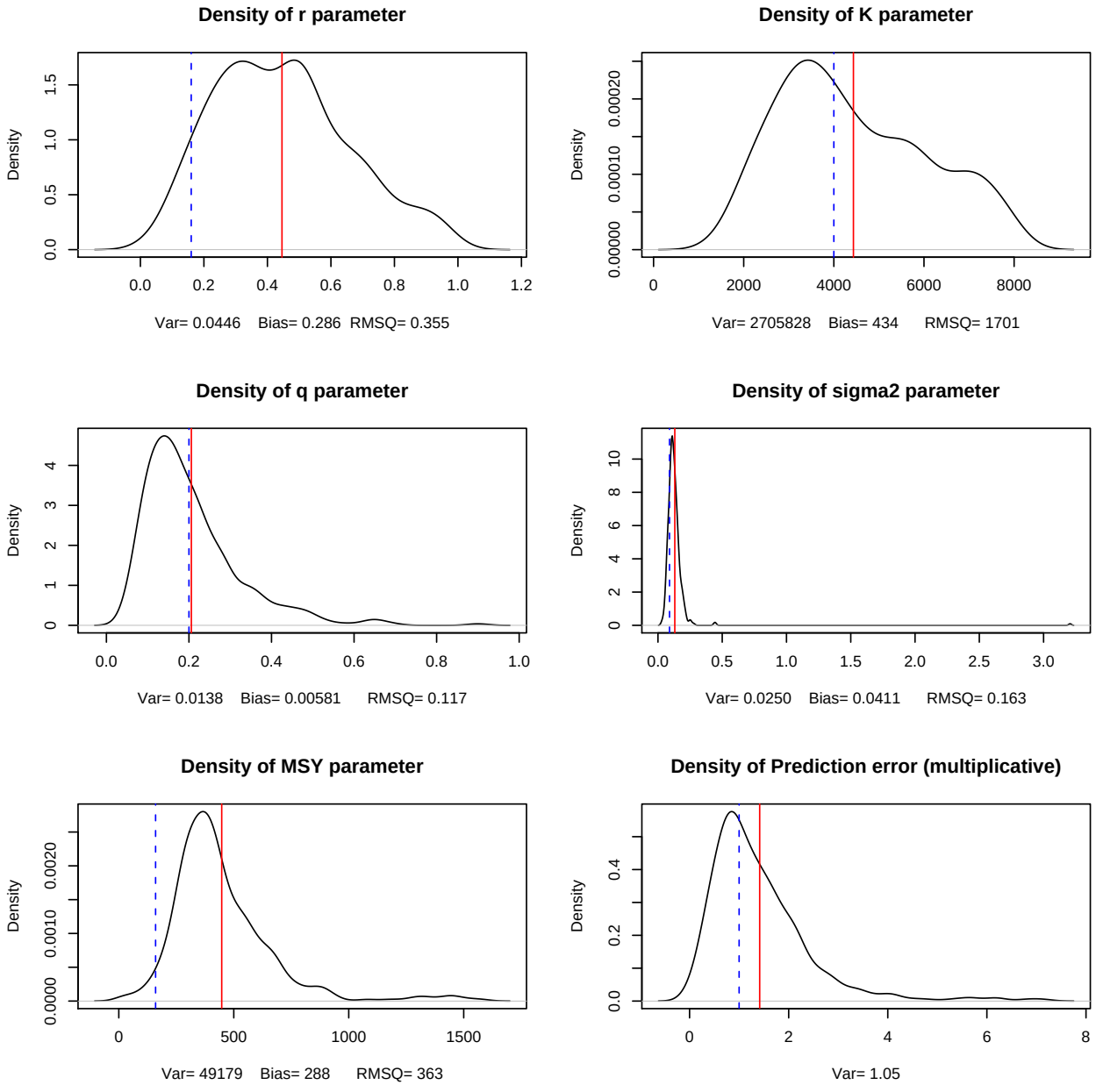


Figure 2.25: These plots represents the kernel density estimation of the parameters estimates for the treatment 7 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and there is no process error

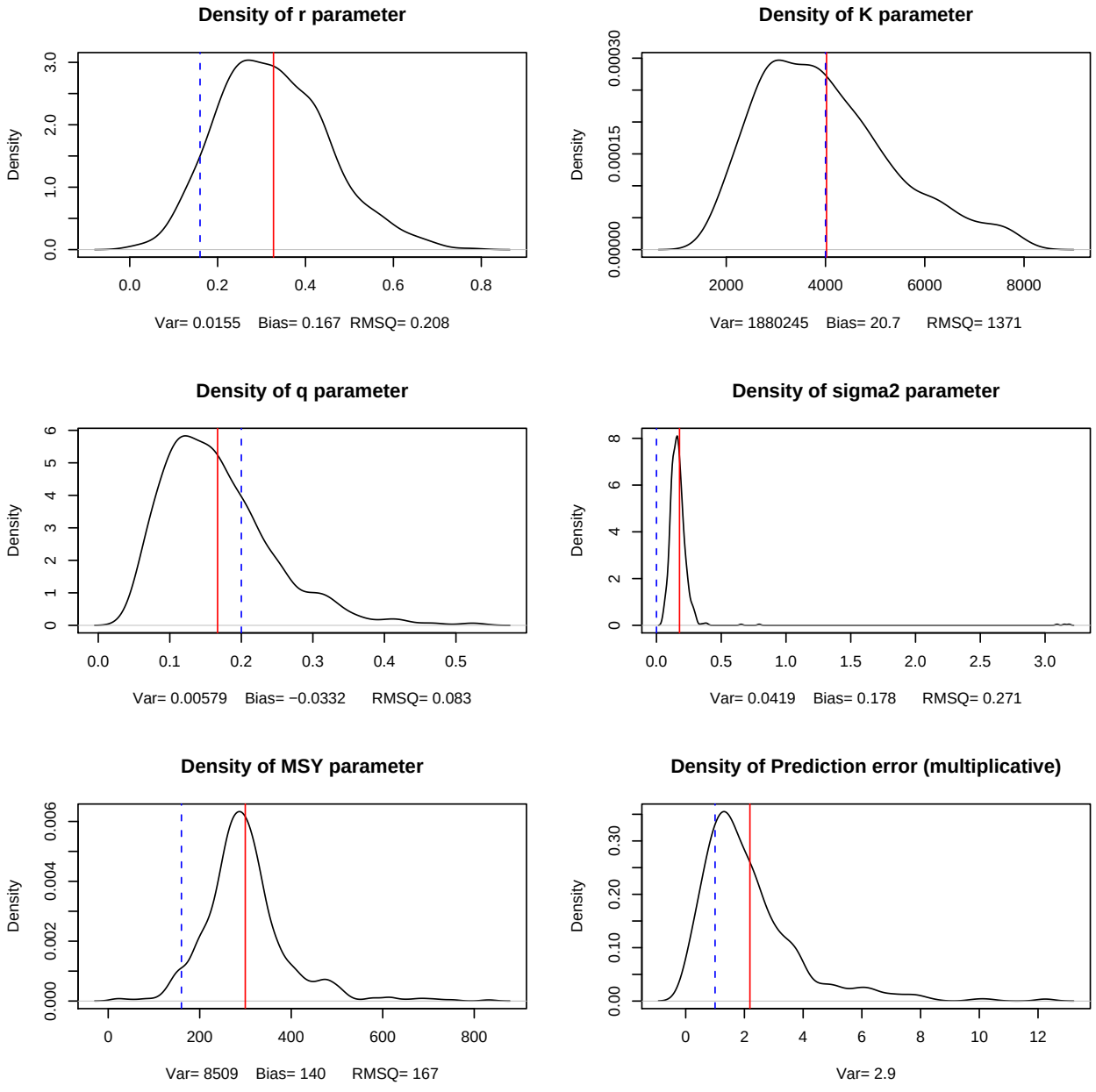


Figure 2.26: These plots represents the kernel density estimation of the parameters estimates for the treatment 8 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is small (0.04)

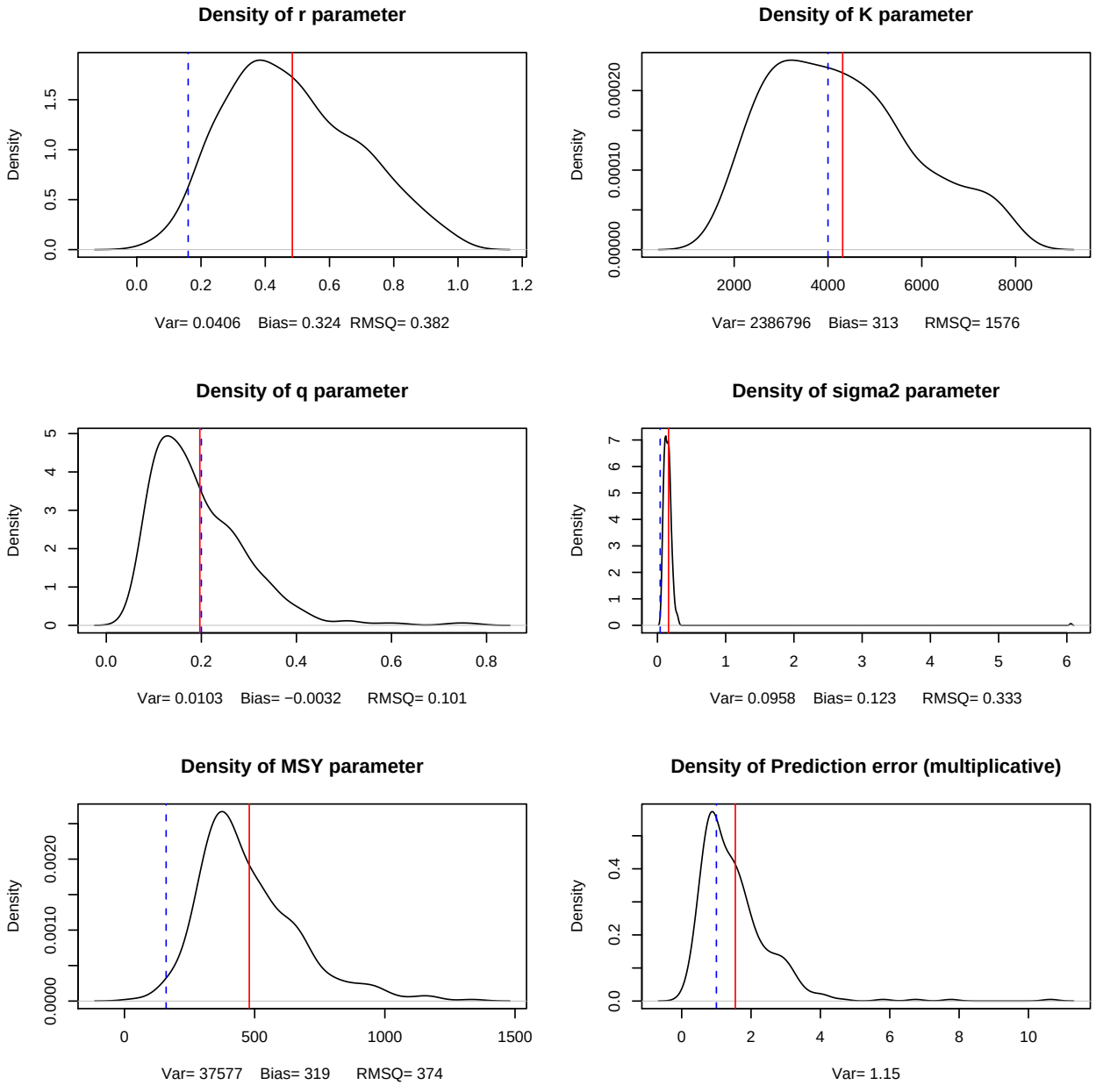


Figure 2.27: These plots represents the kernel density estimation of the parameters estimates for the treatment 9 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is high (0.09)

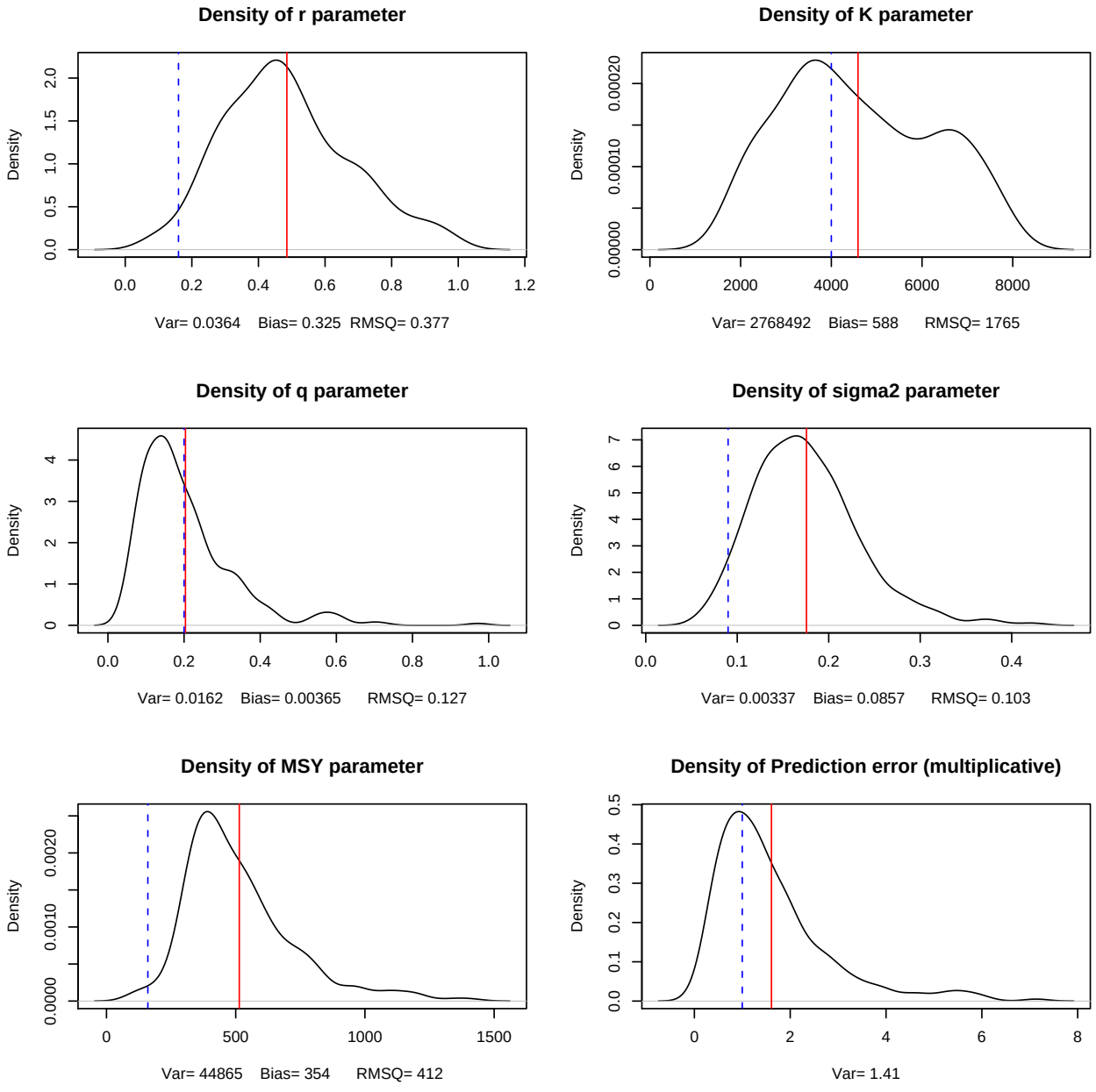


Figure 2.28: These plots represents the kernel density estimation of the parameters estimates for the treatment 11 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is small (0.04)

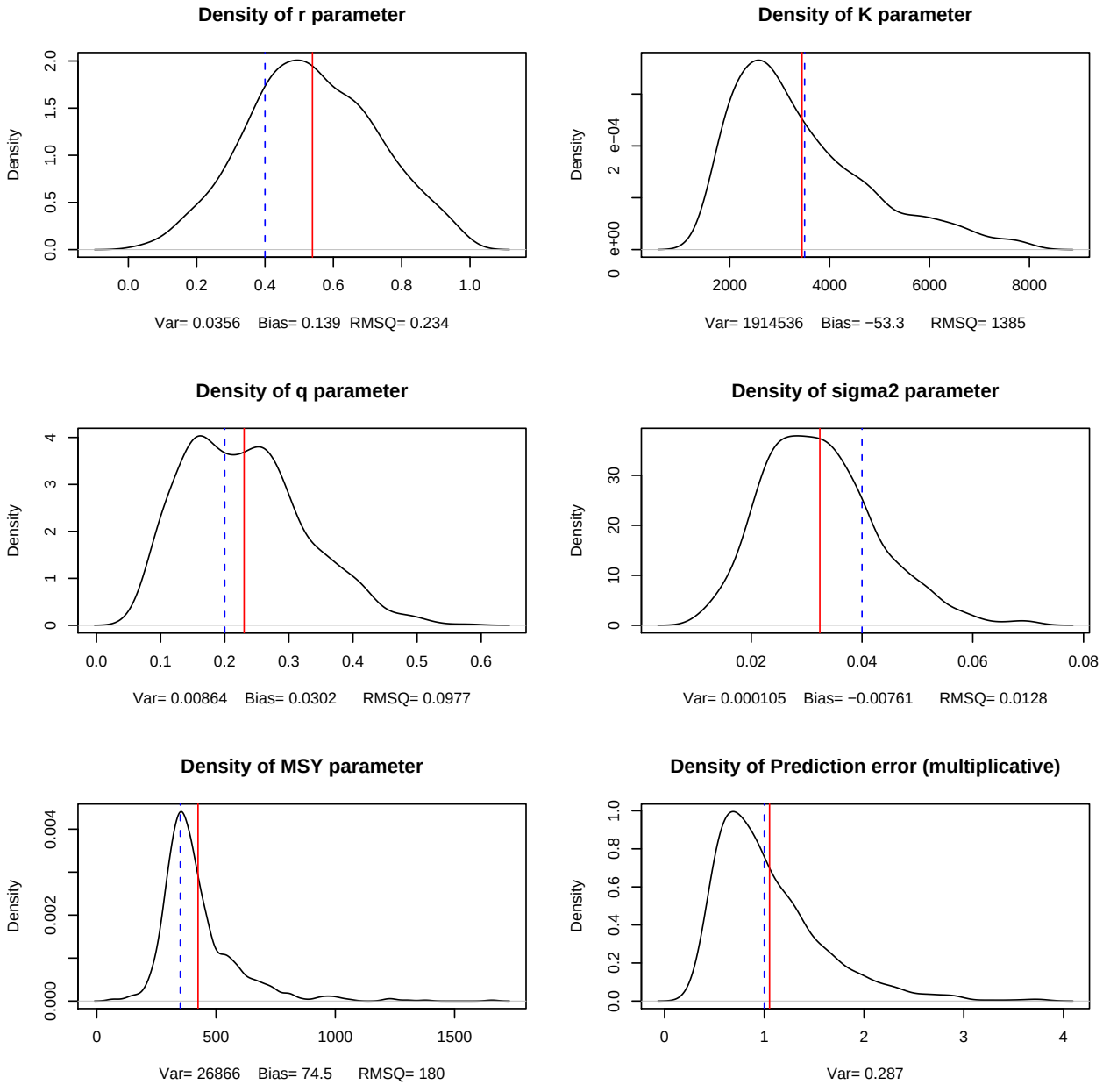


Figure 2.29: These plots represents the kernel density estimation of the parameters estimates for the treatment 12 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no observation error and process error variance is high(0.09)

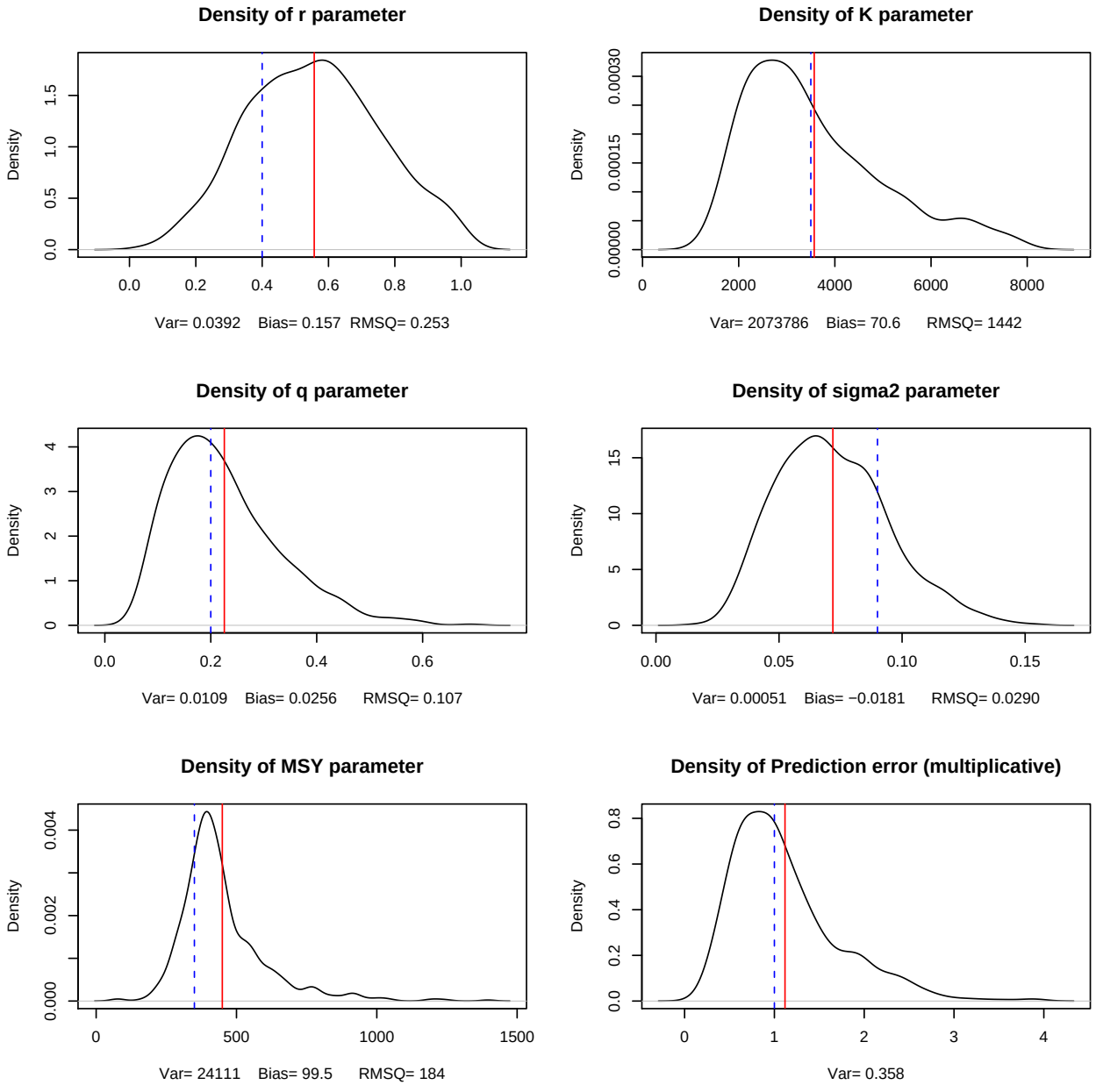


Figure 2.30: These plots represents the kernel density estimation of the parameters estimates for the treatment 13 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case there is no process error and observation error variance is small (0.04)

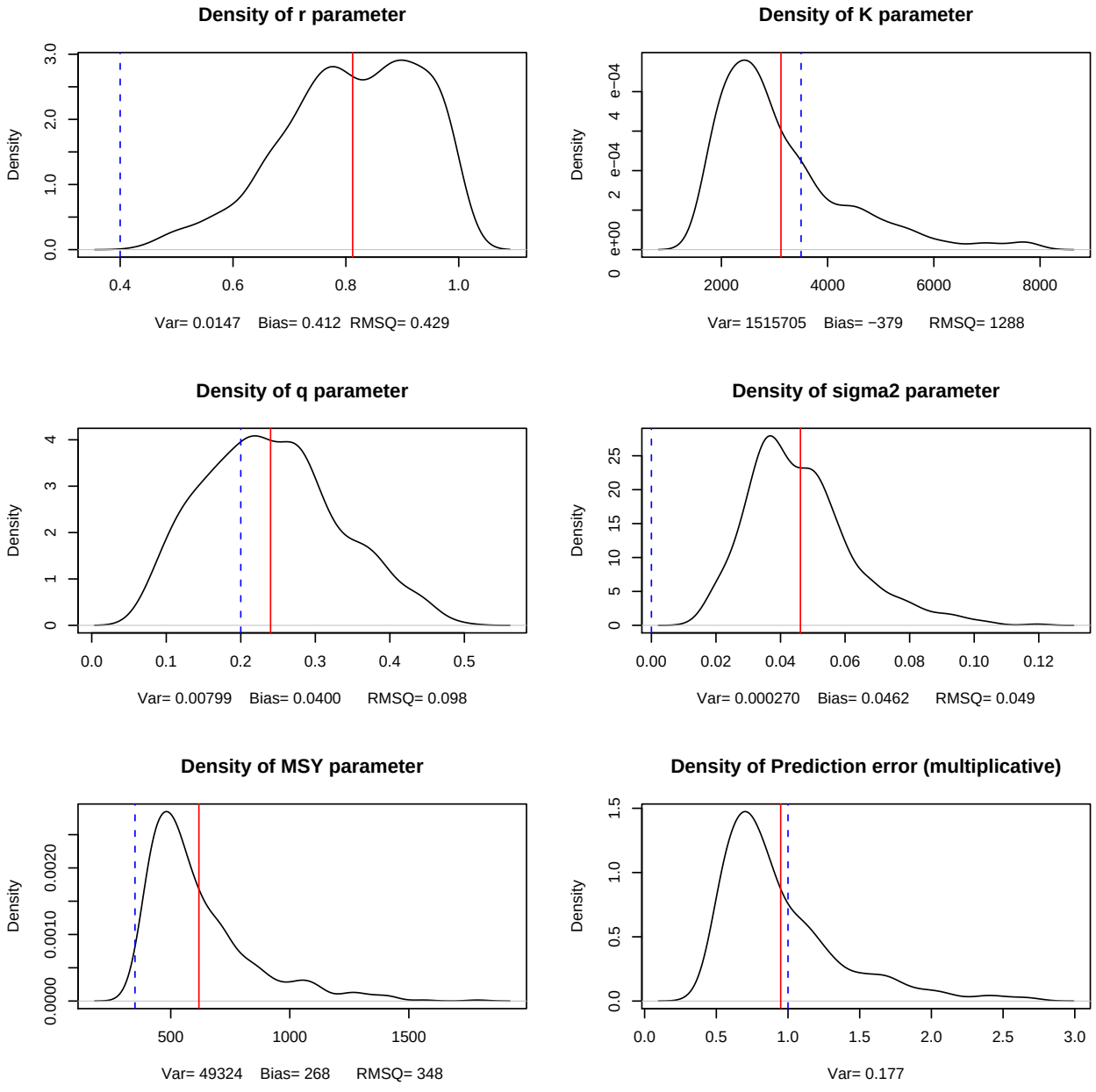


Figure 2.31: These plots represents the kernel density estimation of the parameters estimates for the treatment 14 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance is small (0.04)

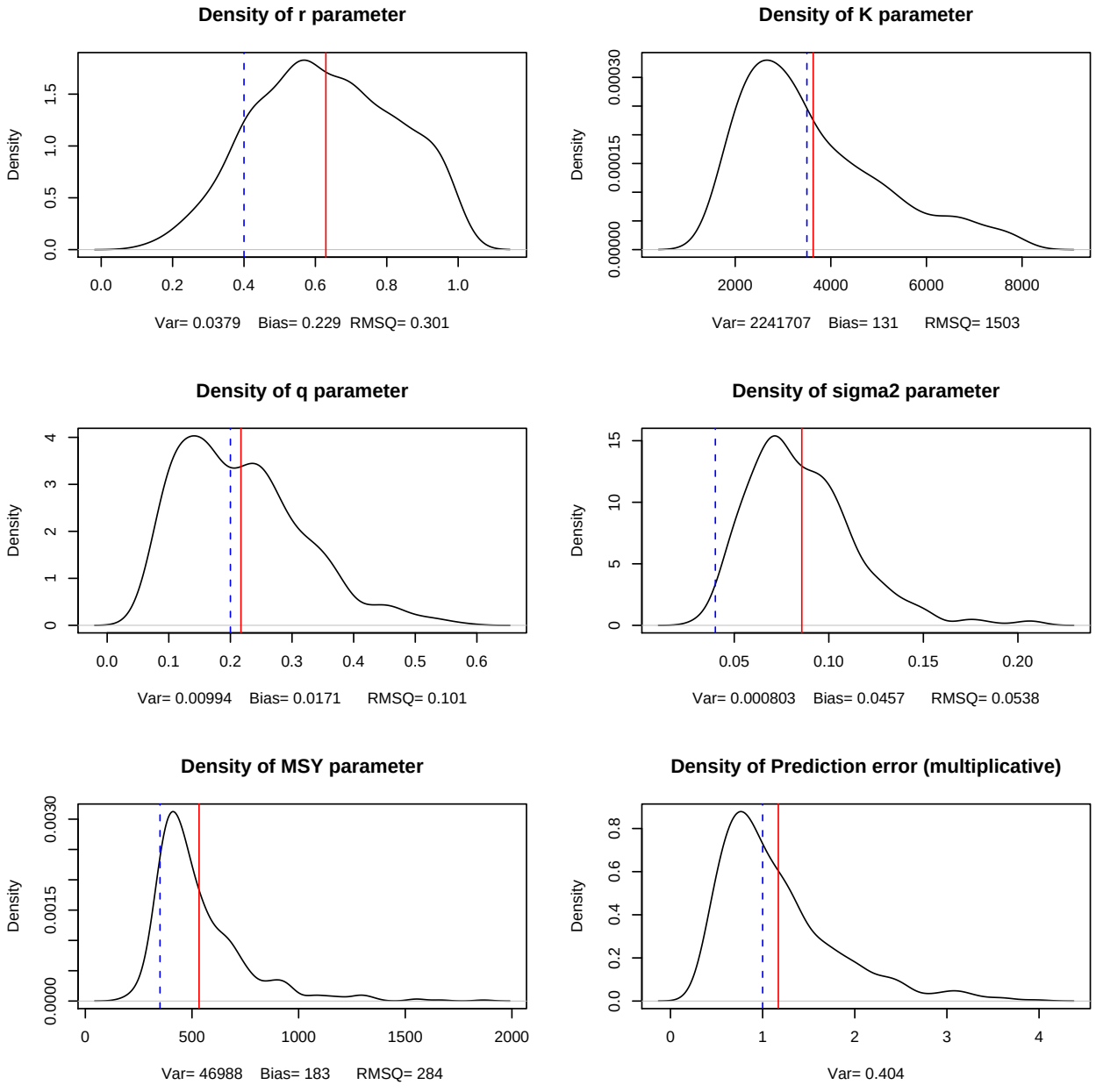


Figure 2.32: These plots represents the kernel density estimation of the parameters estimates for the treatment 15 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is small (0.04) and process error variance had is high (0.09)

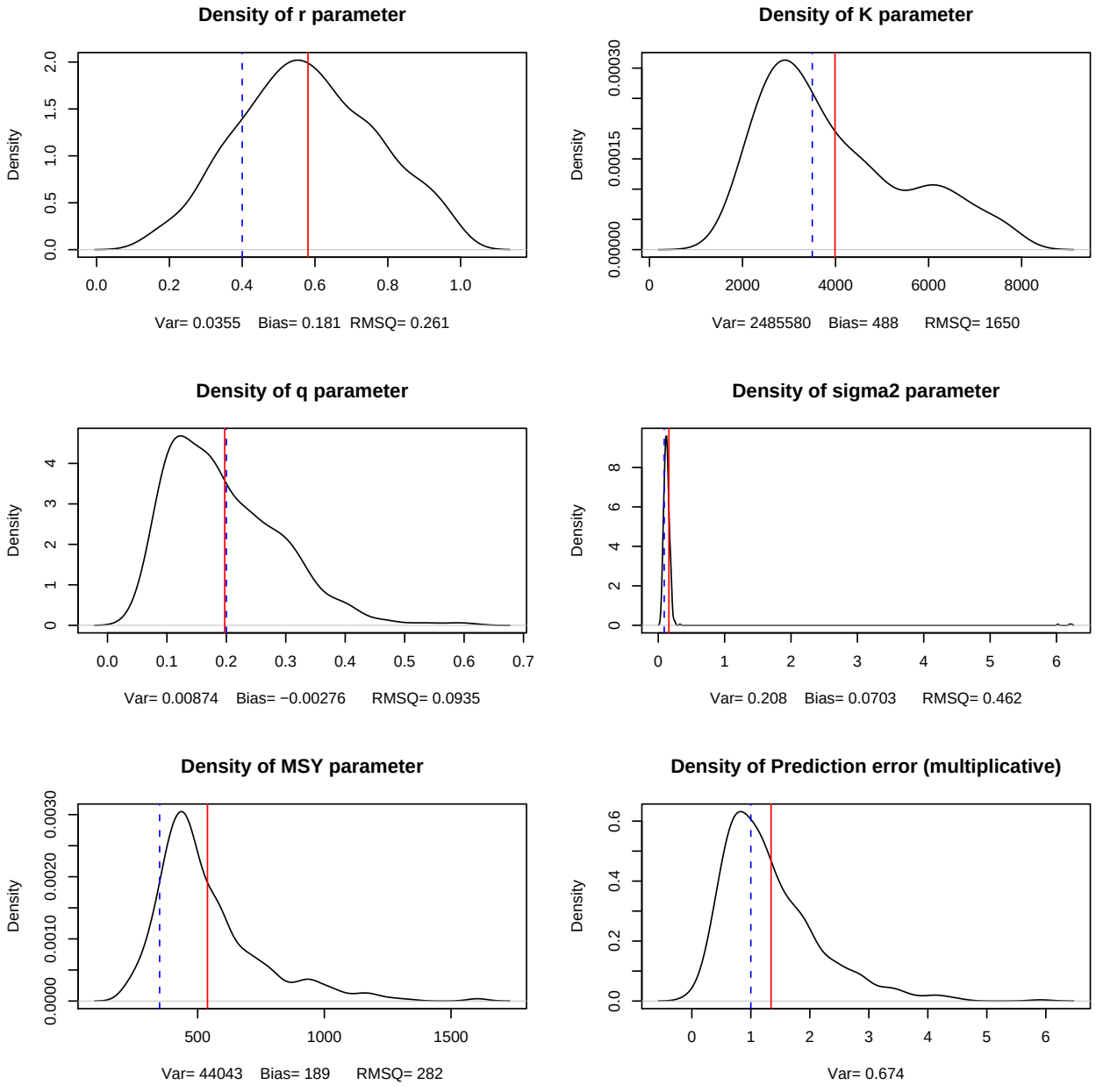


Figure 2.33: These plots represents the kernel density estimation of the parameters estimates for the treatment 16 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and there is no process error

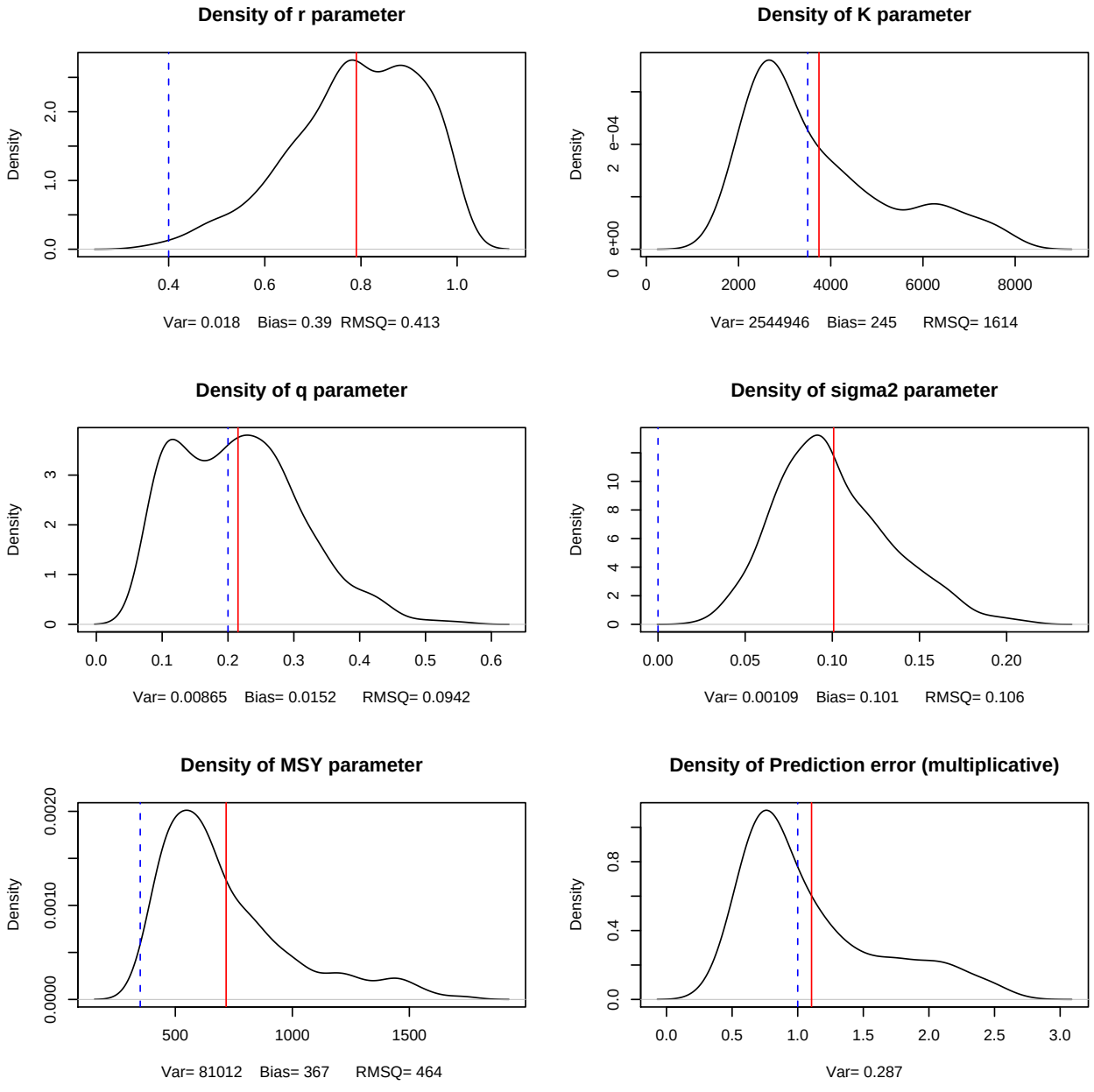


Figure 2.34: These plots represents the kernel density estimation of the parameters estimates for the treatment 17 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is small (0.04)

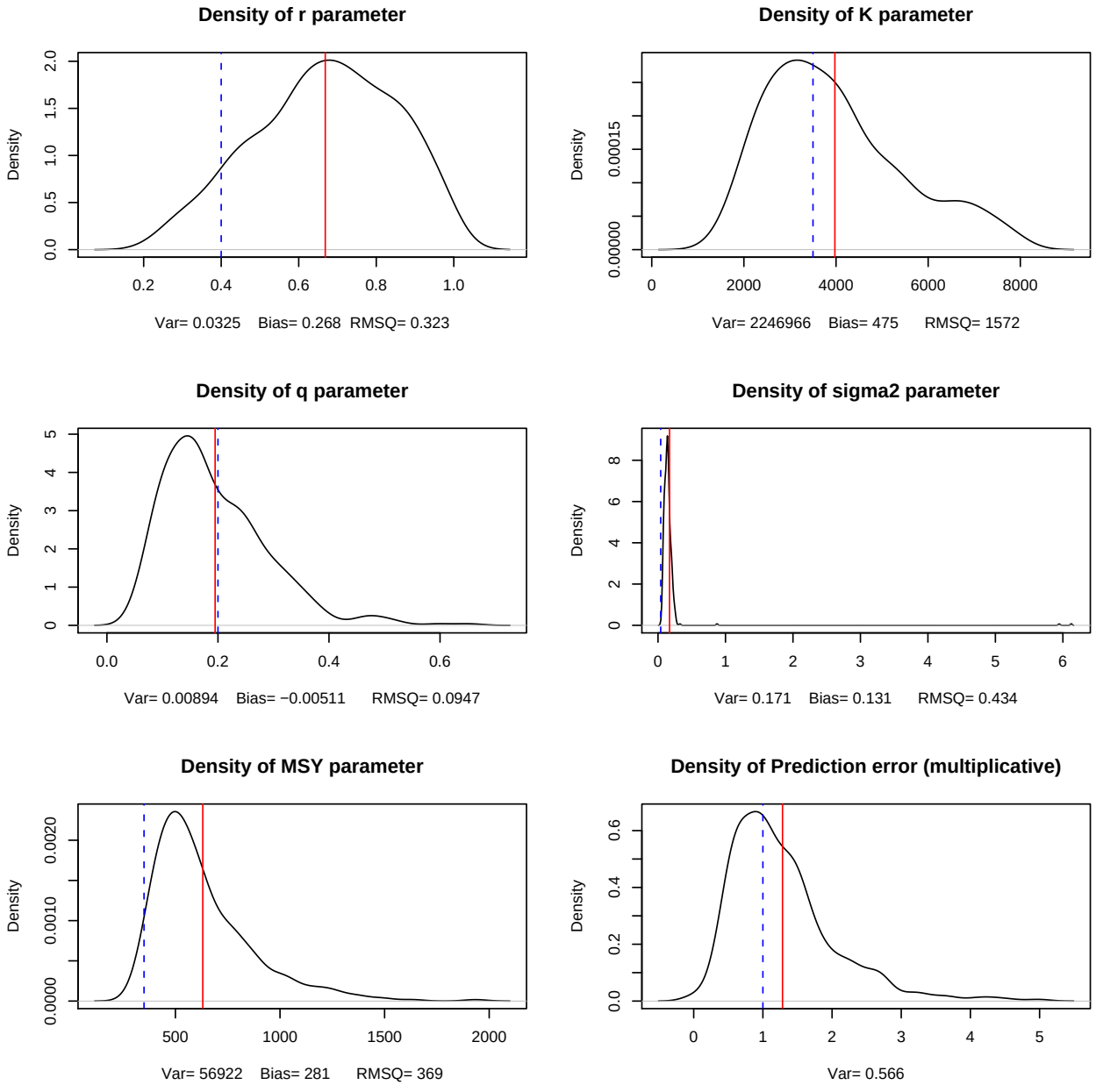


Figure 2.35: These plots represents the kernel density estimation of the parameters estimates for the treatment 18 using MLEP method. The solid vertical line is the mean value of the estimator while the dotted vertical line is the true parameter value. In this case observation error variance is high (0.09) and process error variance is high (0.09)

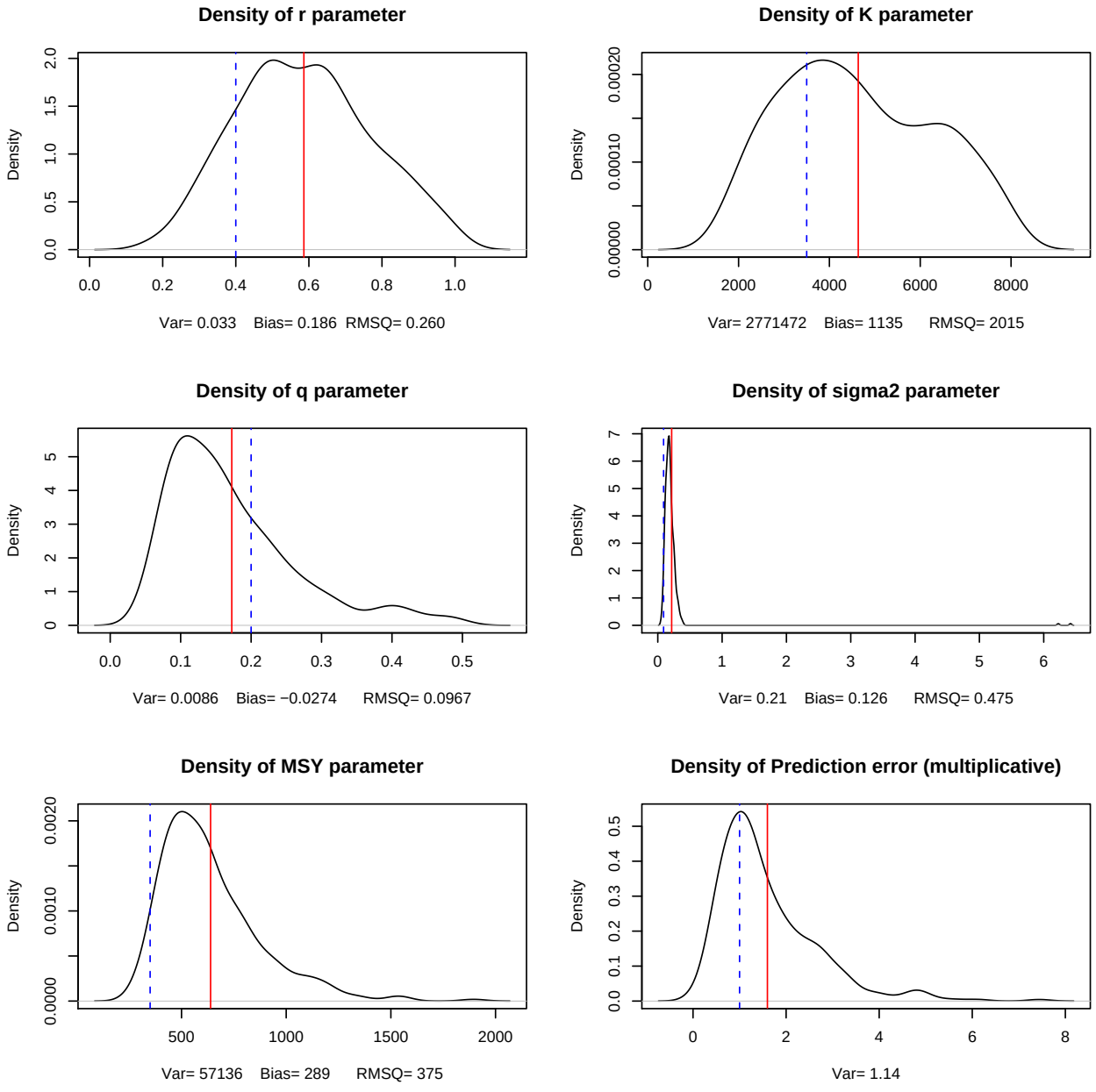


Figure 2.36: Correlation between r and K estimates using the MLEP method. We see that there is less dependency between these parameters comparing with the MLEO method

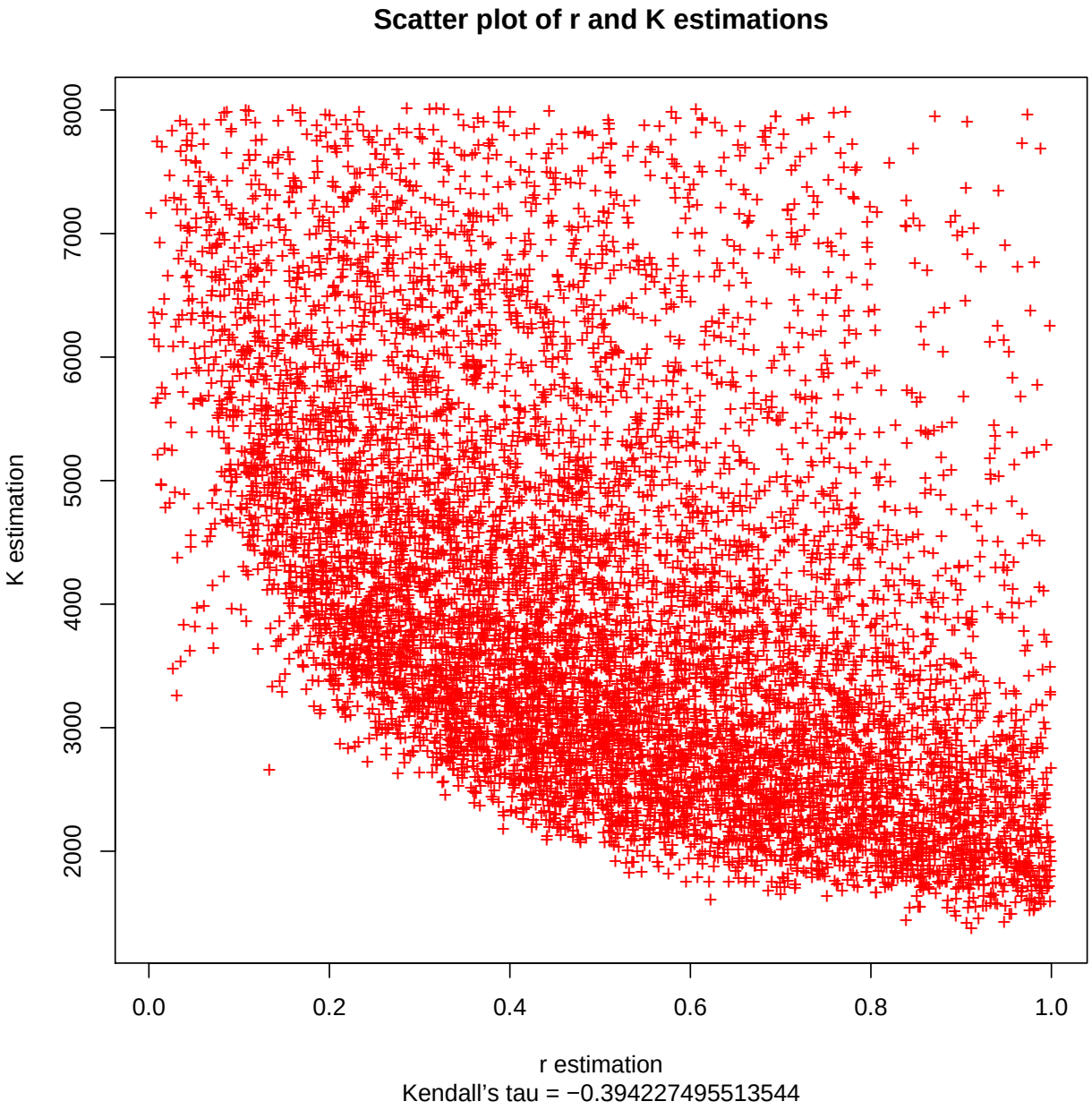


Table 2.6: Estimates means for the MLEP methods

treatment	r	K	q	sigma2	Prediction error
2	0.30	4476.86	0.21	0.03	1.20
3	0.38	4327.50	0.22	0.07	1.26
4	0.25	3856.85	0.20	0.09	1.45
5	0.44	4279.05	0.20	0.09	1.38
6	0.45	4434.40	0.21	0.13	1.42
7	0.33	4020.72	0.17	0.18	2.19
8	0.48	4312.76	0.20	0.16	1.55
9	0.49	4588.37	0.20	0.18	1.61
11	0.54	3446.75	0.23	0.03	1.05
12	0.56	3570.62	0.23	0.07	1.12
13	0.81	3121.20	0.24	0.05	0.95
14	0.63	3631.42	0.22	0.09	1.17
15	0.58	3987.89	0.20	0.16	1.34
16	0.79	3744.59	0.22	0.10	1.11
17	0.67	3975.13	0.19	0.17	1.28
18	0.59	4635.25	0.17	0.22	1.60

Table 2.7: Estimates variance for the MLEP methods

treatment	r	K	q	sigma2	Prediction error
2	0.0383	2426363.2572	0.0084	0.0001	0.3296
3	0.0441	2304495.2527	0.0130	0.0006	0.4885
4	0.0162	1617430.1399	0.0054	0.0317	0.8571
5	0.0430	2358062.3854	0.0085	0.0010	0.6836
6	0.0446	2705827.5925	0.0138	0.0250	1.0523
7	0.0155	1880244.8342	0.0058	0.0419	2.9020
8	0.0406	2386795.6493	0.0103	0.0958	1.1479
9	0.0364	2768492.0569	0.0162	0.0034	1.4142
11	0.0356	1914535.9965	0.0086	0.0001	0.2867
12	0.0392	2073786.2460	0.0109	0.0005	0.3583
13	0.0147	1515705.0257	0.0080	0.0003	0.1769
14	0.0379	2241706.9237	0.0099	0.0008	0.4039
15	0.0355	2485580.0988	0.0087	0.2081	0.6744
16	0.0180	2544945.5865	0.0086	0.0011	0.2870
17	0.0325	2246966.3699	0.0089	0.1714	0.5663
18	0.0330	2771472.2824	0.0086	0.2102	1.1358

Table 2.8: Estimates bias for the MLEP methods

treatment	r	K	q	sigma2	Prediction error
2	0.141	476.860	0.009	-0.008	0.181
3	0.215	327.502	0.018	-0.020	0.215
4	0.091	-143.151	-0.002	0.093	1.454
5	0.276	279.047	0.001	0.050	1.378
6	0.286	434.400	0.006	0.041	1.415
7	0.167	20.716	-0.033	0.178	2.187
8	0.324	312.762	-0.003	0.123	1.547
9	0.325	588.367	0.004	0.086	1.609
11	0.139	-53.250	0.030	-0.008	0.033
12	0.157	70.616	0.026	-0.018	0.072
13	0.412	-378.805	0.040	0.046	0.949
14	0.229	131.418	0.017	0.046	1.170
15	0.181	487.889	-0.003	0.070	1.343
16	0.390	244.589	0.015	0.101	1.105
17	0.268	475.129	-0.005	0.131	1.284
18	0.186	1135.252	-0.027	0.126	1.598

Table 2.9: Estimates root mean square error for the MLEP methods

treatment	r	K	q	sigma2	Prediction error
2	0.24	1629.04	0.09	0.01	0.60
3	0.30	1552.98	0.12	0.03	0.73
4	0.16	1279.81	0.07	0.20	1.72
5	0.35	1560.75	0.09	0.06	1.61
6	0.36	1701.33	0.12	0.16	1.75
7	0.21	1371.38	0.08	0.27	2.77
8	0.38	1576.27	0.10	0.33	1.88
9	0.38	1764.84	0.13	0.10	2.00
11	0.23	1384.69	0.10	0.01	0.54
12	0.25	1441.79	0.11	0.03	0.60
13	0.43	1288.10	0.10	0.05	1.04
14	0.30	1502.99	0.10	0.05	1.33
15	0.26	1650.34	0.09	0.46	1.57
16	0.41	1613.93	0.09	0.11	1.23
17	0.32	1572.49	0.09	0.43	1.49
18	0.26	2015.01	0.10	0.48	1.92

2.3.3 Interpretation of results

MLEO

Of course, we expect this model to perform better when $\sigma^2 = 0$ as in that case, the true model is fitted by maximum likelihood, which should yield consistent and efficient estimators of the parameters. Without any surprises, the simulation study does confirm this. For treatment levels 4, 7, 13 and 16 (no process error):

- The proportion of valid samples when $\sigma^2 = 0$ is always clearly above 80% (in comparison, it only exceeds 60% for treatments 11 and 14 when $\sigma^2 > 0$). Hence the numerical optimization of the likelihood function is stable when there is no process error.
- Parameter estimates are, on average, close to their true theoretical values. Moreover, their root mean squared error (RMSE) are much weaker than at the other treatment levels.
- The effect of increasing the observation error variance does not have much of an impact on the bias of the estimators, but it does increase their variability (and thus their RMSE).
- The effect of going from a linearly decreasing to a two-way trip biomass series decreases the bias, but does not have a systematic effect on the variance.

Though inferences seem to be reasonable for most parameters when there is only process error, an analysis of the correlations between the maximum likelihood estimators of some pairs of parameters raises some interesting questions. As shown on Figure 2.37, the r and K parameters are virtually deterministic functions of each other when the CPUE series is nearly linear (treatments 4 and 7), while they remain very highly correlated, but not as close to perfect dependency, when the series has a two-way trip (treatments 13 and 16). Actually what we can conclude from figures 2.37 to 2.39 is that the three parameters r, K and q_s are barely distinguishable, but MSY and q_s are distinguishable when the biomass series has a two-way trip.

It is difficult to make a good assessment of the effect of the process error in this study because of the modification to the simulation algorithm that had to be used to prevent the occurrence

Figure 2.37: This figure shows a scatter plot of the $(\hat{r}, \hat{K})$ pairs for each of the treatments 4, 7, 13 and 16.

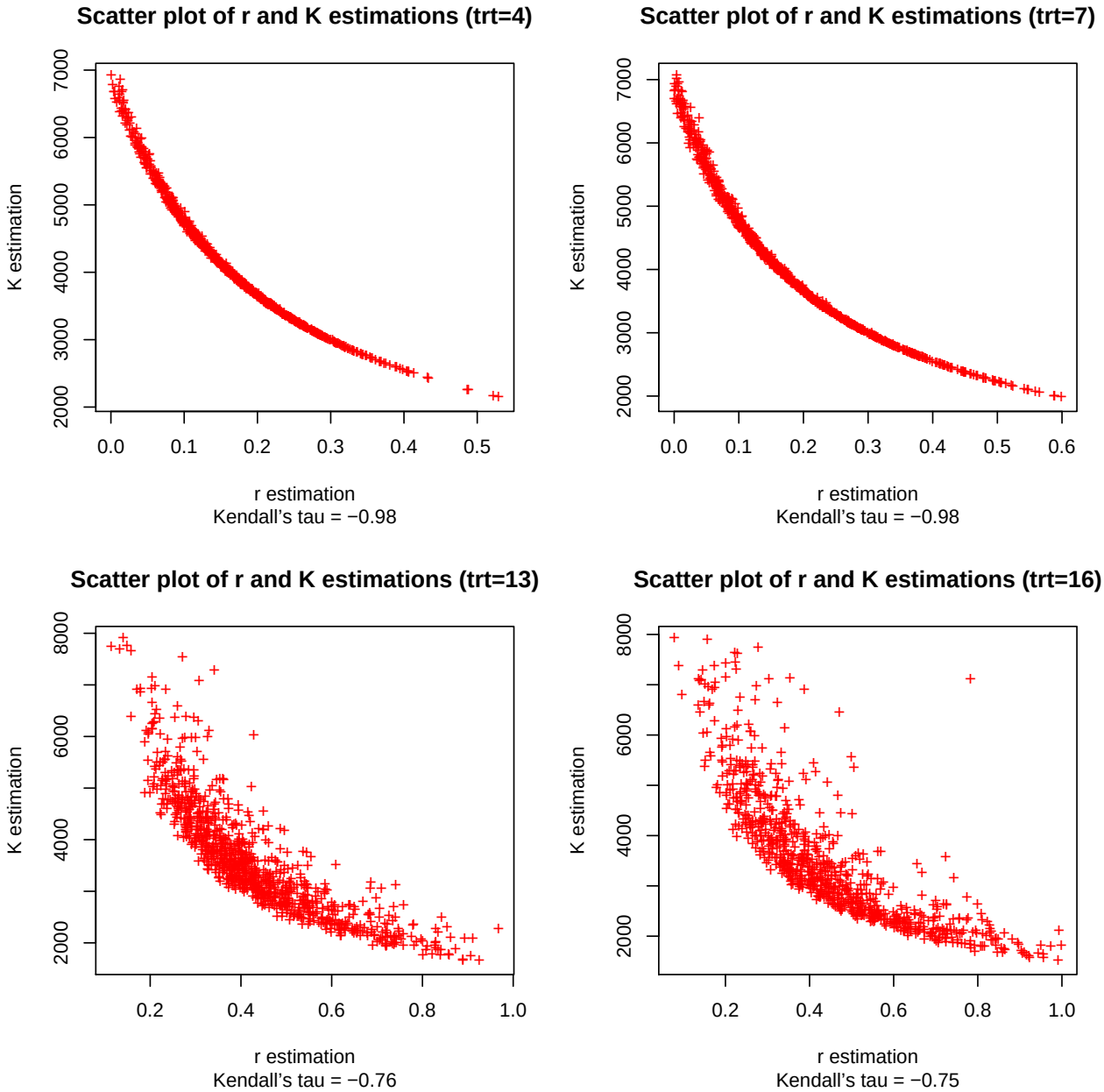


Figure 2.38: This figure shows a scatter plot of the $(\hat{r}, \hat{q}_s)$ pairs for each of the treatments 4, 7, 13 and 16.

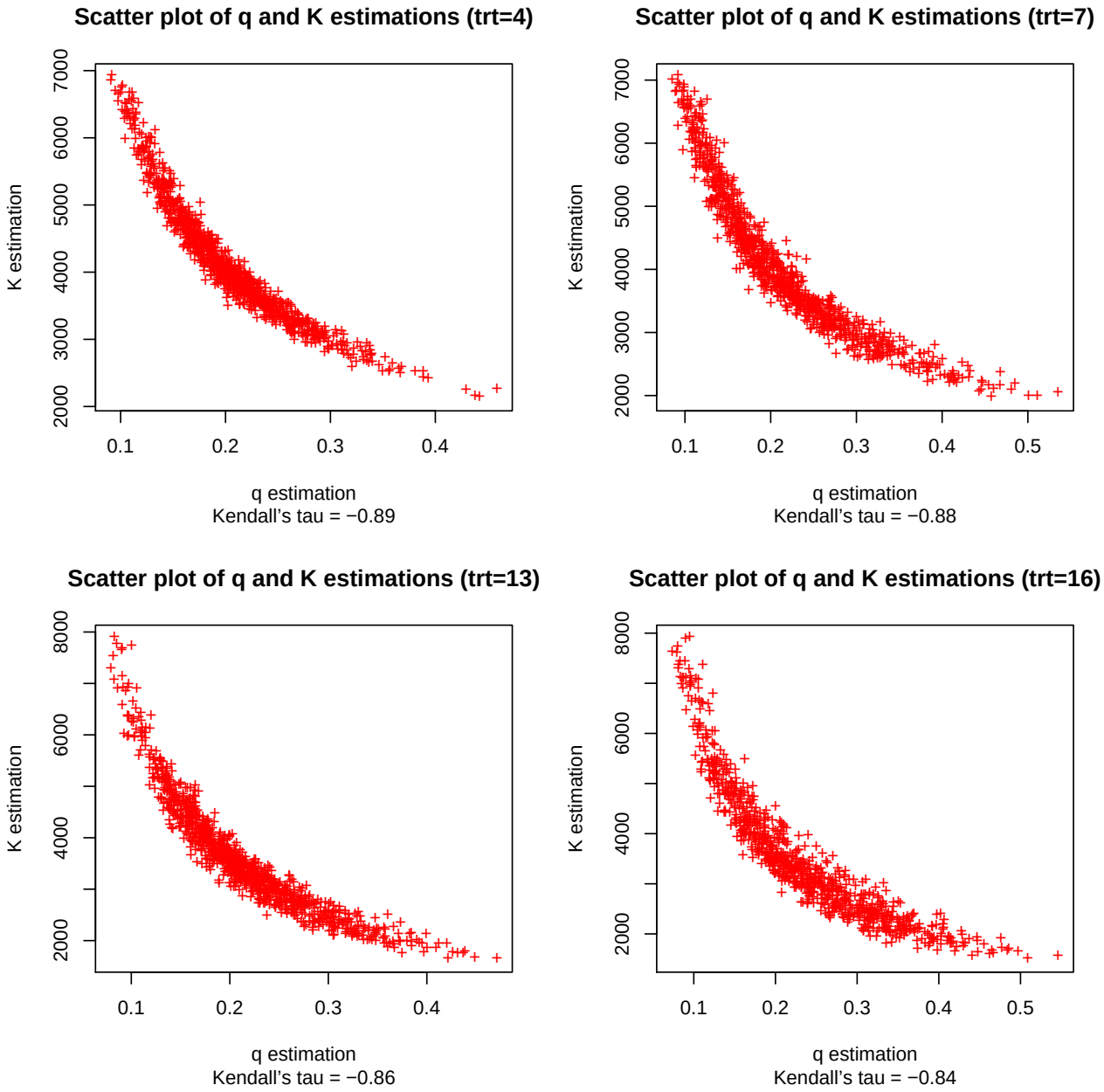
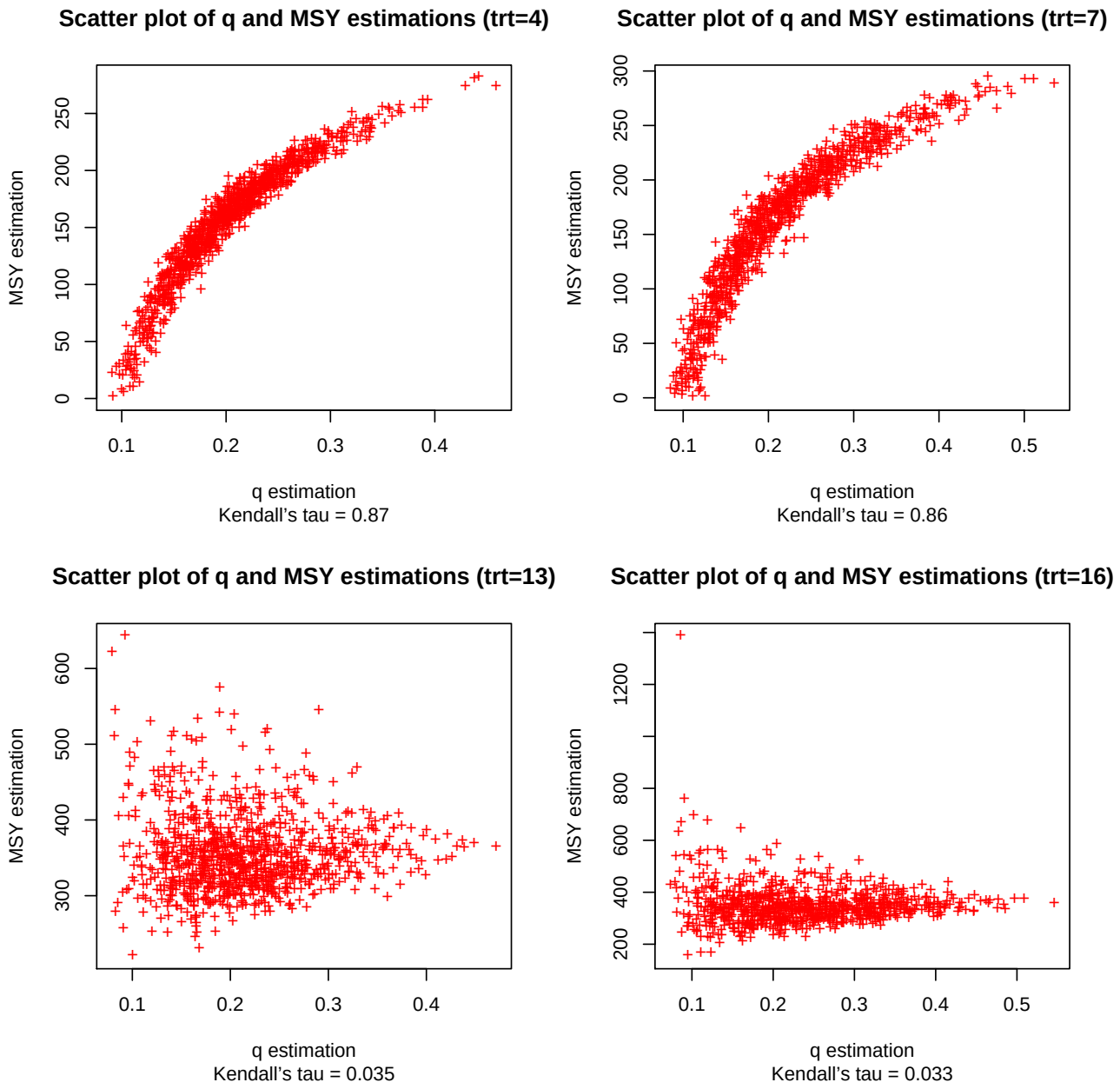


Figure 2.39: This figure shows a scatter plot of the $(\widehat{MSY}, \hat{q}_s)$ pairs for each of the treatments 4, 7, 13 and 16.



of negative biomasses. Indeed, it is very difficult to distinguish between bias in parameter estimates induced by the fact that we are not exactly simulating from the exact SPM anymore and a real bias of the estimator. Nevertheless, we can see that there is a positive bias for r, a negative bias for K, a positive bias for q_s and a positive bias for MSY, and that all these biases worsen as σ^2 increases. As for the prediction error, it generally worsens with increasing values of σ^2, but this tendency is not systematic. We discuss this problem of simulating with process error further in Section 2.4.

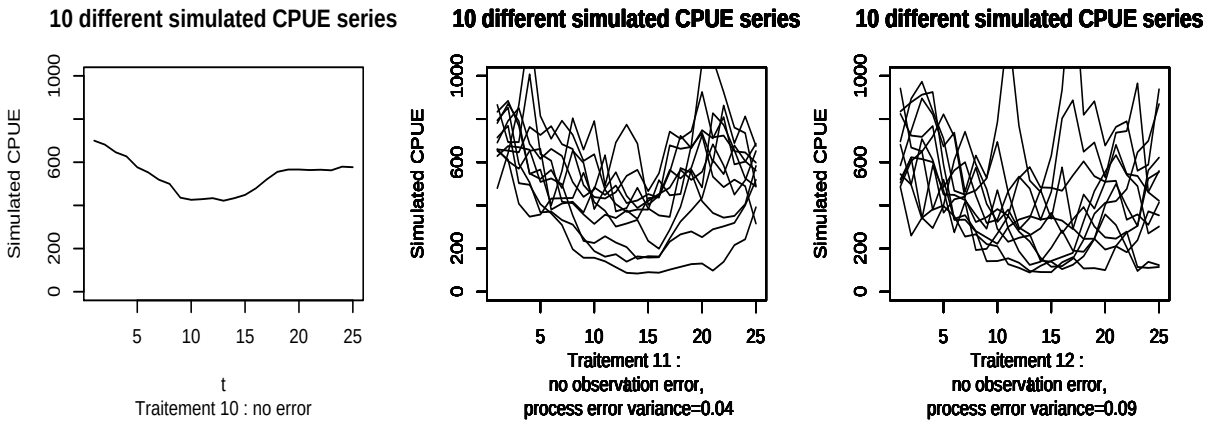
MLEP

Fitting a SPM with process error by maximum likelihood, though similar in essence to fitting a SPM with observation error by maximum likelihood, is much more difficult numerically because of the need to take the natural logarithm of $I_t^*(r, K, q_s)$ given by (**??**). Though in practice this is not much of a problem because one can "manually guide" the maximization procedure, for a simulation study of this magnitude, an automatic fix to keep the maximization going when $I_t^*(r, K, q_s)$ takes on a negative value must be programmed. In our case, we used $I_t^{**}(r, K, q_s) = \max\{0.0001, I_t^*(r, K, q_s)\}$ in our implementation. Unfortunately, this fix leads the Nelder-Mead algorithm to stop at local maxima that do not give the exact maximum likelihood estimators. Unfortunately, the algorithm does not tell whether the maximum found is a global or local maximum. Hence, we suspect that the estimates from Section **??** are in fact a mixture of global and local maximizers of the likelihood function, and hence interpreting these results would make little sense at this time. Note that our suspicions are reinforced by the fact that the proportion of samples that yielded valid (i.e., reasonable) values for the estimators was rather small in the MLEP study.

2.4 Conclusion

What can be concluded from this simulation experiment? The most important conclusion that we have reached is that the SPM model as parameterized is highly volatile and can, even with very mild process error, generate biomass series that are completely unrealistic. Figure 2.40

Figure 2.40: This figure shows simulated biomass series with and without process errors.



shows typical realizations of biomass series with and without process error. As we can see, the latter is extremely volatile and some trajectories are unlikely to be observed in practice. Some authors have circumvented this problem by simulating series with fixed values of the biomasses at the beginning **and** at the end of the series (e.g., Punt 2003). Though this allows one to simulate biomass series that are stable even in the presence of process error, it underestimates the true variability that underlies the SPM and, hence, variances of estimators or prediction errors obtained in such simulation studies are seriously underestimated. Our attempt to put a "floor" on the values that could be taken by the biomasses was not successful, as it biased the inferences in numerous ways: (i) by forcing the biomass series to go up when it is low, we inflated the growth rate and this was reflected by strong positive bias in r estimates in the simulations with process error; (ii) by restraining the possible values of the biomasses, we restrict the values of the error terms and hence diminish their variance, which implies that the variances and prediction errors that we have obtained are also underestimated; (iii) discontinuities were introduced in the likelihood surface, which means that iterative procedures get stuck in local maxima and cannot find the global maximum.

Nevertheless, in the cases were there was no process error we were able to reach some interesting conclusions. First of all, a SPM with process error can be fitted, but the observation error means that the $I_t^*(r, K, q_s)$ evaluated at some parameter values can be negative, and hence traditional optimization methods such as quasi-Newton or Nelder-Mead are not appropriate for

MLEP. But when the SPM with observation error is fitted to data generated from an SPM with observation error only, inferences are good. As expected, bias and estimation/prediction error increase when the biomass series does not have a two-way trip and when the variance of the observation error increases. We also have that MSY is well estimated and that prediction of a future value of biomass is not systematically bias, in the sense that the average ratio of predicted biomass over simulated biomass was not systematically above or below 1. However, a correlation analysis revealed that the parameters r and K are strongly correlated (virtually deterministic functions of each other when the there is no two-way trip in the CPUE series) and, thus, considering a reparameterization of the SPM that would replace the three parameters r, K and q_s by two parameters (e.g., in terms of MSY and q_s) might be relevant.

The previous discussion suggests several avenues for future work. First and foremost, an algorithm to simulate data from the SPM with process error without needing to put a floor on the value of the biomasses or without tying the biomass series at times 1 and N must be derived if we really want to assess if MLEO will still give decent predictions or inferences about MSY in this case. We can think of a few options to achieve this:

1. Use a fixed series of catches, but replace C_t with a random C_t^* between 0 and $B_t + B_t r(1 - B_t/K)$ when $C_t \geq B_t + B_t r(1 - B_t/K)$.

2. Simulate all catch series from a model where C_t would depend on C_{t-1}, B_{t-1} and/or B_t.

3. Use normal rather than lognormal process errors.

Though option 2 seems to be the most natural (the quantity of fish caught in year t is probably a function of the fish caught in previous years as well as the biomass available to be fished during these years). However, properties of SPM in the literature have always been studied based on realized CPUE series. Because of this, option 1 seems to be a promising compromise: mostly rely on a realized CPUE series, but correct the CPUEs of these years where there are more fish caught than available. Though option 3 would solve most numerical issues, it would allow for negative biomasses, which is not realistic. We are currently trying to implement a suitable version of option 1.

Second, the numerical aspect of MLEP should be fixed. Indeed, standard numerical maximization of the log-likelihood function with Nelder-Mead or quasi-Newton methods could not find the global maximum when fitting the SPM with process error even when the data were generated according to a SPM without process error. Once again, there are potential solutions to this problem:

1. Perform a constrained maximization that will only consider values of the parameters for which $I_t^*(r, K, q_s) > 0$ for all t.

2. Use normal rather than lognormal errors.

3. Reparameterize the model.

4. Use a different type of maximization algorithm.

Option 1 seems to be a difficult task, as the constraint $I_t^*(r, K, q_s) > 0$ for all t is quite complex. Once again, option 2 might be a good numerical solution, but allowing for normal errors implies that some I_t or B_t could be negative, which is not practically possible. We have already mentioned option 3 in other parts of this report and it should certainly be seriously considered. Finally, option 4 is an interesting possibility. Indeed, algorithms such as the EM-algorithm or Gibbs sampling may be adapted to the problem at hand. Though these algorithms tend to be much slower than Nelder-Mead or quasi-Newton type methods, they have good robustness properties. Moreover, because they are often used to perform parameter estimation in contexts where some random variables are not observed, they could be useful here since the B_t's are indeed unobserved random variables. We are currently working on the implementation maximum likelihood estimation via the EM-algorithm for both MLEP and MLEPO.

In closing, this study shows that the SPM with process error gives highly volatile CPUE series. This means that without restraining the biomasses, it is very difficult to fit any version of the SPM to a large proportion of simulated CPUE series that all use a same series of catches. However if one wants to assess the robustness of the SPM to misspecification of the error structure, one must be able to simulate valid data with process error and fit the SPM to these simulated data. Perhaps the model needs to be reparametrized, or perhaps better fitting

techniques can solve the problems. We are hoping to shed some lights on those issues in a near future.

2.5 References

Hammond, T. R., and Trenkel, V. M. (2005) *Censored-catch data in fisheries stock assessment.* ICES Journal of Marine Science, **62**: 1118–1130.

Punt, A. E. (2003) *Extending production models to include process error in the population dynamics.* Can. J. Fish. Aquat. Sci. **60** : 1217–1228.

Lemay, J., Duschesne, T. , Rivest, L.-P. (2006) *Review of methods to account for misreported catches in surplus production models using censored-observation methods.* Scientific work, Laval University.

Nelder, J. A. and Mead, R. (1965) *A simplex algorithm for function minimization.* Computer Journal **7**, 308-313.

Polacheck, T., Hilborn, R., and Punt, A.E. (1993) *Fitting surplus production models: comparing methods and measuring uncertainty.* Can. J. Fish. Aquat. Sci. **50**: 25972607.

Robert, P.R, Casella, G. (2004) *Monte Carlo Statistical Methods.* Springer Texts in Statistics, New York: Springer.

Part 3

More analysis about MLEO and MLEP

3.1 Introduction

The Surplus Production Model (SPM) is a widely used fish stock population assessment model. To apply the SPM, all that is required is a series of abundance indices (CPUEs are often used), and the series of catches related to the years to be assessed. In the report that we submitted in December 2006 (included as Part **??** of this document), our interests were centered on the properties of inferences made on SPM parameters by the method of maximum likelihood (we refer the reader who is not familiar with SPM and/or maximum likelihood estimation for SPM to Section 2.2). Our objectives were to investigate the bias and variability of the estimators when SPM with observation error only or process error only were fitted to data simulated from SPM with observation error and/or process error. Because of technical difficulties arising when simulating data from SPM with process error (the main difficulty being the generation of negative biomasses), the properties of estimators were only interpretable when data were simulated from SPM with observation error only. In that latter case, fitting the SPM model with observation error only by maximum likelihood generally led to valid inferences on the model parameters (see Section 2.4 for a detailed interpretation of the simulation results). However, when fitting SPM with process error only to data simulated from SPM with observation error only produced numerical problems that invalidated the simulation results: basically, the numerical procedure used to maximize the likelihood function could only find a global maximum in a limited number of the simulated samples. Hence, the conclusions that could be drawn from the Fall 2006 simulation study were somewhat limited.

Obviously, our main objectives this winter were to solve the problems that we had stumbled upon during the Fall study. More precisely, our objectives were (i) to find a simulation method that can generate biomass series that remain positive without having to simulate new series of catches and that keep the exploitation rate stable and (ii) to improve the stability of the procedure that we use for the numerical maximization of the likelihood function. To tackle objective (i), we propose to simulate the biomasses from a lognormal distribution that is conditional on both the previous and next catch, while our approach to objective (ii) is to use a reparameterization of the SPM parameters. We present these methods as well as the results obtained in the remainder of Part **??**. More precisely, we describe the conditional simulation

model in Section 3.2.1, while we consider maximization of the likelihood function in Section 3.2.2. We present the simulation results and interpretations in Section 3.3 and give our main conclusions and research priorities for the April-June period in Section 3.4.

3.2 Preliminaries

3.2.1 New SPM simulation method

The usual SPM is based on two equations, one for the biomass (B_t) dynamic, one for the observations (I_t):

$$B_{t+1} = B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t; \tag{3.1}$$

$$I_t = qB_t. \tag{3.2}$$

Note that even if this model is using two series of data (the abundance indices I_t, and the catches C_t), only the I_t are explicitely modeled (eq. (3.2)); the C_t are considered a sequence of fixed constants.

In practice, the relationships given by (3.1) and (3.2) are not exact. Hence, random noise can be added to make the model closer to reality. Noise that is added to (3.1) is referred to as *process error* while noise added to (3.2) is referred to as *observation error* or *measurement error*. One common means of including process and observation error is to add a multiplicative lognormal error term to each of (3.1) and (3.2). Let ε_{t+1} and $\tilde{\varepsilon}_t$, $t = 1, 2, \ldots$ be independent zero mean normal random variables with $Var[\varepsilon_t] = \sigma^2$ and $Var[\tilde{\varepsilon}_t] = \tau^2$. Then with process error (3.1) becomes

$$B_{t+1} = \left\{B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t\right\} e^{\varepsilon_{t+1}} \tag{3.3}$$

and with observation error (3.2) is

$$I_t = qB_t e^{\tilde{\varepsilon}_t}. \tag{3.4}$$

Note that when there is no observation error (i.e., $\tau^2 = 0$ and we observe I_t without error), we can replace B_t by I_t/q in (3.3) to get

$$I_{t+1} = \left\{I_t(1+r) - \frac{r}{qK}I_t^2 - qC_t\right\} e^{\varepsilon_{t+1}}.$$

When simulating from a SPM with process error using a fixed series of catches C_t, a problem may arise: extinction of the simulated population (more precisely, negative values for the biomasses can be simulated). Indeed, consider the standard way to simulate from a SPM with process error only:

1. For fixed r, K and σ^2, simulate

$$B_1 = Ke^{\varepsilon_1}$$
$$B_t = \left\{B_{t-1} + rB_{t-1}\left(1 - \tfrac{B_{t-1}}{K}\right) - C_t\right\} e^{\varepsilon_t}, \quad t > 1$$

2. Multiply the B_t series by the fixed q parameter to obtain the simulated series of abundance indices I_t.

Because the simulated biomass at time t depends only on the catch at time $t-1$, it is possible to simulate a biomass at time t that is small in comparison to the catch at time t (recall that catches are fixed and only biomasses are simulated), thereby producing a negative biomass at time $t+1$.

One obvious means of solving this problem would be to use simulated catches, with the distribution of C_t depending on the value of B_t. However this would require a model for the catch as a function of the biomass. Furthermore, the observed series of catches give information about the type of biomass trajectory that is realistic and thus biomass series simulated should be such that an actually observed series of catches is possible. For these reasons, we prefer to keep the catches fixed and to include information about the catches at times $t-1$ **and** t when simulating the biomass value at time t. In order to achieve this, we slightly modify the SPM by modeling the *exploitation rate* (the ratio C_t/B_t) of the population over time. We suppose that the exploitation rates have the same mean in all years, but we let them be random. To do so, we first rewrite (3.3) as

$$\log(B_t)|C_{t-1}, B_{t-1} \sim N\left[\log\left\{B_{t-1} + rB_{t-1}\left(1 - \frac{B_{t-1}}{K}\right) - C_{t-1}\right\},\ \sigma^2\right], \tag{3.5}$$

where "$X \sim N(\mu, \sigma^2)$" means that X follows a normal distribution with mean μ and variance σ^2. Then, we assume lognormal exploitation rates, $C_t/B_t = \phi e^{\varepsilon_t^*}$ with $\varepsilon_t^* \sim N(0, \sigma^{*2})$, to obtain

$$\log(C_t)|B_t \sim N\left\{\log(\phi) + \log(B_t),\ \sigma^{*2}\right\}. \tag{3.6}$$

We can then get the joint distribution of $\log(B_t), \log(C_t)|B_{t-1}, C_{t-1}$ from (3.5) and (3.6):

$$\left(\begin{array}{c} \log B_t \\ \log C_t \end{array} \middle| \, C_{t-1}, B_{t-1} \right) \sim N_2 \left\{ \begin{array}{c} \log(\mu_t) \\ \log(\phi) + \log(\mu_t) \end{array} , \left(\begin{array}{cc} \sigma^2 & \sigma^2 \\ \sigma^2 & \sigma^{*2} \end{array} \right) \right\}, \tag{3.7}$$

where $\mu_t = B_{t-1} + rB_{t-1}\left(1 - \frac{B_{t-1}}{K}\right) - C_{t-1}$. Now because the C_t are fixed, we are interested in the distribution of B_t given C_t, C_{t-1}, B_{t-1}, which we get from (3.7):

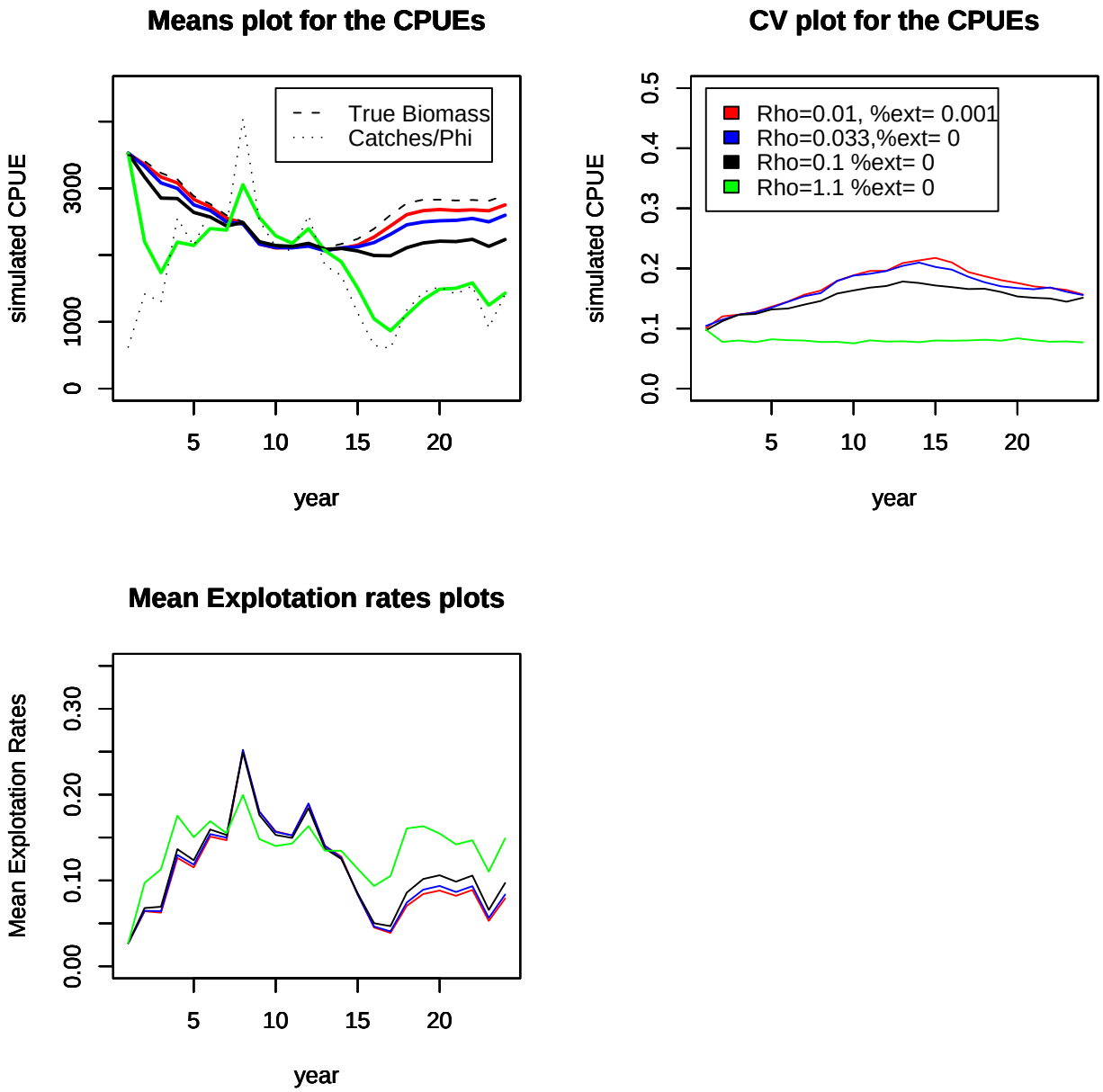
$$\log(B_t)|C_t, C_{t-1}, B_{t-1} \sim N\left[\log(\mu_t) + \frac{\sigma^2}{\sigma^2 + \sigma^{*2}}\left\{\log(C_t) - \log(\phi) - \log(\mu_t)\right\},\ \sigma^2\left(1 - \frac{\sigma^2}{\sigma^2 + \sigma^{*2}}\right)\right]. \tag{3.8}$$

Note that if we let $\rho = \frac{\sigma^2}{\sigma^{*2}}$, the weight given to constant exploitation rate is $\rho/(1+\rho)$. This means that for a small ρ (exploitation rate variance is large compared to process error variance), the model is less driven by the constant exploitation rate hypothesis.

Once the biomass series has been simulated, then we can easily generate the series of abundance indices by setting $I_t = qB_t$ when there is no observation error and by simulating the $\tilde{\varepsilon}_t$ from the $N(0, \tau^2)$ distribution and setting $I_t = qB_t e^{\tilde{\varepsilon}_t}$ when there is observation error.

Using (3.8) with a fixed series of C_t does not guarantee that a series of biomasses will never dip below zero. However, the probability of generating negative biomasses is greatly diminished in comparison to simulation from (3.3). The mean biomass trajectories based on 1,000 simulations from model (3.8) with various values of $\rho = \frac{\sigma^2}{\sigma^{*2}}$ are given in Figure 3.1. The "%ext" values represent the proportion of trajectories that dip below 0. The corresponding mean exploitation rates, C_t/B_t, are depicted in Figure 3.1. As we can see, the greater *rho*, the more constant the exploitation rate. However, with a larger *rho*, the shape of the biomass series will mimic that of the C_t, while a smaller *rho* allows the simulated biomass series to have a shape closer to that prescribed by the SPM (3.1). We also get very few negative biomasses; in the cases shown in the figure, only 1 trajectory out of 1,000 when *rho* took on smaller value.

Figure 3.1: These plots show the mean of 1,000 simulated biomass trajectories from model (3.8) for various values of σ^2 and with the fixed series of C_t on Namibian Hake from Punt (2003), $K = 3500$, $r = 0, 4$, $q = 1$, $\sigma^2 = 0.01$, $\phi = 0.15$ and different values of $\rho = \frac{\sigma^2}{\sigma^{*2}}$. The values of r and K parameters were chosen to give the data a two-way trip shape although it doesn't seem so. The reason why the biomass series seems linear is that the two way-trip relies more on the catches series than the parameters. Note that as ρ increases, the mean biomass tend to follow the series of C_t/ϕ and the mean exploitation rates tend to stabilize around ϕ. However, when ρ is too large, we are not simulating from an SPM but from eq(3.6).



We think that this simulation method gives a better idea of the variability in the biomass trajectories under the SPM than the method used by Punt (2003). Indeed, the latter assumes fixed values for the biomasses at the first and last times of the biomass trajectory. While this has the advantage of keeping the biomasses positive, it has the disadvantage of simulating highly similar biomass trajectories, which is not consistent with a SPM with lognormal process error. Hence, a simulation study that uses the strategy of Punt (2003) may seriously underestimate the variability in the parameter estimators.

3.2.2 Maximization of the likelihood function

The main objective of our statistical analyses is to make inferences on the parameters of the SPM, more precisely the parameters r, K, q, $MSY = rK/4$ and the prediction of the biomass in the year following the last data point. Several methods are available to carry out those inferences, but here we are interested in maximum likelihood based approaches (see rationale in Section 2.1). In this study, we investigate the quality of maximum likelihood estimation when fitting a SPM with observation error only (MLEO) and when fitting a SPM with process error only (MLEP). We will not give a detailed account of these procedures in this section, as they are already described in detail in Section 2.2.2.

When performing maximum likelihood estimation, we must find the values of the model parameters that maximize the likelihood function. In the case of the SPM, in both MLEO and MLEP, the likelihood function is relatively complex and its maximization cannot be done in closed form; we must resort to numerical optimization. In the Fall, we had encountered numerous problem with the numerical optimization, which we did using the Nelder-Mead simplex algorithm as implemented in the `optim()` function of R (R Development Core Team, 2006). We had chosen the simplex algorithm because it is not based on the derivatives of the objective function with respect to its parameters and, hence, is more robust in cases where the objective function may not be smooth in all parameters. In our optimization in the Fall, we did not restrict the search for the maximum over the possible parameter values, but rather let the algorithm scan the entire $(-\infty, \infty)$ range for all parameters. This winter, we modified the parametrization of the SPM so that the simplex algorithm would only search for a maximum

over the proper parametric space. More precisely, we rewrote (3.1) and (3.2) as

$$B_{t+1} = B_t + \frac{e^{r'}}{1+e^{r'}} B_t \left(1 - \frac{B_t}{e^{K'}}\right) - C_t; \tag{3.9}$$

$$I_t = e^{q'} B_t, \tag{3.10}$$

and then maximized the likelihood function, with this new parametrization, using the Nelder-Mead algorithm (Nelder and Mead, 1965) implemented in the `optim( )` function of the package R. The maximum likelihood estimators under the original parametrization are easily retrieved by computing $r = \exp(r')/(1+\exp(r'))$, $q = \exp(q')$ and $K = \exp(K')$. These transformations guarantee that $r \in (0,1)$ and $q, K > 0$, their range of possible values. Another option that we considered to solve the optimization problem was to use the Newton-Raphson algorithm with the gradient of the log-likelihood function provided. Finally, we have also redefined what we term a "valid optimization". In the Fall, it was defined as an optimization yielding parameter estimates in a certain range. This time, a "valid optimization" is an optimization which gives the same parameter estimates when starting from four different starting vector points, regardless of the values obtained for the estimates. The four starting vector points were chosen relatively to the r and K parameters, with combinations of values that are greater or smaller than the true values used for simulation : {(smaller,smaller),(smaller,greater),(greater,smaller),(greater,greater)}. With this new definition of a valid sample, a few simulation runs suggested that the reparameterized simplex gives a higher proportion of valid estimators than Newton-Raphson, so the former is the method used in the simulation study described in Section 3.3.

3.3 Simulation study

3.3.1 Study design

This simulation study has two objectives: (i) to determine if one of MLEO and MLEP is better than the other for making inferences about SPM parameters when data are generated with process error only and with both process and observation error; (ii) to assess the impact of the level of variability in the process error, the exploitation rate and the observation error on the

various parameter estimates. To do so, we have run a complete 2^3 factorial experiment: 1,000 simulations run at each of 8 combinations of high and low values of the variance parameters of the three sources of variability. More precisely, we have run the SPM given by equations (3.8) and (3.4), with $r = 0.4$, $K = 3,500$, $q = 1$, $\phi = 0.15$ and the first 23 years of observation of the Namibian Hake catch series in all simulations, and with the values specified in Table 3.1[1] for σ^2, σ^{*2} and τ^2. Note that the values chosen for the parameters were obtained by looking at what would reasonable values be by fitting the MLEO to the Namibian Hake data. Also, because only a small amount of observation error is enough to make MLEP estimates completely wrong (see Chapter III), we used a small variance (τ^2).

Table 3.1: This table shows the 8 combinations of SPM variability parameters.

Treatment	σ^2	σ^{*2}	ρ	τ^2
1	0.01	0.30	0.033	0.00
2	0.01	0.30	0.033	0.01
3	0.04	0.30	0.133	0.00
4	0.04	0.30	0.133	0.01
5	0.01	0.50	0.020	0.00
6	0.01	0.50	0.020	0.01
7	0.04	0.50	0.100	0.00
8	0.04	0.50	0.100	0.01
9	0.01	0.15	0.067	0.00
10	0.01	0.15	0.067	0.01
11	0.04	0.15	0.267	0.00
12	0.04	0.15	0.267	0.01

We start by giving the raw simulation results in Subsection 3.3.2 in the form of plots and tables, and defer their interpretation to Subsection 3.3.3.

[1]Refer to Part **??** for results about SPM without process error ($\sigma^2 = 0$).

3.3.2 Results

We first give a series of plots that show overlays of density estimates of the maximum likelihood estimators of some SPM parameters of interest when fitting MLEO and MLEP to the same simulated samples. Additional information is provided in the legends given in some of the plots: proportion of valid optimizations for each of MLEO and MLEP, coverage proportion of nominal approximate 95% likelihood ratio intervals and correlation between a predicted and simulated terminal biomass. For comparability purposes, the plots are based on the samples for which both MLEO and MLEP gave valid estimators. Note that the prediction error refers to the difference between the simulated terminal biomass and the estimated terminal biomass. What we are searching for is the nearest mean to zero and the smaller variance around that mean. Finally, the last figure of this section is presenting a comparison of the correlation between r and K for the MLEO and MLEP.

Figure 3.2: These plots show kernel density estimates of the parameter estimates for treatment 1 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.3$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

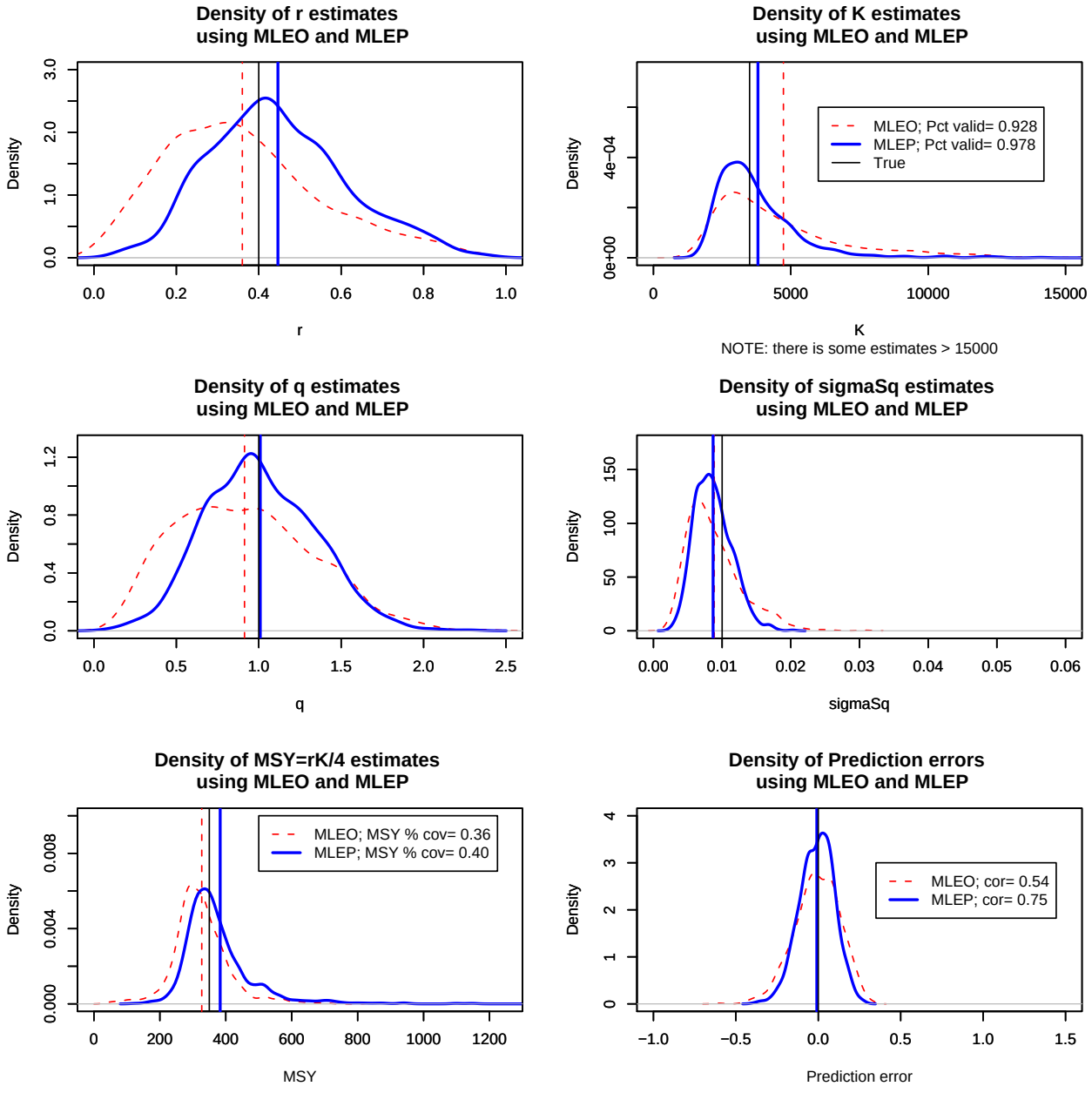


Figure 3.3: These plots show kernel density estimates of the parameter estimates for treatment 2 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.3$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

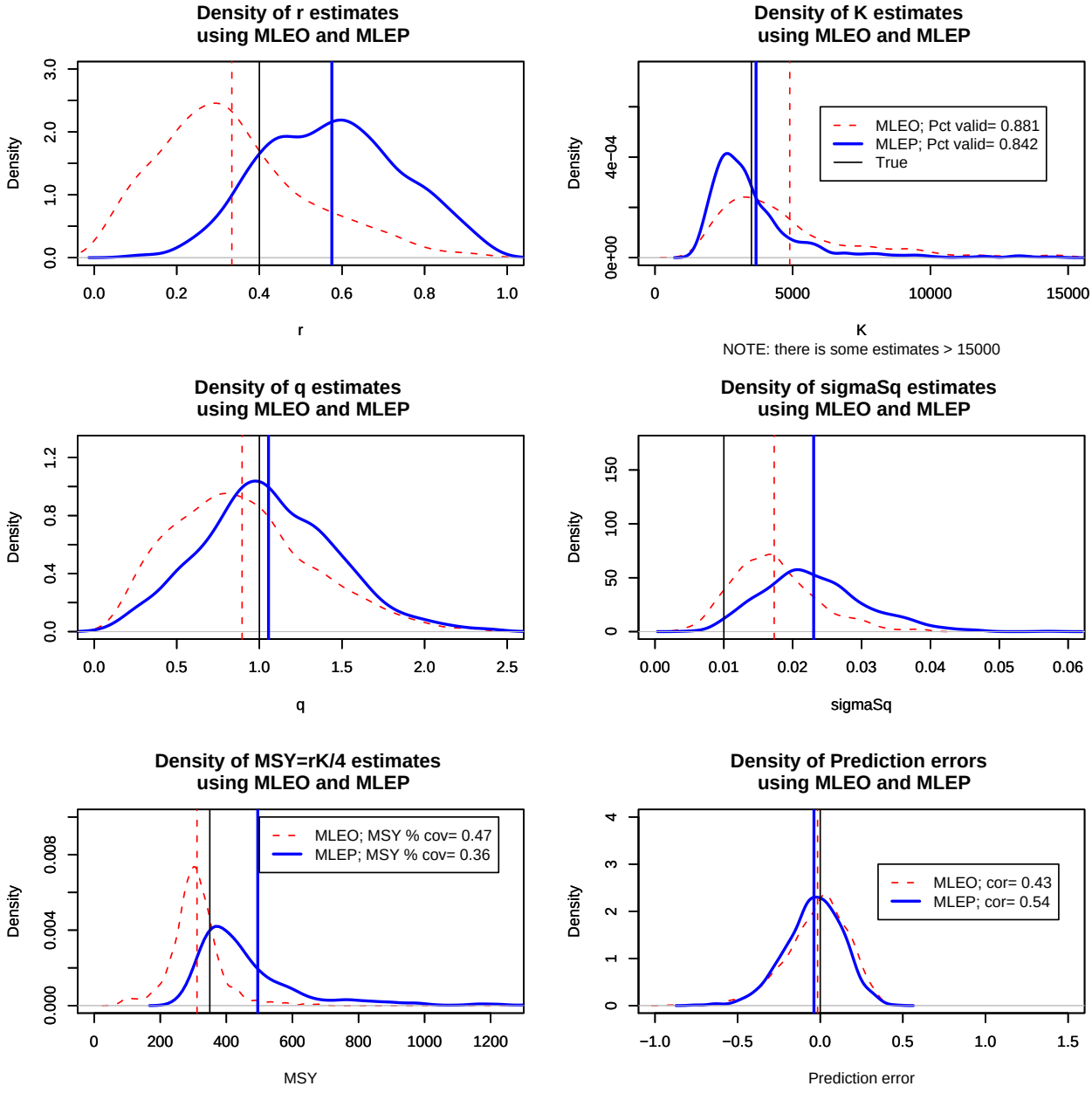


Figure 3.4: These plots show kernel density estimates of the parameter estimates for treatment 3 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.3$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

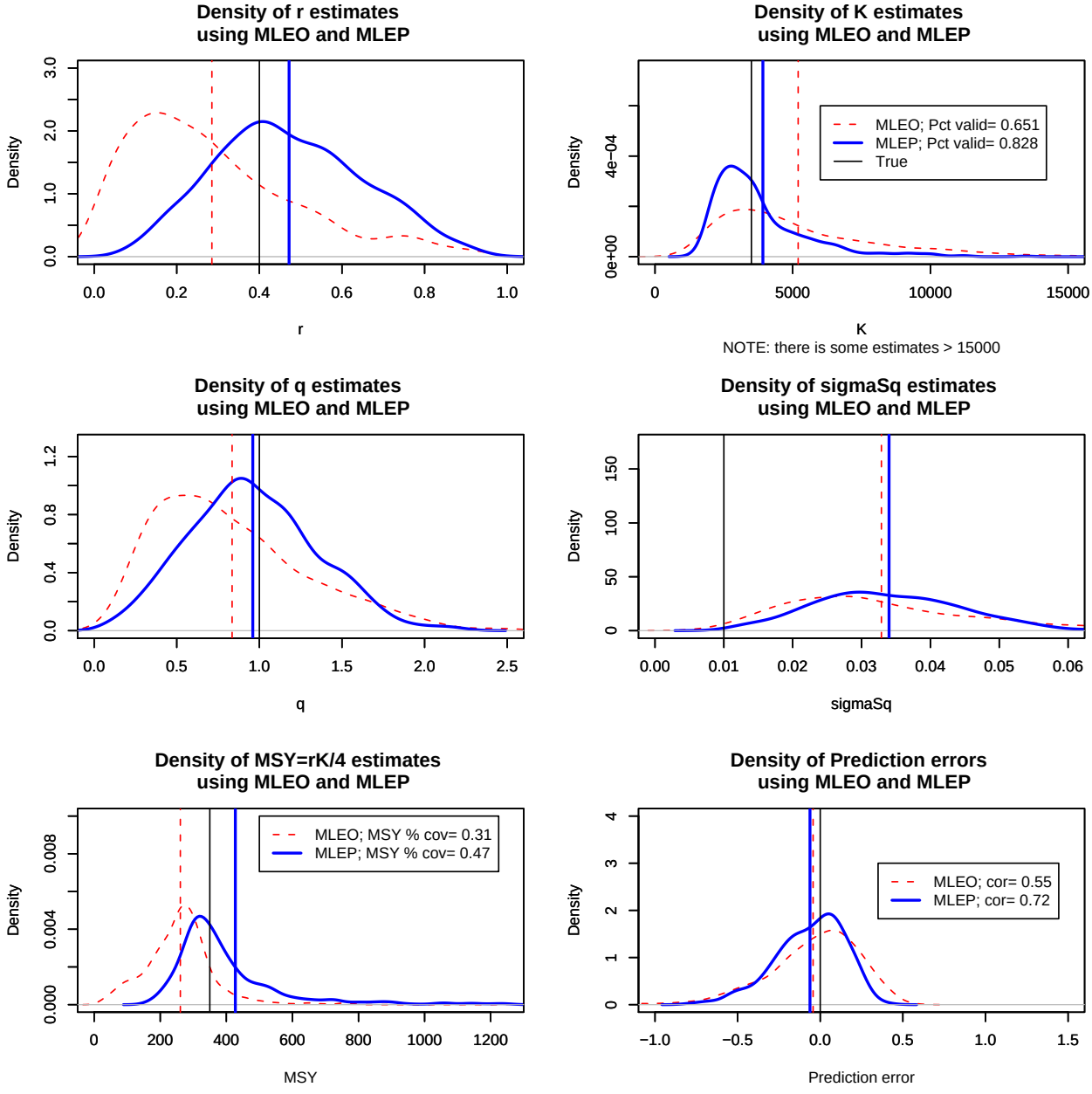


Figure 3.5: These plots show kernel density estimates of the parameter estimates for treatment 4 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.3$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

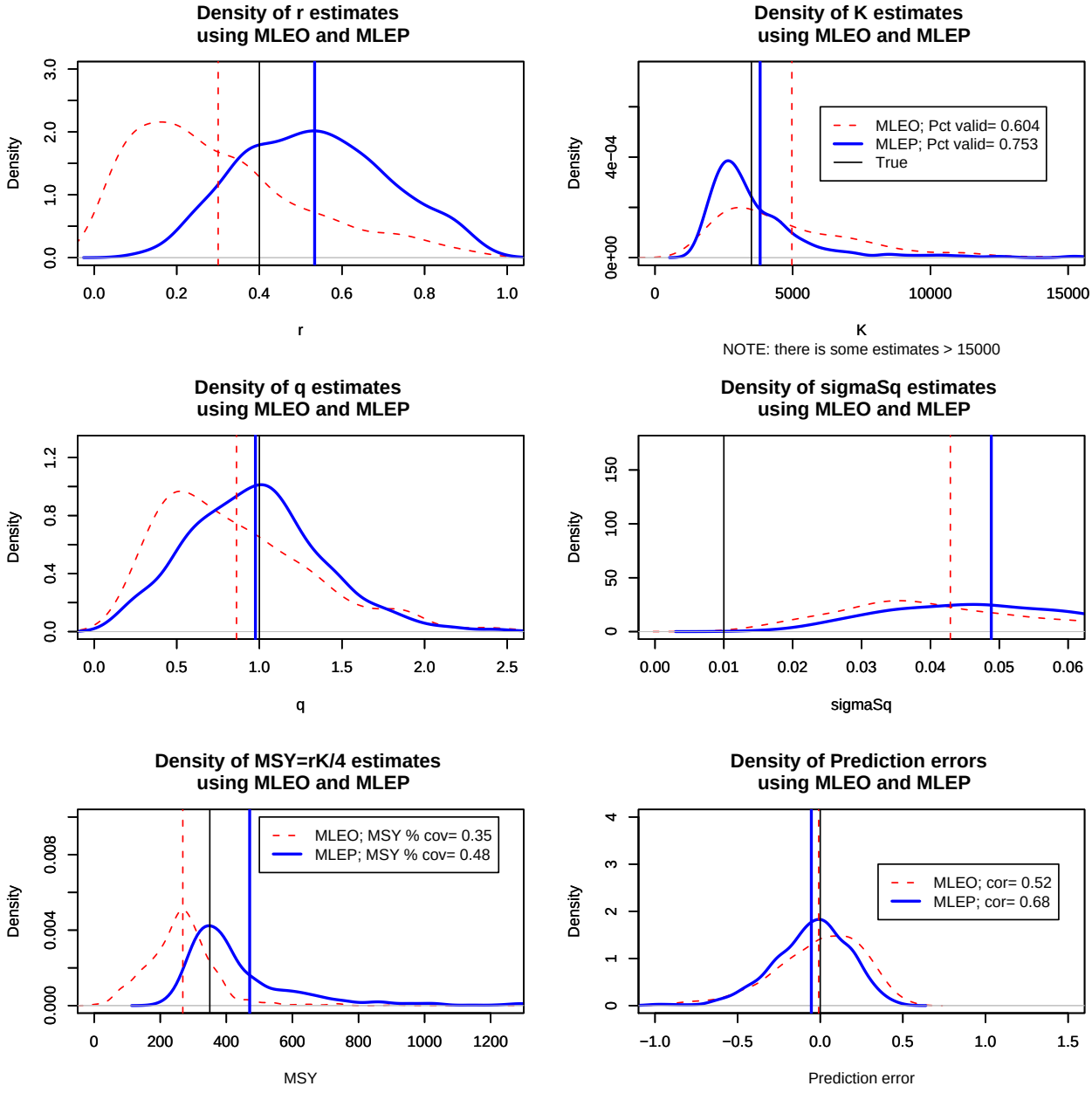


Figure 3.6: These plots show kernel density estimates of the parameter estimates for treatment 5 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.5$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

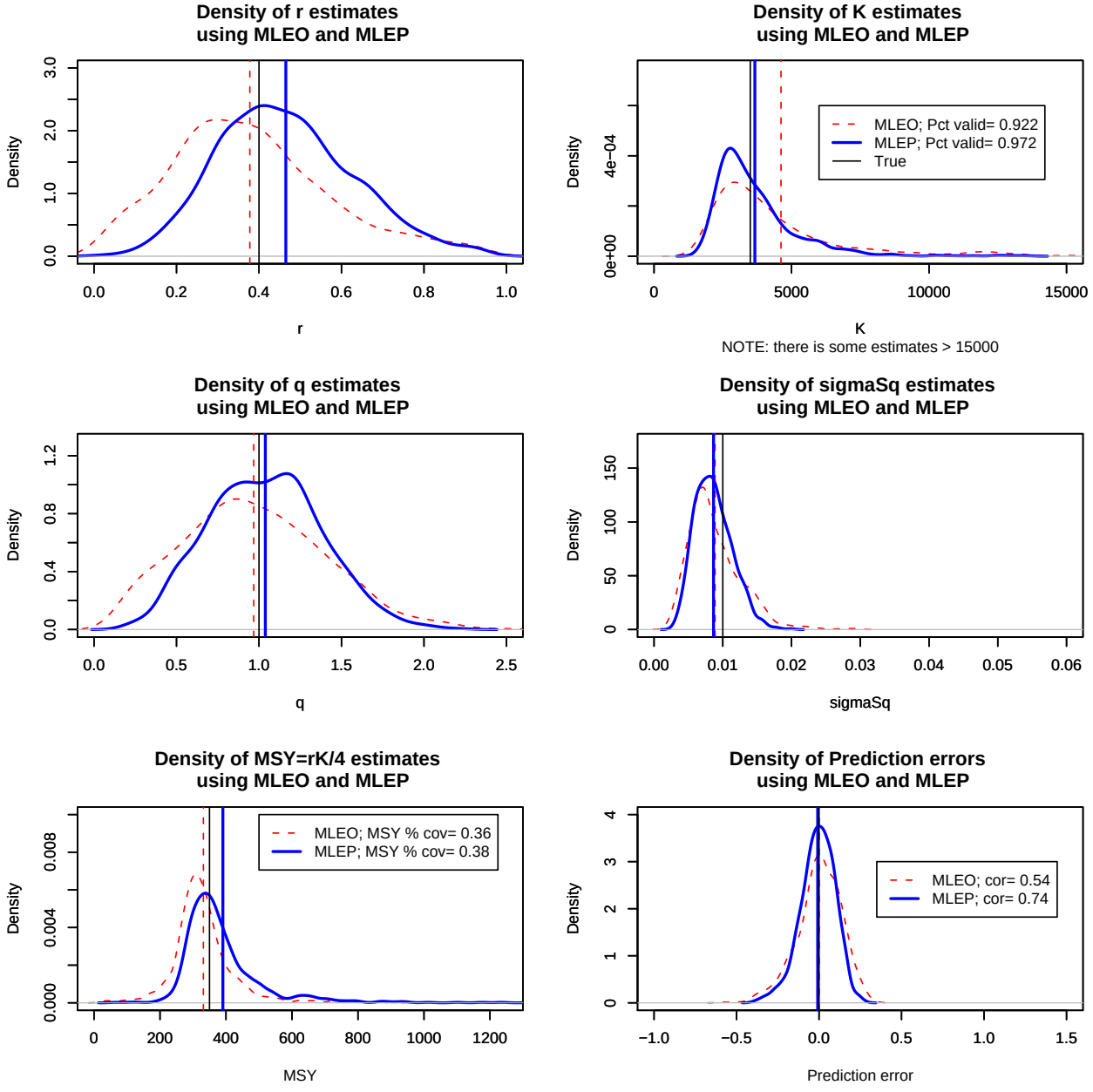


Figure 3.7: These plots show kernel density estimates of the parameter estimates for treatment 6 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.5$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

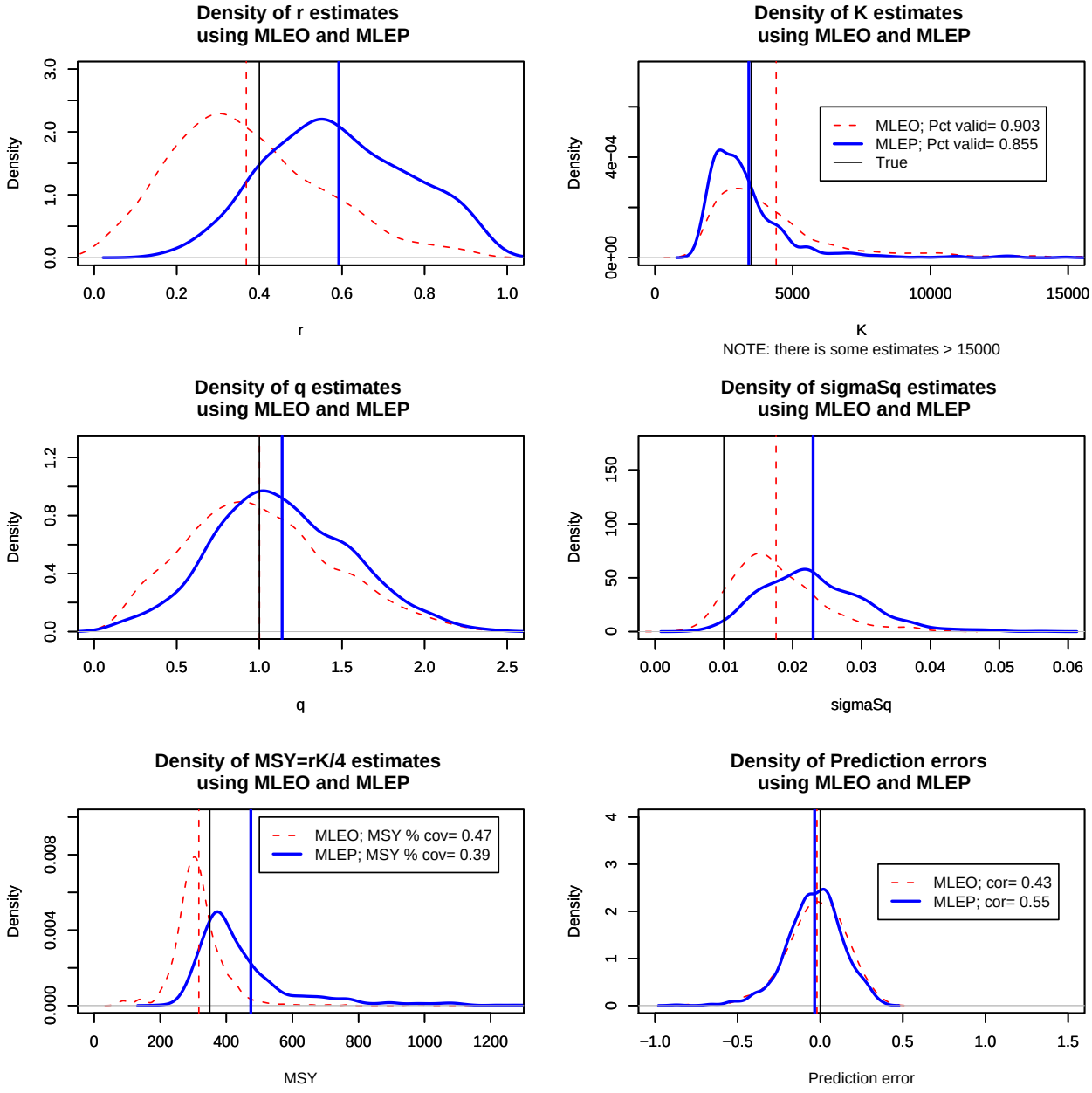


Figure 3.8: These plots show kernel density estimates of the parameter estimates for treatment 7 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.5$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

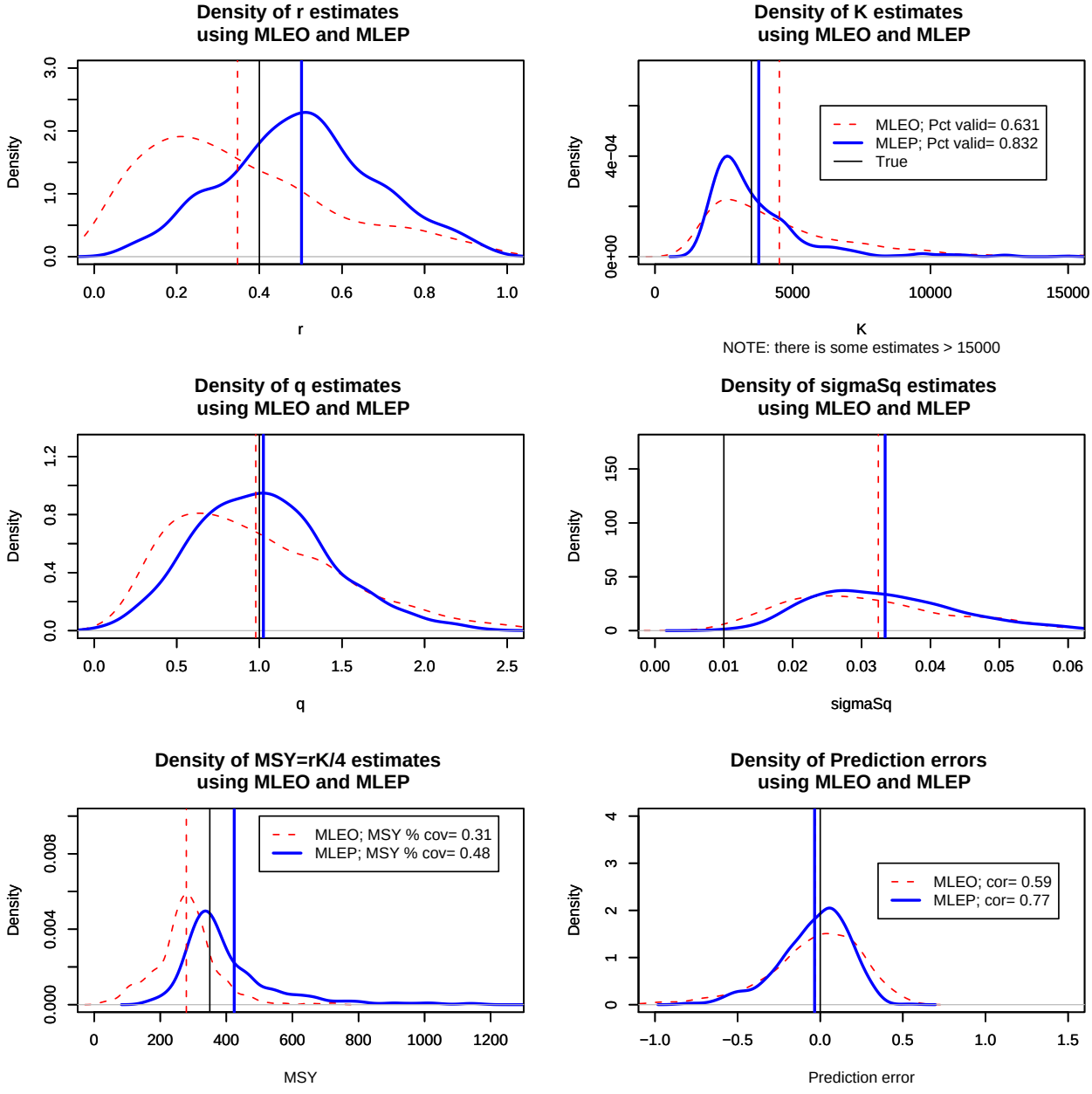


Figure 3.9: These plots show kernel density estimates of the parameter estimates for treatment 8 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.5$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

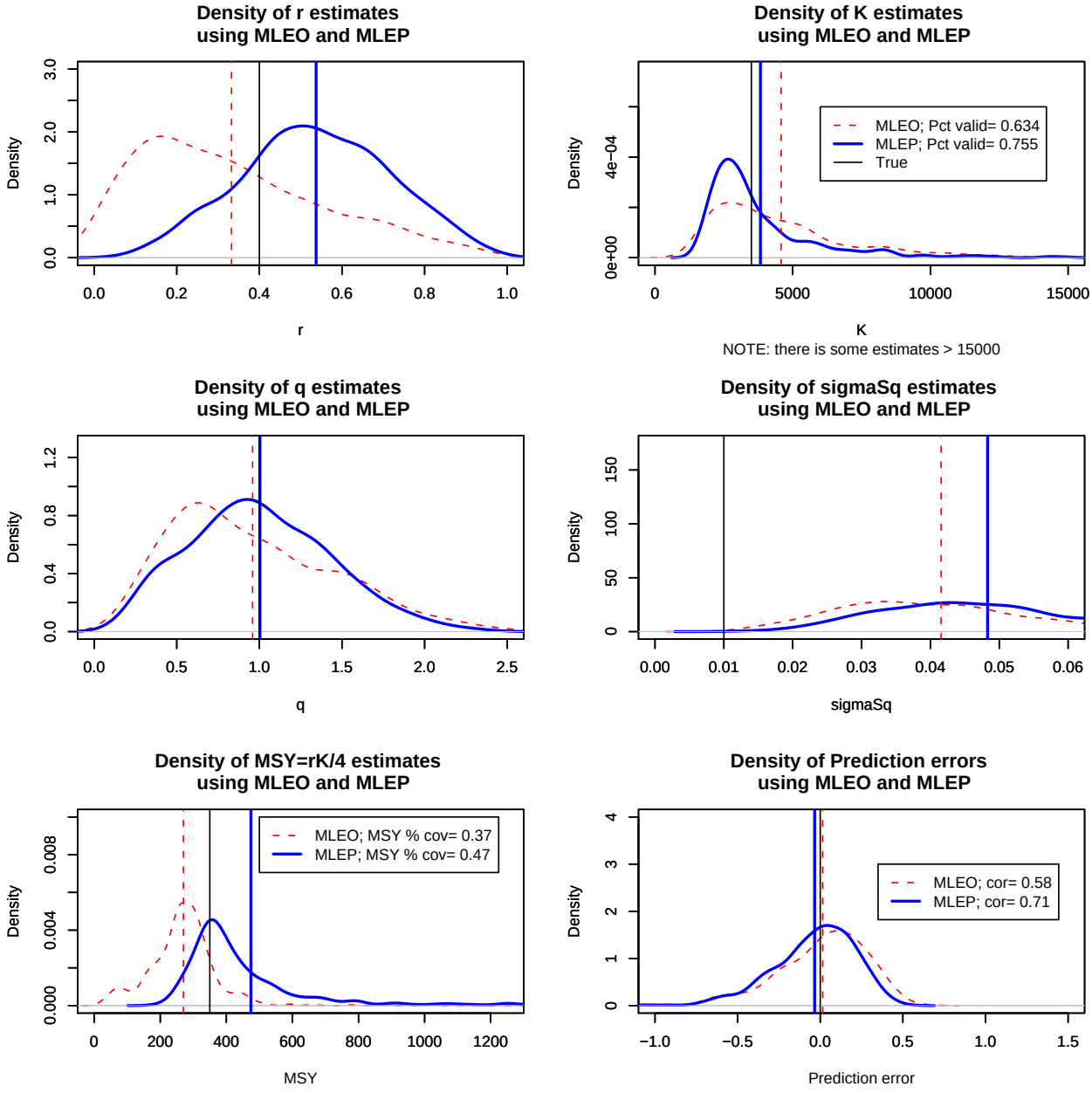


Figure 3.10: These plots show kernel density estimates of the parameter estimates for treatment 9 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.15$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

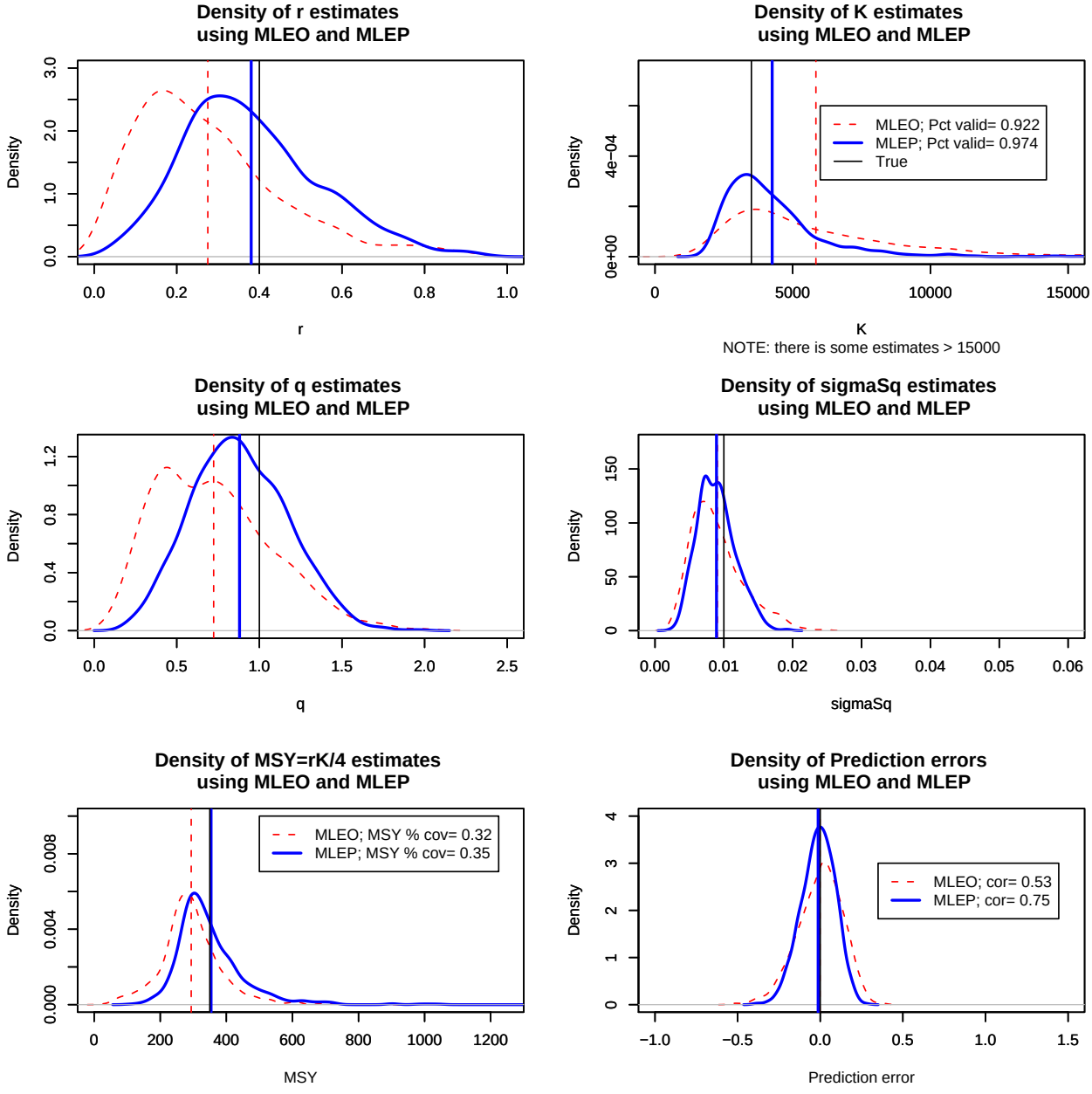


Figure 3.11: These plots show kernel density estimates of the parameter estimates for treatment 10 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.01$ and $\sigma^{*2} = 0.15$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

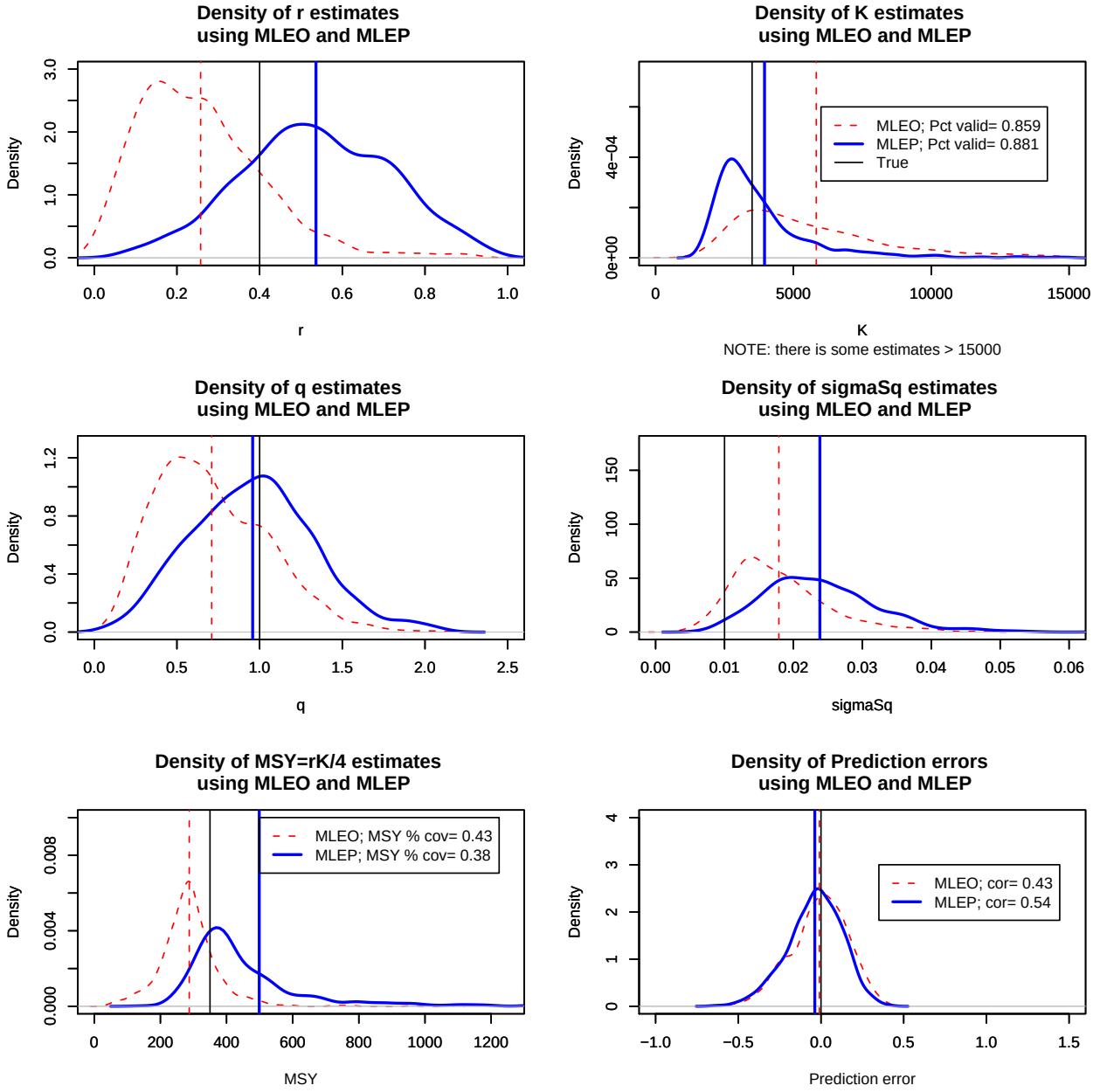


Figure 3.12: These plots show kernel density estimates of the parameter estimates for treatment 11 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.15$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

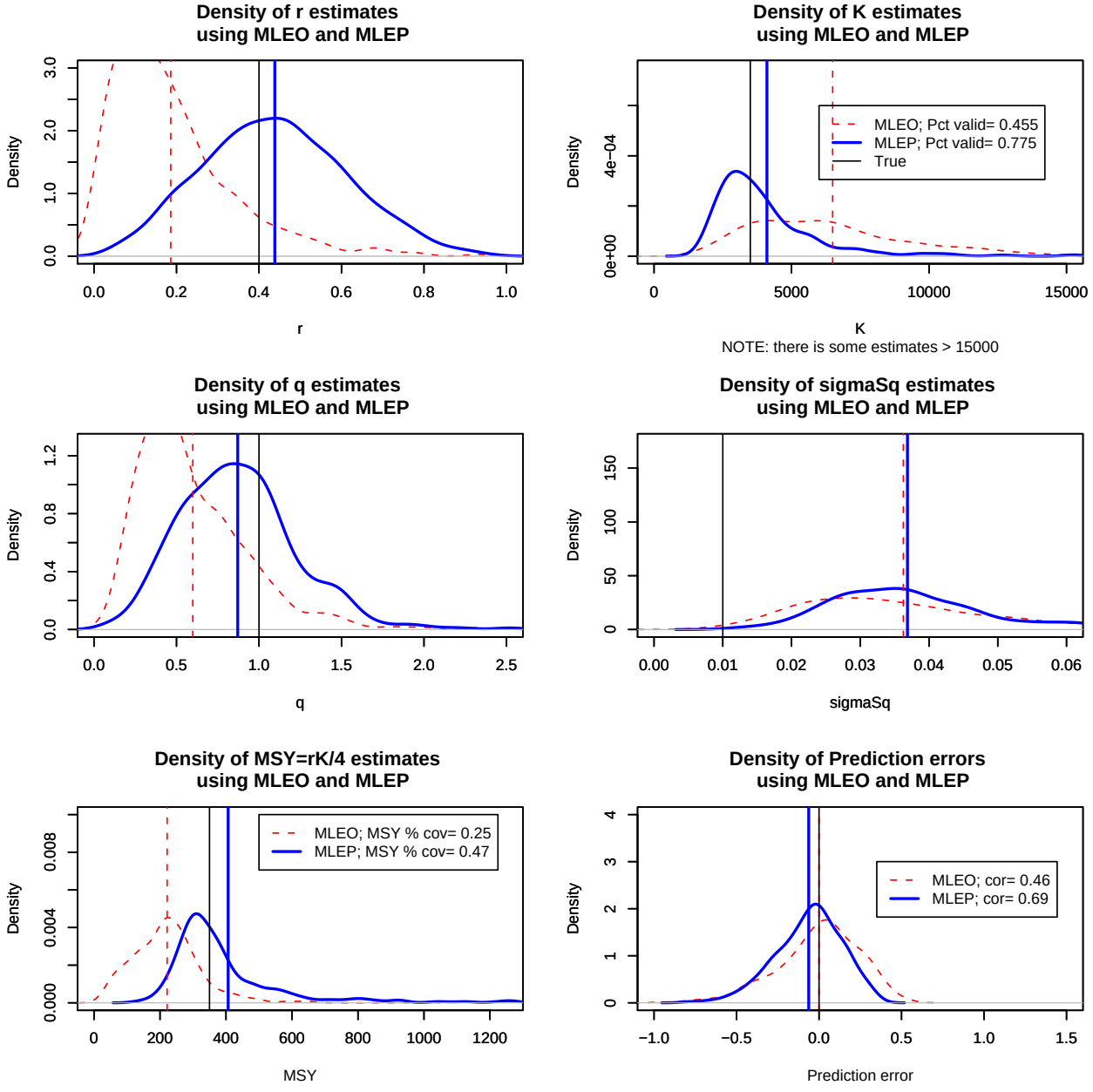


Figure 3.13: These plots show kernel density estimates of the parameter estimates for treatment 12 ($r = 0.4$, $K = 3,500$, $q = 1$, $\tau^2 = 0.01$, $\sigma^2 = 0.04$ and $\sigma^{*2} = 0.15$) using the MLEO and MLEP methods. "Pct valid" gives the proportion of valid optimizations, "% cov" gives the coverage proportion of 95% likelihood ratio intervals and "cor" is the correlation between the predicted and simulated values of a terminal biomass. The solid blue lines and dotted red lines correspond to MLEP and MLEO means, respectively, while the black vertical lines are the true parameter values.

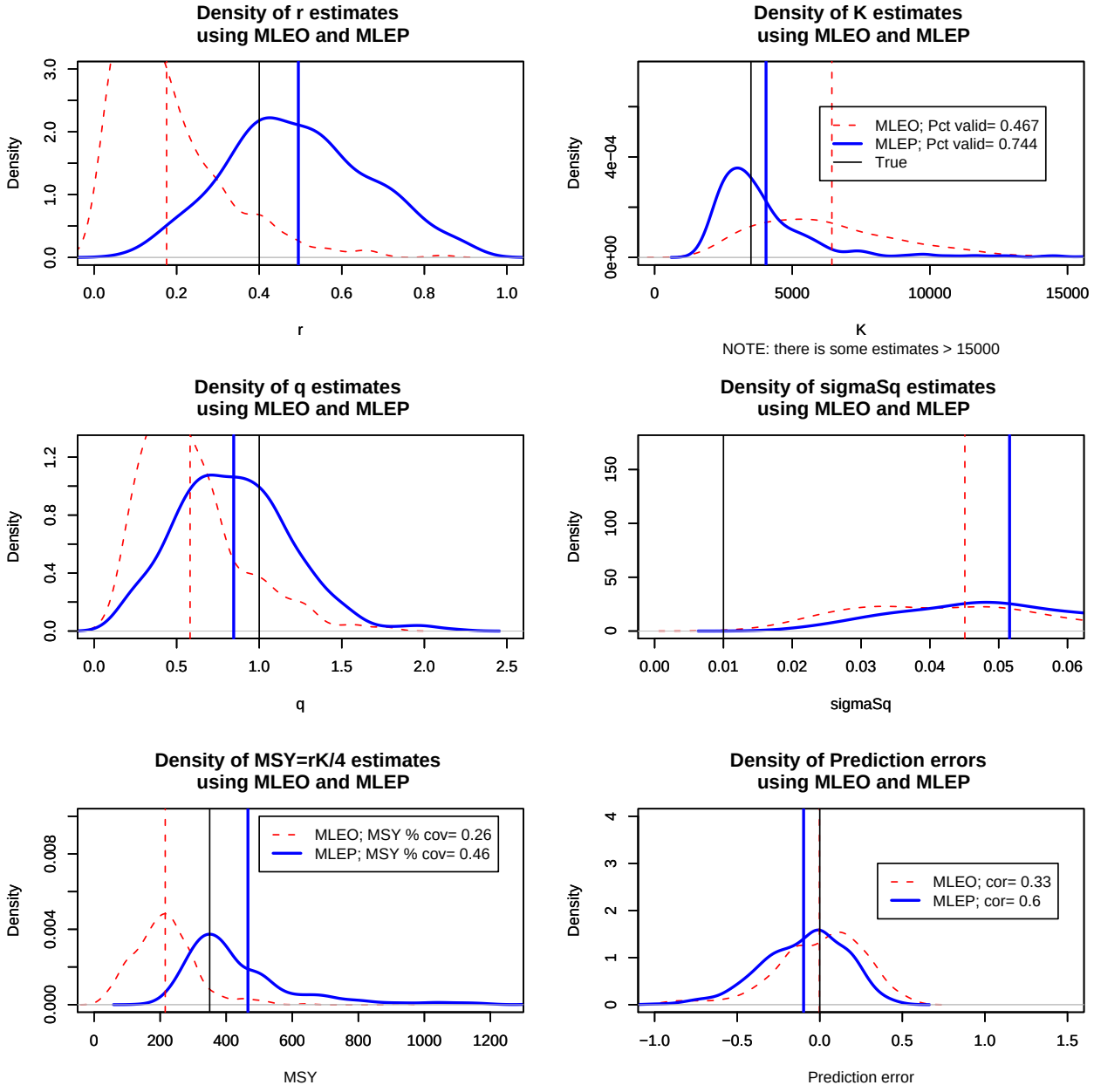


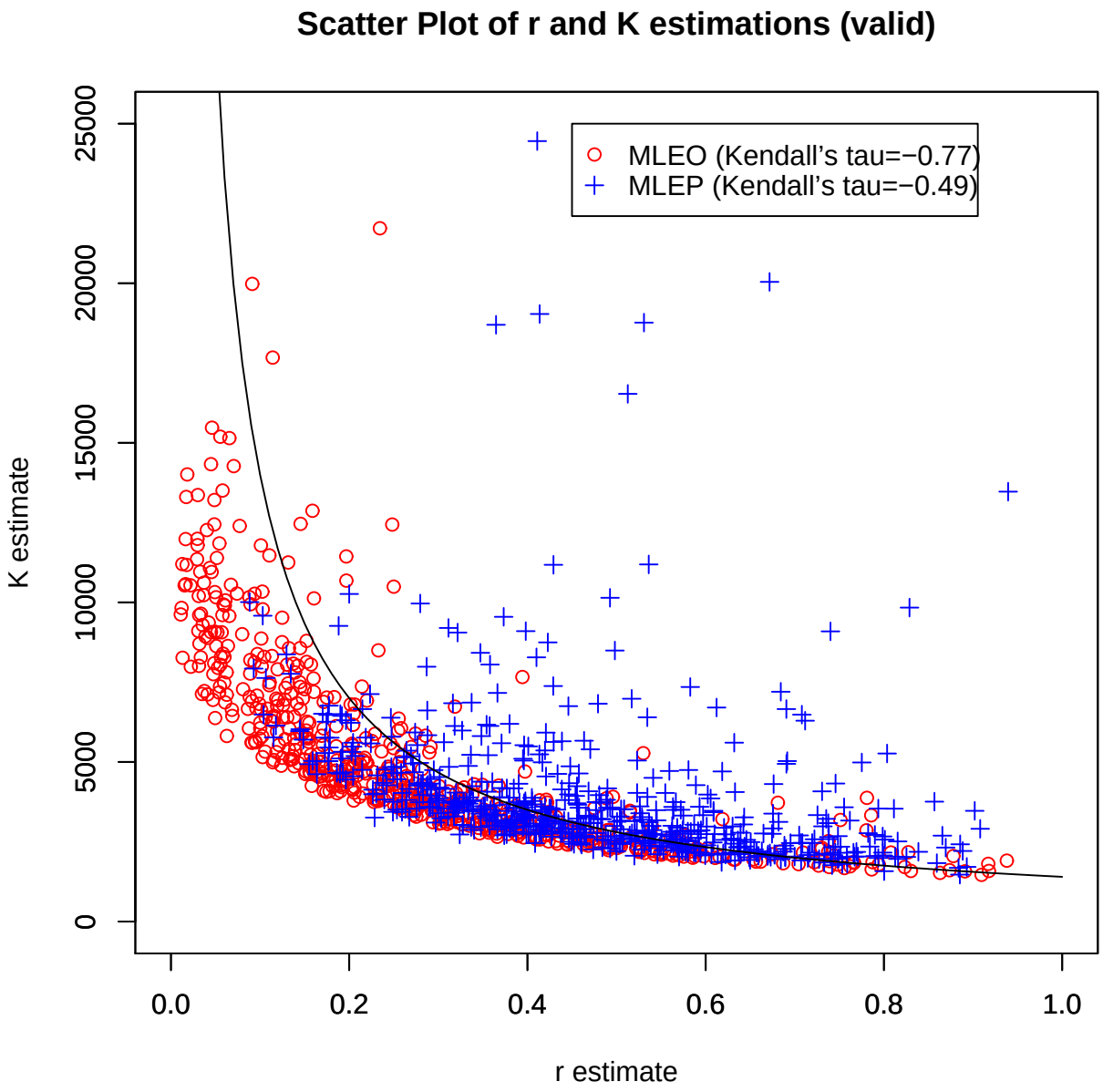
Table 3.2: This table presents the mean (standard error) of the valid estimates from the MLEO and MLEP methods. The values in square brackets next to the parameter names are the true/target values.

Tr.	Method	r [0.4]	K [3500]	q [1]	σ^2 (or τ^2)	MSY [350]	Pred Err [0]
1	MLEP	0.45(0.2)	3936(2225)	1(0.3)	0.0087(0.003)	394(200)	-0.0087(0.1)
	MLEO	0.36(0.2)	4727(2807)	0.91(0.4)	0.0088(0.004)	329(97)	-0.0084(0.1)
2	MLEP	0.58(0.2)	3881(3147)	1.0(0.4)	0.023(0.007)	524(394)	-0.039(0.2)
	MLEO	0.35(0.2)	4923(3089)	0.9(0.4)	0.017(0.006)	325(120)	-0.020(0.2)
3	MLEP	0.47(0.2)	4644(3505)	0.87(0.4)	0.034(0.01)	494(404)	-0.053(0.2)
	MLEO	0.28(0.2)	5299(3054)	0.82(0.5)	0.033(0.01)	265(127)	-0.039(0.3)
4	MLEP	0.53(0.2)	4389(3203)	0.9(0.4)	0.049(0.02)	527(375)	-0.049(0.2)
	MLEO	0.30(0.2)	5172(3013)	0.83(0.5)	0.043(0.02)	275(151)	-0.0037(0.3)
5	MLEP	0.47(0.2)	3804(2426)	1.0(0.4)	0.0087(0.003)	401(188)	-0.0084(0.1)
	MLEO	0.38(0.2)	4627(3167)	0.97(0.4)	0.0089(0.004)	334(102)	-0.00015(0.1)
6	MLEP	0.6(0.2)	3485(2135)	1.1(0.4)	0.023(0.007)	489(302)	-0.036(0.2)
	MLEO	0.39(0.2)	4331(2641)	1.0(0.4)	0.018(0.006)	327(91)	-0.024(0.2)
7	MLEP	0.5(0.2)	4527(5610)	0.95(0.4)	0.034(0.01)	491(489)	-0.031(0.2)
	MLEO	0.34(0.2)	4635(2818)	0.96(0.5)	0.033(0.01)	280(101)	-0.025(0.3)
8	MLEP	0.53(0.2)	4409(3156)	0.94(0.4)	0.048(0.02)	528(384)	-0.041(0.2)
	MLEO	0.33(0.2)	4790(2976)	0.94(0.5)	0.042(0.02)	274(118)	0.011(0.3)
9	MLEP	0.39(0.2)	4347(1953)	0.87(0.3)	0.009(0.003)	366(150)	-0.013(0.1)
	MLEO	0.27(0.2)	5888(3475)	0.72(0.4)	0.009(0.004)	294(96)	-0.0018(0.1)
10	MLEP	0.54(0.2)	4219(3135)	0.93(0.4)	0.024(0.008)	538(468)	-0.039(0.2)
	MLEO	0.27(0.2)	5852(3421)	0.72(0.3)	0.018(0.007)	298(106)	-0.011(0.2)
11	MLEP	0.41(0.2)	5507(4001)	0.71(0.4)	0.038(0.01)	494(396)	-0.046(0.2)
	MLEO	0.18(0.2)	6554(3317)	0.59(0.3)	0.037(0.02)	221(129)	0.008(0.2)
12	MLEP	0.46(0.2)	5219(4259)	0.72(0.4)	0.053(0.02)	552(511)	-0.078(0.3)
	MLEO	0.18(0.1)	6462(2971)	0.58(0.3)	0.046(0.02)	213(100)	0.009(0.3)

Table 3.3: These tables represent summary statistics for the 6 parameters. MSE stands for *standardized Mean Square error* which is $E(\hat{\theta}-\theta)^2/\theta^2$ while MAE stands for *standardized Mean Absolute Error* which is $E|\hat{\theta}-\theta|/\theta$. For the Prediction error, we have not used the standardization because $\theta = 0$. In this particular case $MSE = E(\hat{\theta}-\theta)^2$
and $MAE = E|\hat{\theta}-\theta|$

Tr.	Method	r		K		q		σ^2 (or τ^2)		MSY		Err Pred	
		MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE
1	MLEP	0.21	0.36	0.42	0.35	0.12	0.28	0.088	0.25	0.34	0.25	0.011	0.085
	MLEO	0.24	0.4	0.77	0.54	0.18	0.35	0.17	0.34	0.08	0.2	0.019	0.11
2	MLEP	0.37	0.5	0.82	0.41	0.17	0.33	2.2	1.3	1.5	0.53	0.031	0.14
	MLEO	0.24	0.41	0.94	0.59	0.19	0.36	0.92	0.77	0.12	0.21	0.033	0.14
3	MLEP	0.25	0.4	1.1	0.55	0.18	0.35	0.091	0.25	1.5	0.56	0.047	0.17
	MLEO	0.35	0.51	1.0	0.68	0.25	0.42	0.16	0.34	0.19	0.34	0.085	0.22
4	MLEP	0.32	0.45	0.9	0.52	0.19	0.35	0.2	0.35	1.4	0.58	0.056	0.19
	MLEO	0.34	0.51	0.97	0.66	0.25	0.42	0.2	0.33	0.23	0.34	0.074	0.21
5	MLEP	0.21	0.36	0.49	0.34	0.13	0.29	0.092	0.25	0.31	0.26	0.011	0.084
	MLEO	0.24	0.39	0.92	0.54	0.19	0.35	0.16	0.33	0.087	0.2	0.019	0.11
6	MLEP	0.44	0.54	0.37	0.35	0.19	0.35	2.2	1.3	0.9	0.44	0.030	0.13
	MLEO	0.24	0.4	0.63	0.48	0.2	0.36	1	0.8	0.073	0.19	0.032	0.14
7	MLEP	0.30	0.44	2.7	0.56	0.19	0.35	0.096	0.26	2.1	0.52	0.044	0.16
	MLEO	0.35	0.5	0.75	0.58	0.26	0.42	0.16	0.34	0.12	0.28	0.081	0.22
8	MLEP	0.33	0.47	0.88	0.53	0.20	0.37	0.2	0.33	1.5	0.58	0.063	0.19
	MLEO	0.35	0.5	0.86	0.61	0.25	0.42	0.17	0.32	0.16	0.30	0.076	0.22
9	MLEP	0.19	0.35	0.37	0.38	0.11	0.27	0.087	0.24	0.19	0.25	0.011	0.083
	MLEO	0.30	0.47	1.5	0.78	0.2	0.38	0.16	0.33	0.1	0.25	0.019	0.11
10	MLEP	0.34	0.47	0.84	0.45	0.15	0.31	2.5	1.4	2.1	0.6	0.029	0.13
	MLEO	0.28	0.45	1.4	0.76	0.2	0.38	1.1	0.81	0.11	0.26	0.031	0.14
11	MLEP	0.20	0.37	1.6	0.71	0.21	0.39	0.093	0.24	1.4	0.58	0.042	0.16
	MLEO	0.43	0.6	1.7	0.93	0.28	0.47	0.17	0.33	0.27	0.44	0.061	0.19
12	MLEP	0.22	0.37	1.7	0.64	0.21	0.38	0.27	0.41	2.5	0.67	0.071	0.20
	MLEO	0.43	0.6	1.4	0.9	0.27	0.46	0.23	0.36	0.24	0.43	0.082	0.22

Figure 3.14: This plot shows the correlation between r and K for the estimates in treatment 3. We do not present results for other treatments because they are very similar. The black solid line represents the relation $MSY = rK/4$ or more precisely $K = 4 * 350/r$.



3.3.3 Interpretation of results

We can first try to compare the performance of MLEO and MLEP by interpreting Figures 3.2-3.13. Clearly, when $\sigma^{*2} = 0.15$ (Figures 3.10-3.13) (and hence the shape of the biomass trajectory is close to that of the catch series), MLEO is way off the mark and MLEP is a clear winner. This is probably due to the fact that the MLEP is based on the simulation model. Facts that are common to all other cases (Figures 3.2-3.13) include

- Estimates of K are better with MLEP than with MLEO.
- Estimates of r are better in terms of bias with MLEO than with MLEP.
- The terminal biomass predicted by MLEP is more correlated with the biomass simulated from the model than the terminal biomass predicted by MLEO.
- Estimates of r and K are still highly correlated (see Part **??**). The correlation pattern is also stronger with the MLEO.

Then there are conclusions that can be drawn in most, but not all, of the first 12 figures:

- The proportion of valid estimates is greater with MLEP than MLEO.
- Estimates of q are better with MLEP than with MLEO.
- MLEO is better at giving a point estimate of MSY but likelihood ratio intervals have slightly better coverage with MLEP (though neither method yields coverage that is anywhere near the 95% nominal level).

Finally, some other remarks inspired by Figures 3.2-3.9:

- MLEP is very close to the true model when $\tau^2 = 0$. Not surprisingly, in those cases MLEP seems to get better than MLEO as σ^2 increases.
- As we add observation error, estimators of r under MLEP deteriorate. Estimators of the other parameters are also affected, but not as badly. Note that when $\tau^2 > 0$, MLEP's estimate of σ^2 is actually an estimate of roughly $\sigma^2 + \tau^2$, which is what transpires from Figures 3.3, 3.5, 3.7 and 3.9.

Now we can assess the effect of the three variability parameters from the tables.

- Effect of σ^2: When the variability in process error increases, the bias in the parameter estimates generally increases except for parameter r in the case of MLEP and r and MSY in the case of MLEO. The MSE/MAE of all parameter estimates tend to dramatically increase for MLEP and moderately increase for MLEO.

- Effect of σ^{*2}: Going from $\sigma^{*2} = 0.3$ to $\sigma^{*2} = 0.5$ did not have much of an impact on any parameter estimate. However going $\sigma^{*2} = 0.3$ to $\sigma^{*2} = 0.15$ induced serious bias in MLEO.

- Effect of τ^2: When we go from no observation error to small observation error, there is a small increase in the bias of the r and MSY estimates under MLEP and a major increase in the MSE/MAE of all estimates under MLEP; bias and MSE/MAE of parameters under MLEO barely change.

3.4 Discussion

The main conclusions that can be drawn from this report are that

1. Restricting the parameters to the proper parameter space when maximizing the likelihood function greatly helps in getting valid estimators under both MLEO and MLEP. It is worth noting that the number of valid estimations was almost always slightly greater with MLEP than with MLEO, which is not surprising as MLEP was closer to the true model from which the data were simulated than MLEO.

2. Conditioning on the subsequent catch greatly limits the number of biomass trajectories that dip below zero during simulations.

3. The impact of conditioning on the subsequent catch by fixing the exploitation rates depends on the variability allowed in the exploitation rates. If the variability is very small, then the simulated biomass series follow the catch series more closely than the SPM model and the parameter estimates exhibit more bias. This seems to be more of a problem with MLEO than with MLEP.

4. Except in the case $\sigma^{*2} = 0.15$, MLEO was surprisingly robust to process error, especially in point estimation of r and MSY.

5. Coverage of likelihood ratio intervals under both MLEO and MLEP was always well below the nominal 95% level, and was usually slightly better with MLEP than with MLEO. Is this due to the fact that the chi-square with one degree of freedom approximation to the distribution of the likelihood ratio statistic was used despite the small sample of 23 observations?

6. Comparison of the performance of MLEO and MLEP on the basis of the correlation between simulated and predicted biomasses is of little value, as the model from which biomasses are simulated is almost the model on which MLEP is based. But one could argue that with process error, MLEP seems to be slightly better at predicting the next biomass than MLEO in most of the cases considered.

7. The correlation between r and K seems to still be a problem. The results suggest that the data are more informative in terms of the MSY than r and K.

These conclusions raise a few questions, such as why is MLEO so good at estimating r and MSY, or can fitting a model with two errors (observation and process) help in getting better confidence interval coverage? Thus, as future work, our first priority will be on implementing maximum likelihood estimation of SPM with both process and observation error. Perhaps this will enable us to take advantage of the good properties of both models, as well as to get better coverage of the confidence intervals. Then, the next step will consist in modifying the methods such that they can handle misreported catches.

3.5 References

Hammond, T. R., and Trenkel, V. M. (2005) *Censored-catch data in fisheries stock assessment*. ICES Journal of Marine Science, **62**: 1118–1130.

Punt, A. E. (2003) *Extending production models to include process error in the population dynamics*. Can. J. Fish. Aquat. Sci. **60** : 1217–1228.

Lemay, J., Duschesne, T. , Rivest, L.-P. (2006) *Review of methods to account for misreported catches in surplus production models using censored-observation methods.* Scientific work, Laval University.

Nelder, J. A. and Mead, R. (1965) *A simplex algorithm for function minimization.* Computer Journal **7**, 308-313.

Polacheck, T., Hilborn, R., and Punt, A.E. (1993) *Fitting surplus production models: comparing methods and measuring uncertainty.* Can. J. Fish. Aquat. Sci. **50**: 25972607.

Robert, P.R, Casella, G. (2004) *Monte Carlo Statistical Methods.* Springer Texts in Statistics, New York: Springer.

Nelder, J. A. and Mead, R. (1965) *A simplex algorithm for function minimization. Computer Journal* **7**, 308-313.

Part 4

Bayesian Inference for Censured data using the SPM

4.1 Introduction

The purpose of this report is to present the results of simulation studies that were conducted to validate the approach proposed by Hammond and Trenkle (2005) (henceforth referred to as HT) to estimate the parameters of the surplus production model (SPM). These authors propose a method that takes into account the fact that reported landings are usually a lower bound to the true size of the catches. To make inferences about the model and population parameters under this censored-catch[1] approach, they rely on Bayesian inference methods. Our main objective is to investigate the overall validity of this approach by simulation; proceeding in this manner is appropriate since (i) theoretical properties of estimators in this context are difficult to derive and, at best, will be based on asymptotic results (i.e., assuming very large samples) and (ii) by simulating the model, we know the true parameter values and we are thus able to directly assess the accuracy of the inferences.

4.1.1 Specific objectives

We divide our investigation of the HT approach into two main objectives:

1. To assess whether the censored-catch approach is efficient.

2. To validate the use of a Bayesian approach.

In order to achieve objective 1, we simulated data under three setups: (i) SPM with no misreporting (i.e., catches and landings equal); (ii) very volatile misreporting (i.e., landings represent a proportion of catches, with this proportion varying between 40% and 100%, as in HT); (iii) volatile misreporting (i.e., landings represent a proportion of catches, with this proportion varying between 62.5% and 70%). Three different models were fitted to the simulated datasets by Bayesian inference: (a) a regular SPM that does not take misreporting into account; (b) the SPM proposed by HT, which assumes that catches are a function of fishing effort and are censored between landings and twice the landings; (c) same as HT, but without taking fishing

[1] In statistics, "censoring" refers to the fact that only partial information on the value of an observation is available, not its actual exact value. In the catch vs landings example, the true catch might not be known, but the reported landings certainly give a lower bound to the value of the true catch.

effort into account. All the simulation details (models, results) as well as our analysis of these results are given in Chapter 3. Though no general conclusion can be drawn, it looks as though the HT method works best if the catches are indeed misreported, while both the HT method and the standard SPM work well when there is no misreporting.

To tackle objective 2, we studied the sensitivity of the inferences to the choice of prior distributions. The rationale behind this idea is that if parameter estimators are highly sensitive to changes in prior distributions, this implies that the data do not contain enough information to conduct precise inferences about these parameters. If this is the case, then frequentist inference methods (such as maximum likelihood) or Bayesian inference based only on uninformative priors might be more appropriate. In order to do so, we fitted a standard SPM to the dataset on South Atlantic albacore tuna (1967-1989) presented by Meyer and Millar (1999) using several combinations of prior distributions for the various parameters of the model; these priors were derived by modifying the mean and variance of the prior distributions used in the Meyer and Millar (1999) analysis. The main conclusion of this part of the study is that some of the SPM parameters are indeed sensitive to the specification of the prior distributions.

The remainder of this report is organized as follows. Background information on SPM and Bayesian inference are given in Chapter 2. A simulation study carried out to compare the effect of correction for misreporting in SPMs is described and analyzed in Chapter 3. The assessment of the sensitivity of inferences to prior distributions is done in Chapter 4. A discussion of the results as well as ideas for future investigations conclude the report in Chapter 5.

4.2 Surplus production model and Bayesian estimation

In this chapter we give background information on the SPM and Bayesian estimation methods that will be used in the two studies of chapters 3 and 4.

4.2.1 The Surplus Production Model (SPM)

We investigate the Schaefer annual SPM,

$$B_{t+1} = B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t, \tag{4.1}$$

where B_t represents the biomass (e.g. 1000 tons) in year t, r is the intrinsic population growth rate parameter, K is the virgin population biomass (or the biomass when the population is in equilibrium) and C_t represents the catches in year t (1000 tons).

Stock biomass usually cannot be measured explicitly to estimate the r and K parameters in (4.1). Additional information is required to estimate these parameters. Often a CPUE time series is used, but a research survey biomass index is also commonly used. We need a second equation to include the information provided by a survey index,

$$I_t = q_s B_t, \tag{4.2}$$

where I_t corresponds to the survey index at time t, and q_s represents the fish catchability in the survey. The parameters to estimate are r, K and q_s.

The above model is deterministic; that is, it does not include any error. However, we consider at least to kinds of error:

1. observation errors (within the CPUE equation (4.2)),

2. process errors (within the dynamic equation (4.1)).

The observation errors imply that the surveys are not perfect while the process errors imply that the SPM cannot exactly reflect the reality.

We consider the same setting as HT; that is, an SPM model with lognormally distributed observation errors and normally distributed process errors. Including the error terms and using a little modification, the model can be written as

$$\begin{aligned} P_{t+1} &= P_t + rP_t(1 - P_t) - C_t/K + \varepsilon_{t+1}; & (4.3)\\ I_t &= q_s K P_t \varepsilon_t^*, & (4.4) \end{aligned}$$

where $P_t = B_t/K$, $\varepsilon_t \sim \mathbf{N}(0, \sigma^2)$ and $\log(\varepsilon_t^*) \sim \mathbf{N}(0, \tau^2)$.

Another interesting aspect of the SPM is how easy it is to obtain some management parameters. For example, the *maximum sustainable yield* (MSY) is easily derived from the model and is equal to $rK/4$. This parameter will be used later in a comparison between estimation methods.

The SPM is based on some important assumptions. For example, the population intrinsic growth rate (r) and the fish catchability (q_s) do not depend on time. Finally, it is important to note that this model does not include any information on age, but some others, such as virtual population analysis (VPA) models can (see, e.g., Cadigan and Farrell, 2005).

4.2.2 Bayesian inference and SPM

Bayesian inference is a statistical way of thinking that often appears in problems with few observations. Bayesian analysis relies on Bayes' rule, which states that for two events A and B,

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}.$$

In a Bayesian analysis, parameters to be estimated in a model are considered as random variables. Information about the distribution of these random variables that is available **before** data collection is quantified in the *prior distribution* of the parameters. When data are collected, Bayes' rule is used to get the distribution of the parameters given the observed data, the so-called *posterior distribution*. In the Bayesian paradigm, all inferences are based on the posterior distribution of the parameters. Mathematically, if the data are distributed as $f(\underline{\mathrm{x}}|\underline{\theta})$, where $\underline{\theta}$ represents the model parameters, and $\pi(\underline{\theta})$ is the prior distribution, then the posterior distribution of $\underline{\theta}$ given the data is

$$g(\underline{\theta}|\underline{\mathrm{x}}) = \frac{f(\underline{\mathrm{x}}|\underline{\theta})\pi(\underline{\theta})}{f(\underline{\mathrm{x}})}, \tag{4.5}$$

with $f(\underline{\mathrm{x}}) = \int f(\underline{\mathrm{x}}|\underline{\theta})\pi(\underline{\theta})d\underline{\theta}$. Point estimates of the parameters are usually taken as the mean value of these parameters under the posterior distribution, while confidence intervals are given by percentiles (e.g., 2.5th and 97.5th percentiles) of the posterior distribution. Bayesian analysis is often used when few data are available; in these cases, information additional to that

provided by the data is useful and should be included in the analysis, which is done through prior distributions in that case.

In the case of the SPM of Section 2.1, the unknown parameters are $\underline{\theta} = (K, r, q_s, \tau^2, \sigma^2, P_1, \ldots, P_N)$, the data are $\underline{\mathrm{x}} = \{(I_t, C_t), t = 1, \ldots, N\}$ and $f(\underline{\mathrm{x}}|\underline{\theta})$ is the joint distribution of the data given the parameter values (Meyer and Millar, 1999, eq. (9)):

$$f(\underline{\mathrm{x}}|\underline{\theta}) = \left\{ \prod_{t=2}^{N} f_P(P_t|P_{t-1}, C_{t-1}, K, r, \sigma^2) \right\} \left\{ \prod_{t=1}^{N} f_I(I_t|P_t, q_s, \tau^2) \right\}. \tag{4.6}$$

Now if we substitute $f(\underline{\mathrm{x}}|\underline{\theta})$ given by (4.6) into (4.5), then no matter what we choose as the prior distribution for the parameters, the evaluation of $f(\underline{\mathrm{x}}) = \int f(\underline{\mathrm{x}}|\underline{\theta})\pi(\underline{\theta})d\underline{\theta}$ will not be feasible in closed form. In this type of situation, Markov Chain Monte Carlo (MCMC) algorithms, such as the Gibbs sampler (Robert and Casella, 2004, Chapter 9), are used to simulate observations from the posterior distribution, from which we can derive values for the posterior mean and percentiles; Meyer and Millar (1999) discuss how Bayesian SPMs can be fitted with the Gibbs sampler using the BUGS software.

4.3 Comparison of methods to account for misreported catches

4.3.1 Introduction

Assessments of international (i.e. straddling) stocks are often complicated by incomplete information on fishery catches, more so than for purely domestic stocks. This is because of the difficulties in monitoring and accessing information about catches taken by some foreign fleets. Also, when fishing quotas are restrictive and market conditions are good then there may be economic incentives to misreport catches. Often reported catches are considered to be underestimates of the actual catches, but over-reporting of catches occasionally occurs for some fleet sectors.

Information on commercial catches is usually a fundamental component in a stock assessment. Tracking how changes in catches affect a stock size index, such as a research survey

index of relative abundance or catch per unit of effort (CPUE), is the basis of most stock assessments. Examples of analytic assessment models are age-aggregated surplus production models (SPM's), and age disaggregated virtual population analysis (VPA). A SPM is a simple description of how stock biomass responds to harvesting. It does not explicitly account for stock reproduction, growth, age-structure, or natural mortality. In VPA, information on fishing and natural mortality are used to quantify the size of historic cohorts. If a stock size index that covers the historic and current periods is also available then the index to stock size ratio for the historic period can be estimated and used to convert the current stock size index to absolute stock size. VPA provides of estimates of stock recruitment rates which can be used to forecast future stock size and evaluate stock productivity characteristics.

It is well known that SPM's and VPA's are sensitive to errors in reported catches. Examples of simulation and sensitivity studies are given by Lapointe, Peterman, and MacCall (1989), Megrey (1989), Rivard (1989), Mohn (1999), and Cadigan and Farrell (2005). These studies involve examining the impact of errors in reported catches in stock assessment models that assume catches are known without error. They do not propose methods to accommodate erroneous catches. Some stock assessment models explicitly incorporate errors in landings or catch-at-age (e.g. ICA, Stock-Synthesis); however, the errors are assumed to be of a measurement-type in which reported catches, while uncertain, are unbiased. This measurement-error approach is not appropriate for dealing with misreported catches.

Catch-free stock assessment models (e.g. SURBA; Beare et. al. 2005) have been used to deal with misreported landings. These methods appear to sensitive to some modelling assumptions, and their accuracy is poor in some situations. We suggest that ignoring reported landings and catch sampling information is too drastic in some situations.

Recently, Hammond and Trenkel (2005) used the theory of Bayesian censored estimation methods with a simple formulation of an SPM to address misreported catches. In this context censored is taken to mean truncated, and in the SPM application the catches were assumed to be under-reported. The method may offer a very reasonable way to address uncertainties in reported catches and may be a good compromise between assuming landings are uninformative (e.g. SURBA) and assuming landings are exact (e.g. VPA); however, further studies are

required.

4.3.2 Censored data

In some situations, especially in human clinical studies, the variable of interest is not observed exactly, but is represented as an interval. This is often the case when our interest is time-to-event data. Sometimes, the time-to-event cannot be observed due to financial restrictions or mortality. In these cases, the observations are intervals (e.g., $[t, \infty), (\infty, t]$, or $[t_1, t_2]$).

The use of censored data methods can also be applied to fisheries (see HT). The catch data may be greater than reported for various reasons (discards, misreporting, black market, etc). In these situations we can consider that the *true-catch* is in the interval $[L_t, 2L_t]$, where L_t represents the landings in year t. This indicates that the real catch lies between the total landings and twice the total landings, but we don't know exactly where. The upper bound of $2L_t$ is rather arbitrarily chosen and may not be appropriate in all cases. It will be important to examine the sensitivity of our results to this arbitrary value.

4.3.3 Objectives

The objectives are:

1. Graphically compare the use of 3 different methods (described below) to fit a SPM when the catch data are misreported;

2. Graphically compare the same 3 methods when the catch data are **not** misreported;

3. Graphically compare the 3 methods when the catch data are misreported, but **less** than we assume.

Methods to be compared

The first method we will use is the true-catch method (TCM) in which we assume the catch is equal to landings ($C_t = L_t$). This method is the *standard* method used to fit SPM's when we do not consider misreporting (see Meyer and Millar, 1999).

The second method is the censored method described in HT which uses effort data. We denote this method as CCME (censored catch method with effort). Effort data are a time series that represents the effort applied by fishermen to produce their catch. The reason why HT used these effort data is because catch is supposed to be proportional to biomass times effort. In this sense, they modeled the catches as

$$C_t = q_c E_t B_t \xi_t$$

where q_c is the catchability of the commercial fishing (a different quantity than q_s), E_t is the effort applied in year t, and ξ_t is a random error term, were $\log(\xi_t)$ is iid $N(0, \theta^2)$. Note that censoring has been taken into account in the estimation process only. In fact, instead having an exact observations for the C_t, we consider the intervals C_t as lying in $(L_t, 2L_t)$.

The last method is also a kind of censored method but does not require effort data. We explore this because effort data in some situations may not be available or is poorly estimated. In this sense, we model the catches as

$$C_t \sim Unif(L_t, 2L_t).$$

We denote this method as UCCM (uniform censored catch method).

4.3.4 Methodology

We examined each objective using six simulations with different parameter values. For each simulated data set we applied the three methods (TCM, CCME, and UCCM), and then plotted the simulated biomass series, the estimated biomass series (mean posterior density - MPD) along with its 95% credible interval (CI). We also compared the MSY MPD estimate to its "true" simulation value. However, the preliminary number of simulations is clearly insufficient

to conclude much about the MSY estimations. As typical in a Bayesian simulation design, we have simulated both data and parameters. Our simulation design is exactly the same as HT.

Simulation Design

In each of the six simulations, there were eight steps:

1. Simulate a 20 year series of effort (E_t) using the following method:

   i. Simulated 5 numbers from a $Unif(0.2, 1.2)$. These 5 numbers represent the effort data for the $1^{th}, 6^{th}, 10^{th}, 15^{th}$ and 20^{th} years.

   ii. All the other effort data were linearly interpolated between the step i. values.

2. Draw a set of parameters from their priors (see Table 4.1).

3. Create an initial proportion (P_0) of virgin biomass (this assumes that the population was already depleted before the first year). This was done by drawing P_0 from a $beta(20, 6)$.

4. Prior to the simulation of the biomass and catch series, simulate the proportion of the biomass for the first year: $P_1 \sim \mathbf{N}(P_0, \sigma^2)$.

5. In order to add some *hyper-depletion* (see next step), δ is drawn from a $Unif(0.7, 1.3)$. This is not considered in the estimation process.

6. Create the C_t and P_t series.

   i. $C_t \sim \mathbf{logN}\left\{log(q_c E_t P_t^{\delta} K), \theta^2\right\}$

   ii. $P_{t+1} \sim \mathbf{N}\left[\left\{P_t + rP_t(1 - P_t) - C_t/K\right\}, \sigma^2\right]$

7. Simulate landings. Choose one of the following three options for each objective.

   i. Misreporting (objective 1): simulate a mean landing rate, p_L, from a $Unif(0.5, 0.9)$ and then draw a series of $p_L(t) \sim Unif(p_L - 0.1, p_L + 0.1)$, iid for $t = 1, \ldots$.

   ii. No misreporting (objective 2): $p_L(t) = 1$ for all t.

iii. Less misreporting than assumed (objective 3): $p_L(t) \sim Unif(0.625, 0.7)$, iid for $t = 1, \ldots$. The mean landing rates were constant in all 6 simulations.

8. Finally, generate a series of I_t from a lognormal distribution :

$$I_t \sim \mathbf{logN}\{log(q_s K P_t), \tau^2\}$$

Table 4.1: Description of the parameters priors. Note the log normal distribution is described by the mean and variance of its corresponding normal distribution. Also, The gamma distribution has a mean equal to its first parameter divided by its second.

Parameter	Description	Prior	BUGS alias
r	Intrinsic growth rate	logN(-1.4,0.25)	`r`
K	Virgin Biomass	logN(log(700),0.25)	`K`
P_0	Initial P_t	beta(20,6)	`Pinit`
σ^{-2}	Process error Precision	gamma(100,0.05)	`isigma2`
τ^{-2}	Survey Precision	gamma(44,2)	`itau2`
θ^{-2}	Catch model precision	Gamma(70,1)	`itheta2`
q_c	Fleet catchability	beta(5.5,44.5)	`qc`
q_s	Survey catchability	beta(4,8)	`qs`

The **R** code for our simulation design can be found in appendix.

Estimation

Our estimation method is roughly the same as HT. We used a Bayesian approach to estimate parameters. We evaluated the mean of the posterior density of each parameter using the Gibbs sampler within the OpenBugs software. Basically, Openbugs enables us to sample from the posterior density without having any idea of its form; then we can approximate the posterior mean of each parameter by the sample mean of its posterior sample. Additional information on the Bayesian approach and/or the Gibbs sampler is given in, for example, Robert & Casella (2004).

Note that we used the same OpenBugs code as in HT but we randomly generated our initial values from the priors instead of specifying them. We used 20 years time series of landings and survey indices. This is a fairly common amount of catch information. We have obviously adapted the HT code for the third objective.

The OpenBugs code for our estimation can be found in appendix. A good way to understand the differences between the 3 models is to examine this code.

4.3.5 Results

The results are decribed as follows:

Objective 1: (with misreporting), figures 3.1 and 3.2;

Objective 2: (without misreporting), figures 3.3 and 3.4;

Objective 3: (less misreporting), figures 3.4 and 3.5.

In each plot, the dashed line represents the MPD estimate, the solid line represents the simulated true value and the dotted lines represent 95% credible intervals. Plots on the same row are based on the same simulated data set, which is why they have the same MSY value and solid line.

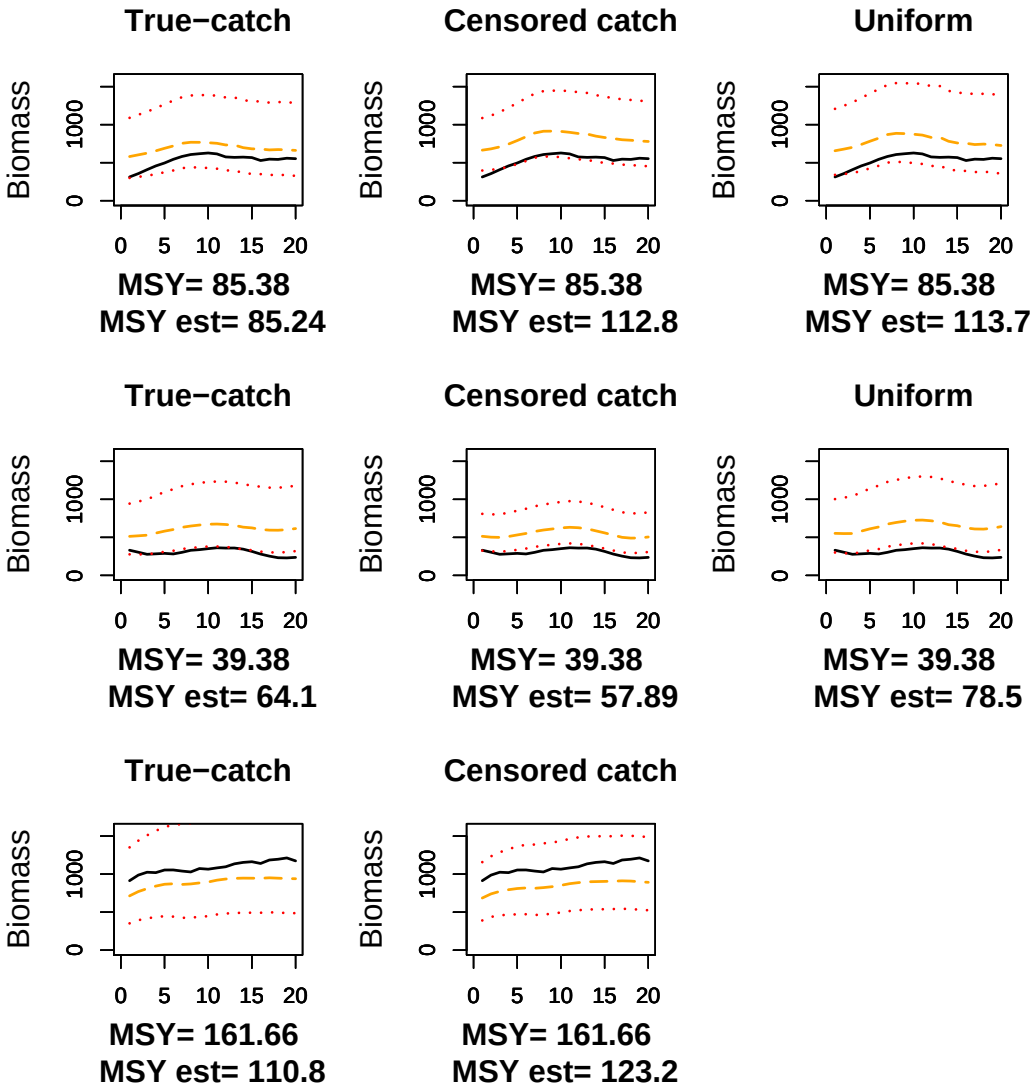


Figure 4.1: **Objective 1: Data with misreporting**. Each plot on a row represents the same simulated set of parameters and data (first 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

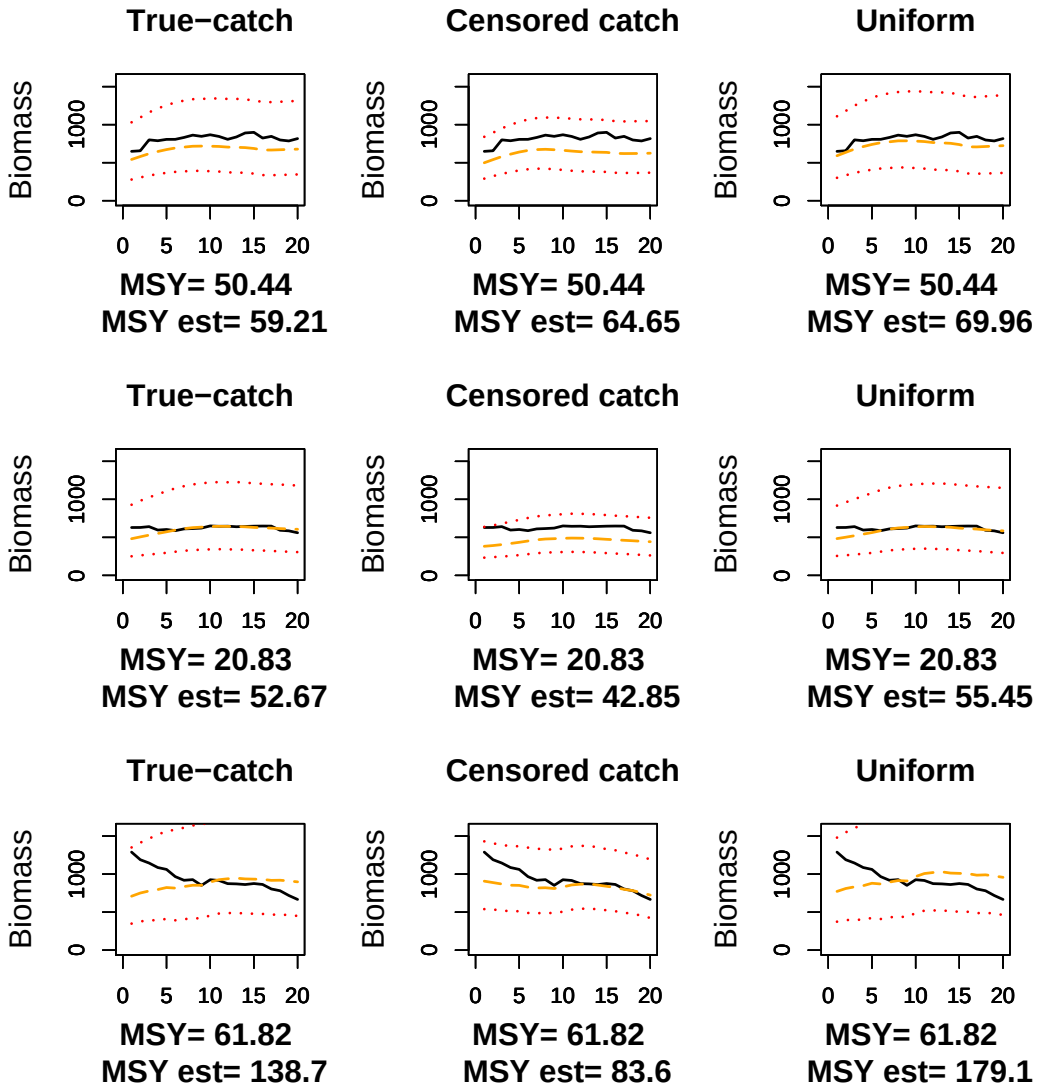


Figure 4.2: **Objective 1: Data with misreporting**. Each plot on a row represents the same simulated set of parameters and data (last 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

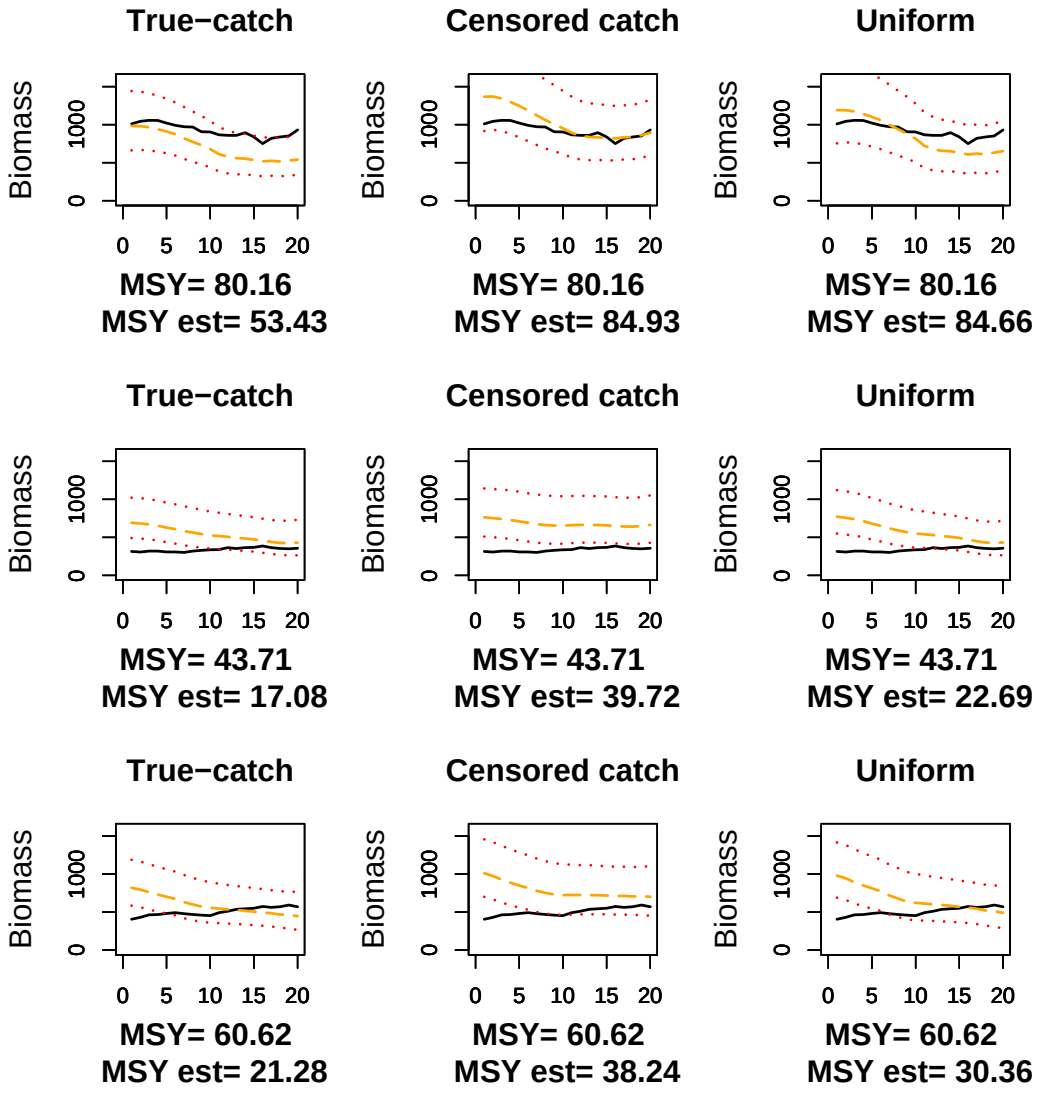


Figure 4.3: **Objective 2: Data without misreporting**. Each plot on a row represents the same simulated set of parameters and data (first 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

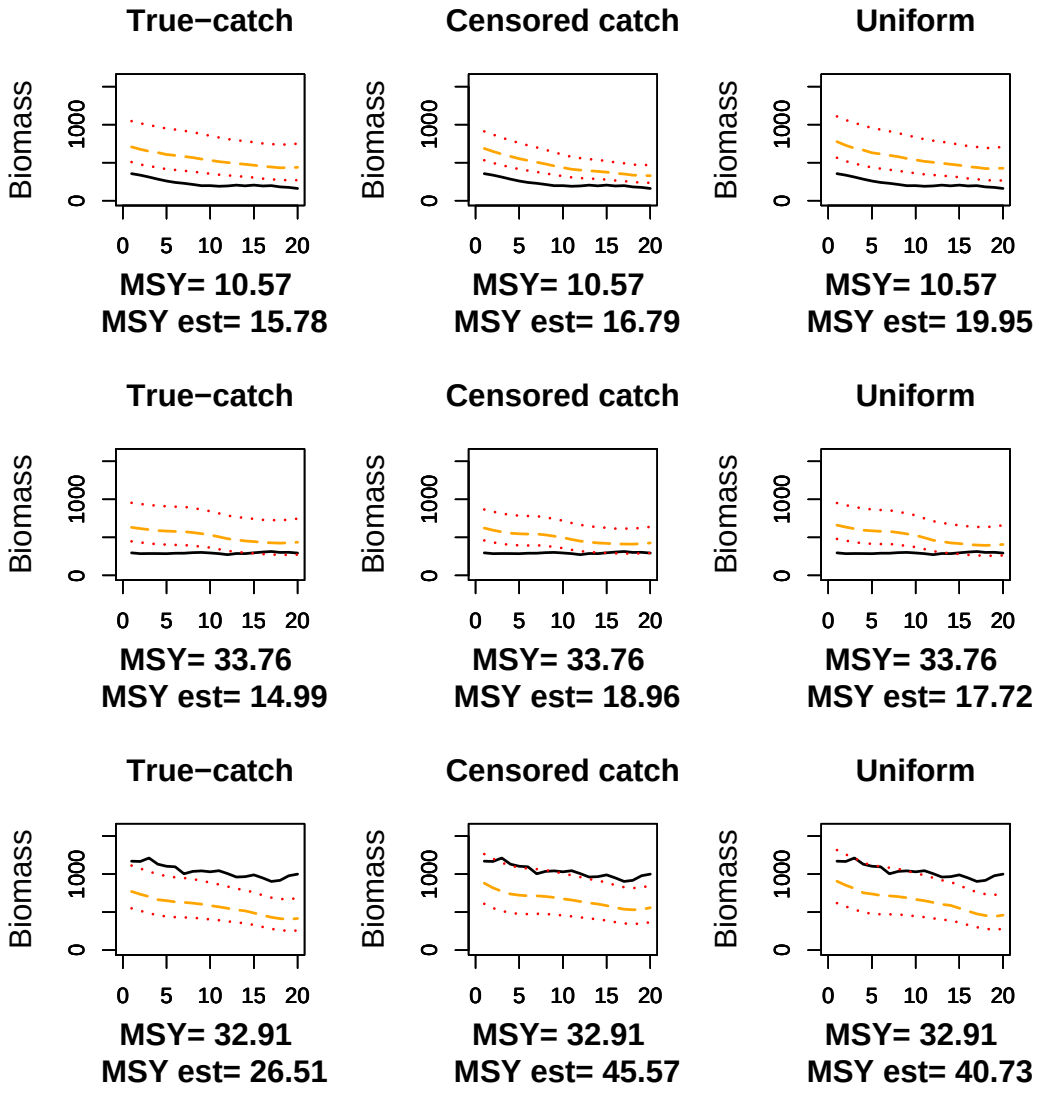


Figure 4.4: **Objective 2: Data without misreporting**. Each plot on a row represents the same simulated set of parameters and data (last 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

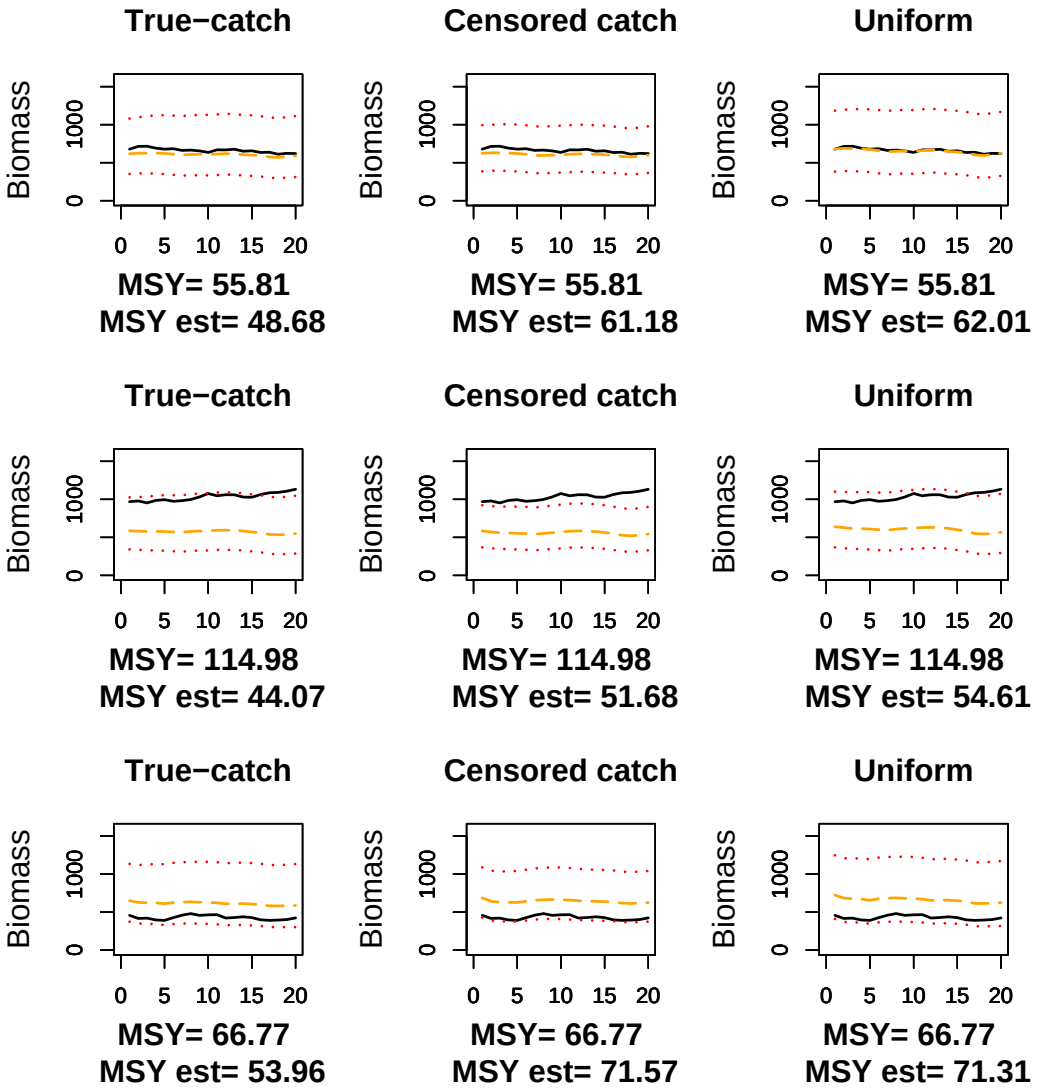


Figure 4.5: **Objective 3: Data with less misreporting**. Each plot on a row represents the same simulated set of parameters and data (first 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

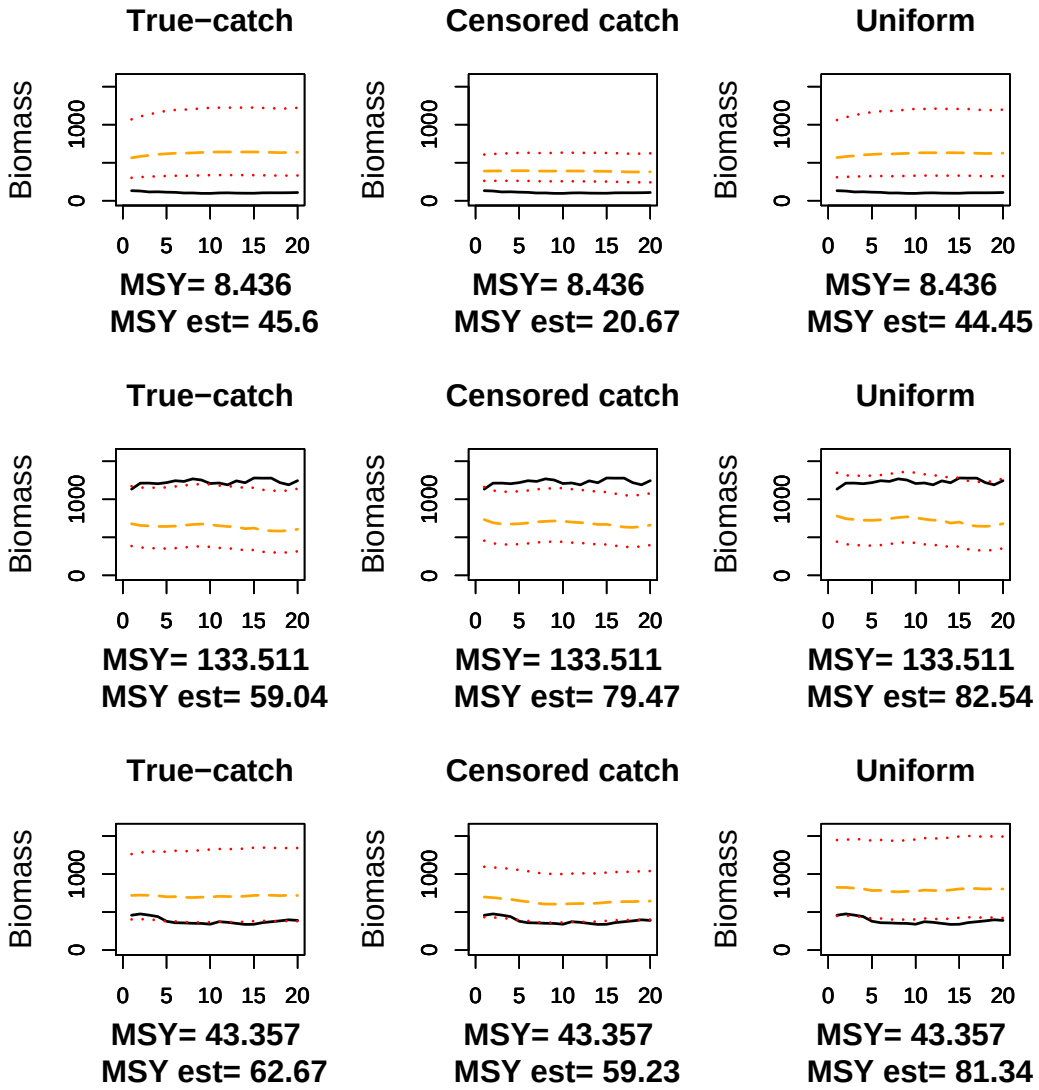


Figure 4.6: **Objective 3: Data with less misreporting**. Each plot on a row represents the same simulated set of parameters and data (last 3 of 6) and each column represents an estimation method, identified in the title. The dash line is the estimation result, the solid line represents the simulated value and the dotted lines are for the 95% credible intervals. **MSY est** is the MSY estimate.

4.3.6 Discussion

General

For an obscure reason, we have encountered some problem with the third estimation method (UCCM). Actually, we can't run two different chains at the same time in OpenBugs and we can't figure why!

Also, we have noticed that the biomass estimation for the uniform method often looked like the estimation from the true catch method, even if the MSY estimates were far from each other. Thus, if a method has the best MSY estimate for a simulation set, the estimated biomass series with this method is not necessarily the best.

Objective 1

For the first objective, out of six simulations, for four of them, the MSY was better estimated by the censored method (CCME), for two of them by the true-catch (TCM) method while the uniform (UCCM) method was always the worst.

Finally, we were not able to generate 50000 samples from the posteriors in the third parameter sets of objective 1. For an unknown reason, the Gibbs sampler got *stuck* on the 21000^{th} sample.

Another interesting thing is that, in the sixth simulation (Figure 3.2, row third row), the only method which was able to detect the population decline was the censored method.

Objective 2

For the second objective, out of six simulation, the best MSY estimate was found with the censored method (CCME) 3 times, the true-catch method (TCM) 2 times and the uniform method (UCCM) 1 time. Note that the only time the UCCM was better than then CCME, it was not really significative (see Figure 3.3, row 1).

Also, the estimated biomass series seems to be worst than in the first objective. We mean that the real biomass series is often out of the 95% credible interval produced by each method.

Objective 3

This time, we observed that the CCME and UCCM have obtained the best MSY estimate 3 times each. However, there was still a uniform (UCCM) estimate that was only slightly better the censored CCME one (see Figure 3.5 third row).

Conclusion

The rationale for the UCCM approach to deal with misreported catches without effort data was that usually in cases where catches are misreported there will also not be reliable effort data available. In fact, the HT model seems somewhat unrealistic for this reason. Good effort data acts like a surrogate measure of catch when CPUE is constant, and this may be part of the reason why these authors found that their censored approach produced better results than the alternative methods they examined. At least the performance of their method needs to be investigated when effort data are measured with error, which is the reality in most cases.

Another problem was the simulation design used by HT, which was also used in our preliminary analyses. It is well known that considerable contrast in a stock size time series (i.e. a 2-way trip) is required to reliably estimate the parameters of a surplus production model. HT studied simulated populations with relatively short time-series (i.e. only 10 years) that did not guarantee in all simulations sufficient contrast in stock size to estimate surplus production models. It is commonly understood that in cases where low data contrast occurs the likelihood surface for the parameters tends to be flat. This can have two consequences. First, differences between methods observed by HT may not be significant. Indeed, the variability from simulation to simulation under their design is very large and it looks as though the differences between estimators are well within the range of the random variation observed from simulation to simulation and can therefore not be attributed to one method being superior to the other. Second, Bayesian HT's estimates and credibility intervals may be heavily influenced by the assumed priors. In such case, the results would be essentially pre-determined by the priors, and a more appropriate simulation design to generate data is required to compare the performance of the different methods. This issue of sensitivity to prior distributions is investigated in the next chapter.

4.4 Sensitivity of parameter estimates to the specification of prior distributions

As we have explained in Section 2.2, Bayesian methods are often used in situations where few data are available, as they allow for the incorporation of prior knowledge about the model parameters to be included in the inferences, thereby making them more precise. However, in situations where no prior information is available, one has to make sure that the inferences are not wrongly influenced by the specification of prior distributions. This last situation seems to be specifically relevant to SPMs, as the series of catch and survey index data usually only span a few years (10 to 20), and with both process and observation errors, these are very few data points to infer about 5 model parameters.

Though many simulation studies of SPMs have been published (see introduction of Chapter 3), there seems to be little knowledge about the sensitivity of SPM parameter estimates to the specification of prior distributions. We investigate this sensitivity by looking at how the posterior densities vary for different choices of prior distributions for the parameters in Section 4.1. An analysis of the correlation between the parameters is given in Section 4.2. We assess the informativeness of the data themselves about the model parameters by looking at log-likelihood profiles in Section 4.3. A discussion of the results wraps up this chapter in Section 4.4.

4.4.1 Sensitivity to the choice of prior

Scenarios

To test the sensitivity of the Bayes estimators, we have used the dataset on South Atlantic albacore tuna from 1967 to 1989 given by Meyer and Millar (1999). For each of the four parameters r, K, σ^2 and τ^2, we have tried to assess the sensitivity to the choice of different priors. This assessment is made at two levels. The first level is an analysis of the change in the posterior distributions under mild modification of the prior distributions. The second level is an analysis of the posterior correlation between the parameters under vague priors.

We have studied the impact of changes in the priors on posterior distributions by modifying the prior of one parameter at a time and by looking at summary statistics and plots of the

posterior distributions of every parameter. For example, for the r parameter, we have used four different priors (four "scenarios"), so we have plotted the four posterior densities associated with them for the six parameters r, K, σ^2, τ^2, q and MSY (6 plots which contain overlays of 4 posterior densities each).

For each of the 4 parameters, our first scenario was the prior used by Meyer and Millar (1999). The second scenario was the same prior, but wider and flatter (slightly less informative). Our third scenario was the same as Scenario 1, but with a change on the mean of the prior. Finally, our last scenario was as vague as the second scenario and with the same mean as the third scenario. This means that, in each of the four figures representing the posterior densities for each scenario (figures 4.2 to 4.5), we have the set of priors used by Meyer and Millar (1999) as a reference (Scenario 1). These prior distributions are shown in Figure 4.1 and described in tables 4.1 to 4.4.

Figure 4.7: These plots represent the priors used in each scenario. Clearly, we can see that there is a change in scale between Scenario 1 (original) and Scenario 2, a change of location between scenarios 1 and 3, and finally a change in scale and location between scenarios 1 and 4. For more details on these priors, please refer to tables 4.1 to 4.4. Note that each plot on this page corresponds to a figure in the results section. For example, the first plot, "r priors", corresponds to the scenarios used to obtain the results in Figure 4.2.

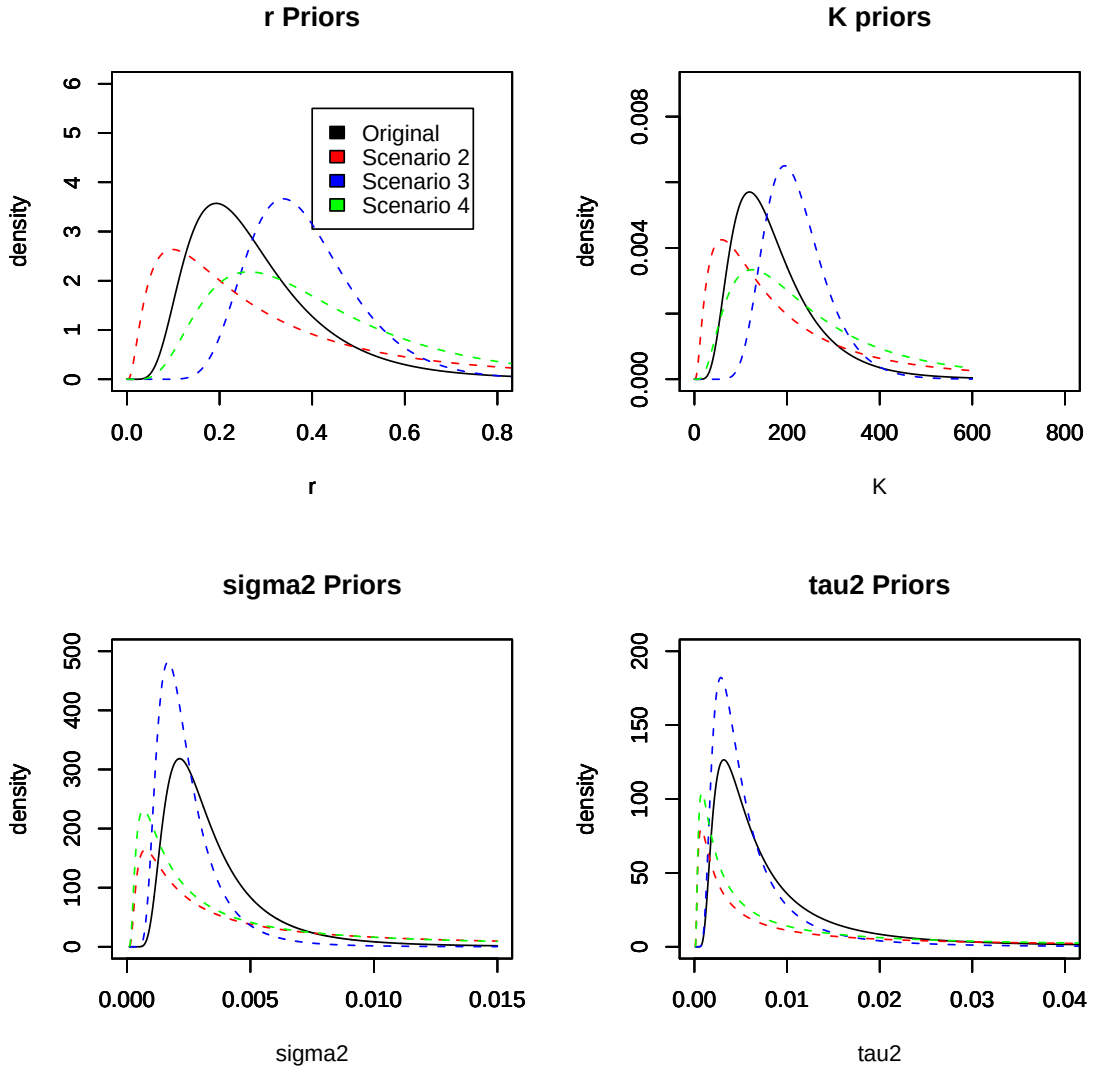


Table 4.2: Scenarios for r parameter

Scenario	Prior	Description
Original	lnorm($\mu = -1.387, \sigma = 0.509$)	.10 quantile=0.13 ; .90 quantile=0.48
2	lnorm($\mu = -1.387, \sigma = 0.968$)	.25 quantile=0.13 ; .75 quantile=0.48
3	lnorm($\mu = -.9915, \sigma = 0.308$)	.10 quantile=0.25 ; .90 quantile=0.55
4	lnorm($\mu = -.9915, \sigma = 0.585$)	.25 quantile=0.25 ; .75 quantile=0.55

Table 4.3: Scenarios for K parameter (priors are in terms of $1/K$)

Scenario	Prior	Description
Original	lnorm($\mu = -5.043, \sigma = 0.516$)	.10 quantile=1/300 ; .90 quantile=1/80
2	lnorm($\mu = -5.043, \sigma = 0.980$)	.25 quantile=1/300 ; .75 quantile=1/80
3	lnorm($\mu = -5.363, \sigma = 0.301$)	.10 quantile=1/350 ; .90 quantile=1/130
4	lnorm($\mu = -5.363, \sigma = 0.734$)	.25 quantile=1/350 ; .75 quantile=1/130

Table 4.4: Scenarios for τ^2 parameter (priors are in terms of $1/\tau^2$)

Scenario	Prior	Description
Original	Gamma($\alpha = 1.709, \lambda = 0.009$)	E($1/\tau^2$)=170.9, VAR($1/\tau^2$)=17090
2	Gamma($\alpha = 0.171, \lambda = .0009$)	E($1/\tau^2$)=170.9 VAR($1/\tau^2$)=1709000
3	Gamma($\alpha = 2.5, \lambda = 0.01$)	E($1/\tau^2$)=250 VAR($1/\tau^2$)=25000
4	Gamma($\alpha = 0.25, \lambda = 0.001$)	E($1/\tau^2$)=250 VAR($1/\tau^2$)=2500000

Table 4.5: Scenarios for σ^2 parameter (priors are in terms of $1/\sigma^2$)

Scenario	Prior	Description
Original	Gamma($\alpha = 3.786, \lambda = 0.010$)	E($1/\sigma^2$)=378.6, VAR($1/\sigma^2$)=37860
2	Gamma($\alpha = .3786, \lambda = 0.0010$)	E($1/\sigma^2$)=378.6 VAR($1/\sigma^2$)=3786000
3	Gamma($\alpha = 5.0, \lambda = 0.010$)	E($1/\sigma^2$)=500 VAR($1/\sigma^2$)=50000
4	Gamma($\alpha = 0.5, \lambda = 0.001$)	E($1/\sigma^2$)=500 VAR($1/\sigma^2$)=5000000

Results

Let us now look at the posterior distributions obtained under the various scenarios detailed in Section 4.1.1. Note that we look at the effect of changing the prior distribution of **one** parameter on the posterior distributions of all SPM parameters. Therefore, each of the figures 4.2 to 4.5 presented below shows the posterior distribution of all parameters of interest when the prior distribution of one parameter varies according to the four scenarios, and the priors of all other parameters are fixed at the Meyer and Millar (1999) values.

Table 4.6: This table shows the mean posterior density of each parameter along with its 95% CI. Each column represents a different scenario for the r parameter (see table 4.2)

	Original	Scenario 2	Scenario 3	Scenario 4
r	0.3(0.15,0.48)	0.30(0.13,0.52)	0.32(0.12,0.54)	0.32(0.13,0.54)
K	277(182,423)	276(172,456)	270(168,450)	268(168,446)
q	0.3(0.15,0.48)	0.25(0.13,0.39)	0.25(0.14,0.39)	0.25(0.14,0.39)
σ^2	0.0031(0.0011,0.0083)	0.0031(0.0011,0.0083)	0.0032(0.0011,0.0082)	0.0032(0.0011,0.0086)
τ^2	0.012(0.0057,0.023)	0.012(0.0058,0.023)	0.012(0.0058,0.023)	0.012(0.0057,0.024)
MSY	19.4(14.2,23.9)	19.4(13.2,23.9)	19.6(13.2,24.2)	19.6(13.1,24.2)

Figure 4.8: These plots show the posterior densities obtained from a change in the r prior only. Differences between posterior densities for parameters other than r are all due to the changes in the r prior and nothing else.

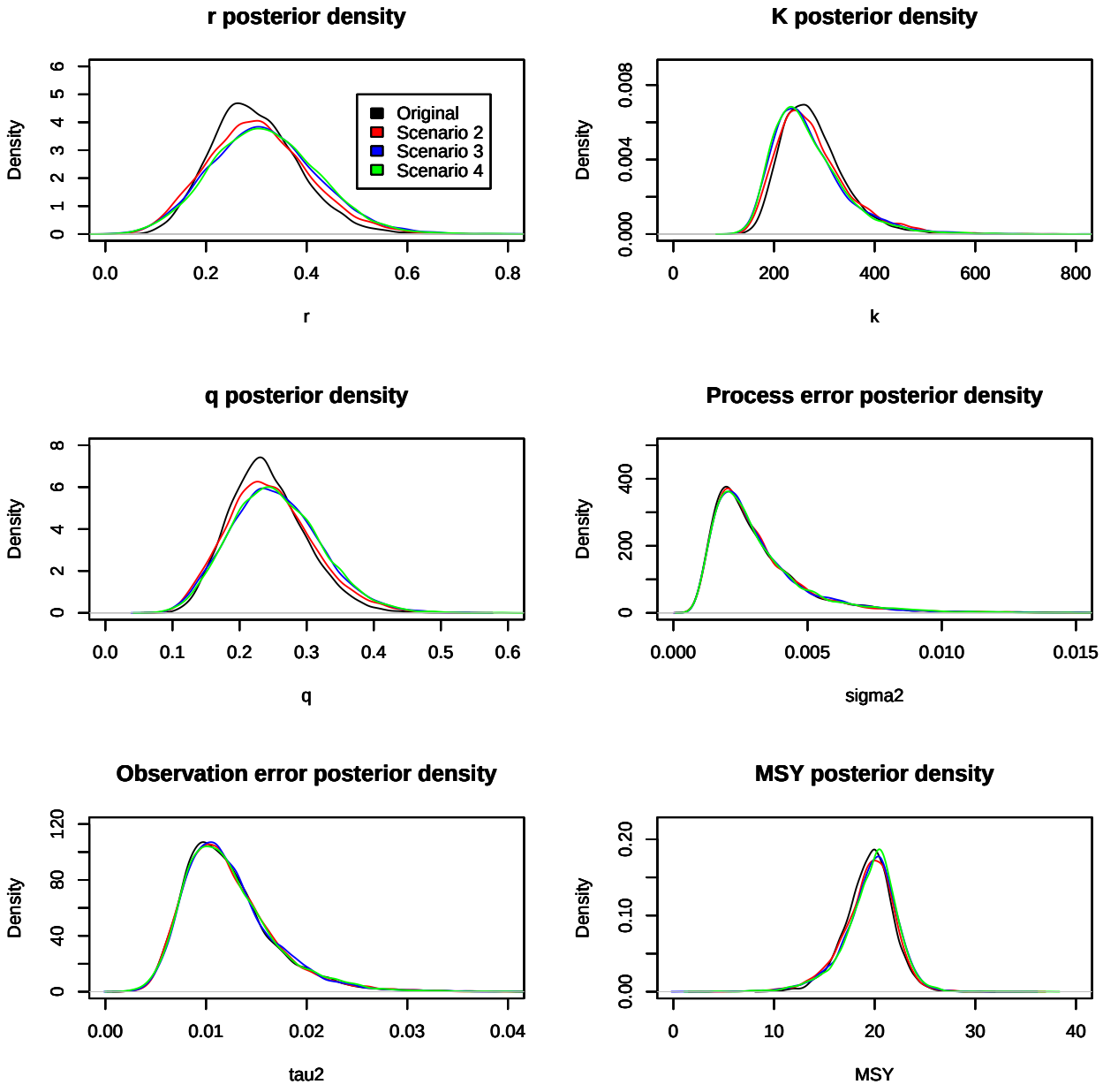


Table 4.7: This table shows the mean posterior density estimates of each parameter along with its 95% CI. Each column represents a different scenario for the K parameter (see table 4.3)

	Original	Scenario 2	Scenario 3	Scenario 4
r	0.3(0.15,0.48)	0.27(0.12,0.46)	0.30(0.17,0.47)	0.27(0.12,0.45)
K	277(182,423)	300(189,485)	268(186,383)	304(192,485)
q	0.3(0.15,0.48)	0.22(0.13,0.35)	0.25(0.16,0.36)	0.22(0.13,0.35)
σ^2	0.0031(0.0011,0.0083)	0.0031(0.0011,0.0081)	0.0031(0.0011,0.008)	0.0031(0.0011,0.008)
τ^2	0.012(0.0057,0.023)	0.012(0.0057,0.023)	0.012(0.0058,0.023)	0.012(0.0058,0.024)
MSY	19.4(14.2,23.9)	19.0(13.5,23.6)	19.5(14.9,23.8)	18.9(13.2,23.6)

Figure 4.9: These plots show the posterior densities obtained from a change in the K prior only. Differences between posterior densities for parameters other than K are all due to the changes in the K prior, and nothing else.

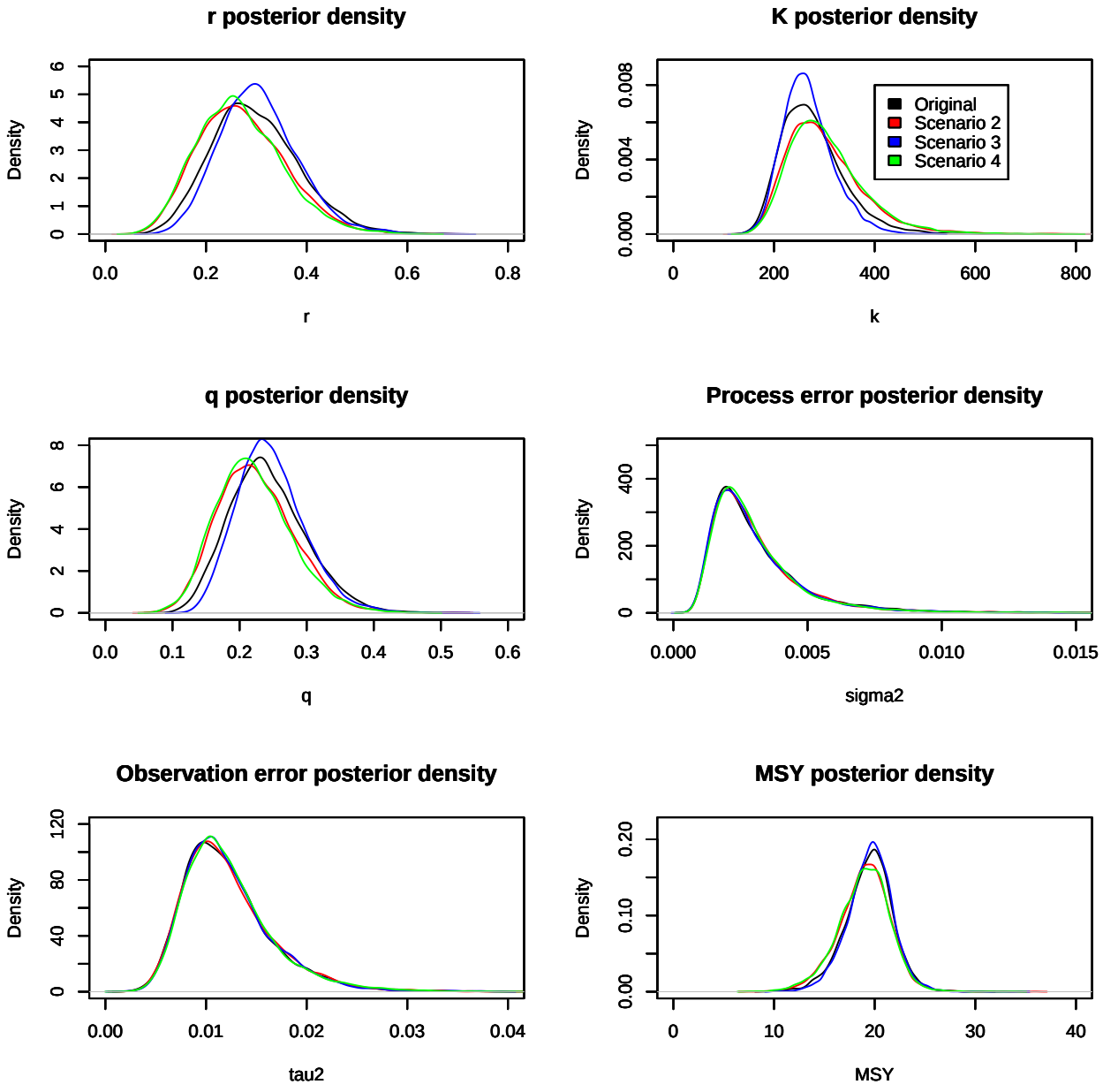


Table 4.8: This table shows the mean posterior density estimates of each parameter along with its 95% CI. Each column represents a different scenario for the τ^2 parameter (see table 4.4)

	Original	Scenario 2	Scenario 3	Scenario 4
r	0.3(0.15,0.48)	0.3(0.15,0.5)	0.3(0.15,0.48)	0.3(0.15,0.49)
K	277(182,423)	273(175,422)	277(181,422)	276(177,426)
q	0.3(0.15,0.48)	0.25(0.14,0.38)	0.24(0.14,0.36)	0.24(0.14,0.37)
σ^2	0.0031(0.0011,0.0083)	0.003(0.0011,0.0076)	0.0032(0.0011,0.0086)	0.0030(0.0011,0.0077)
τ^2	0.012(0.0057,0.023)	0.014(0.0062,0.028)	0.011(0.0053,0.021)	0.014(0.0061,0.027)
MSY	19.4(14.2,23.9)	19.4(14.2,23.6)	19.4(14.2,23.8)	19.4(14.2,23.8)

Table 4.9: This table shows the mean posterior density estimates of each parameter along with its 95% CI. Each column represents a different scenario for the σ^2 parameter (see table 4.5)

	Original	Scenario 2	Scenario 3	Scenario 4
r	0.3(0.15,0.48)	0.30(0.15,0.49)	0.3(0.15,0.48)	0.3(0.15,0.48)
K	277(182,423)	271(179,412)	272(180,409)	273(182,421)
q	0.3(0.15,0.48)	0.25(0.15,0.37)	0.25(0.15,0.37)	0.25(0.14,0.36)
σ^2	0.0031(0.0011,0.0083)	0.0036(0.00035,0.018)	0.0022(0.00095,0.0052)	0.0031(0.00031,0.016)
τ^2	0.012(0.0057,0.023)	0.012(0.0045,0.023)	0.013(0.0062,0.024)	0.012(0.0048,0.023)
MSY	19.4(14.2,23.9)	19.5(14.4,24.4)	19.4(14.8,23.1)	19.4(14.5,24.0)

Figure 4.10: These plots show the posterior densities obtained from a change in the τ^2 prior only. Differences between posterior densities for parameters other than τ^2 are all due to the changes in the τ^2 prior and nothing else.

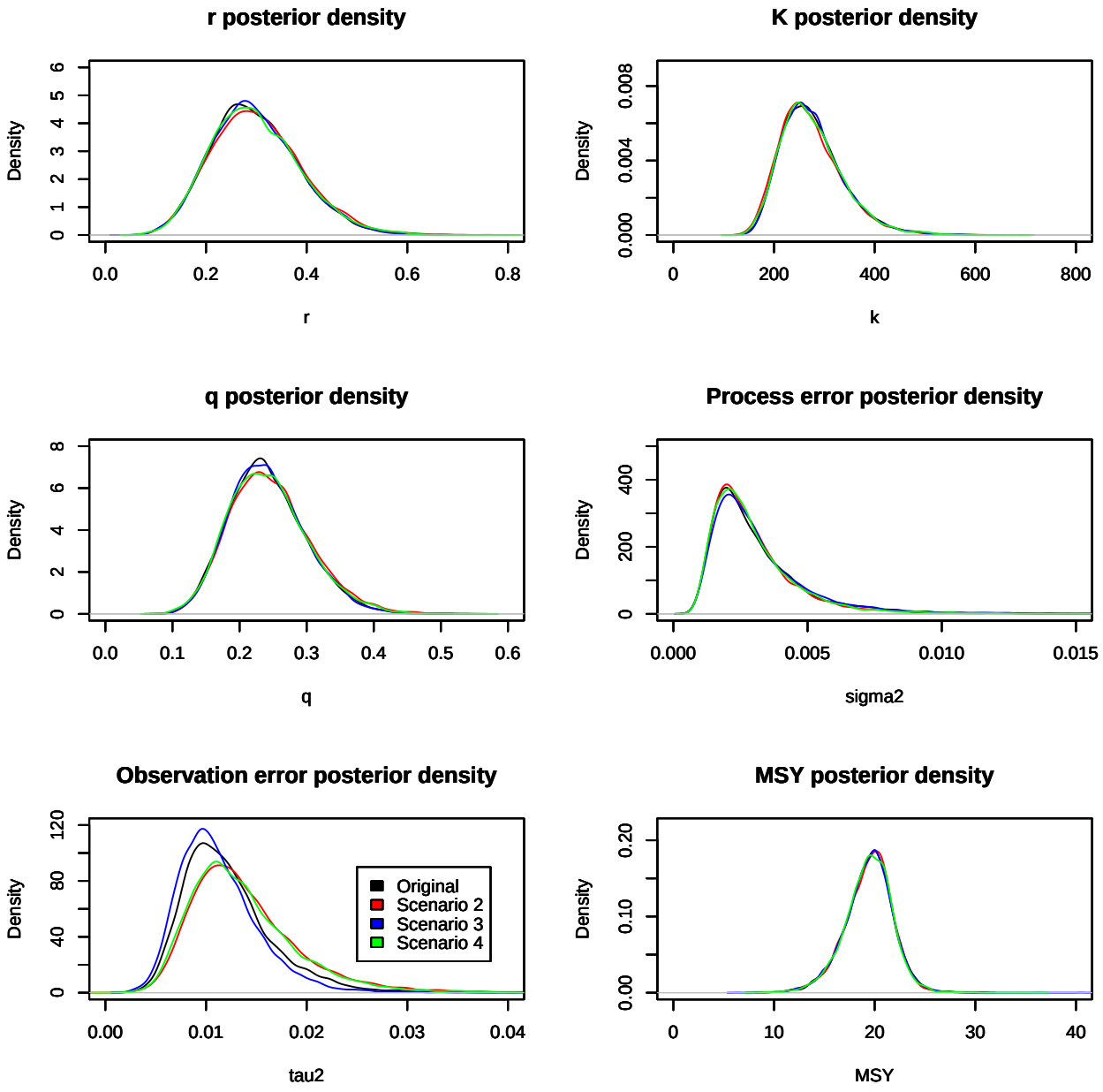
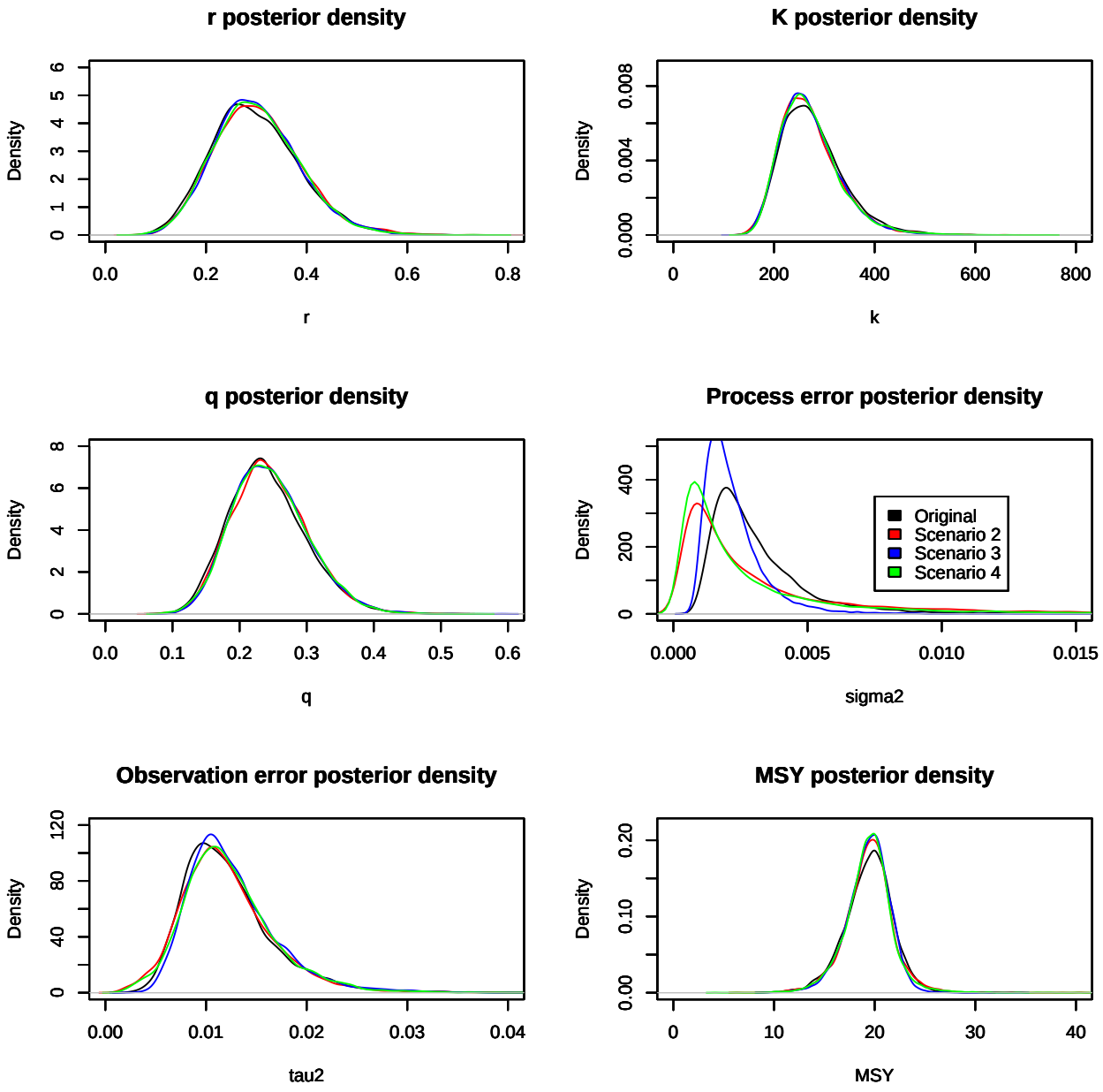


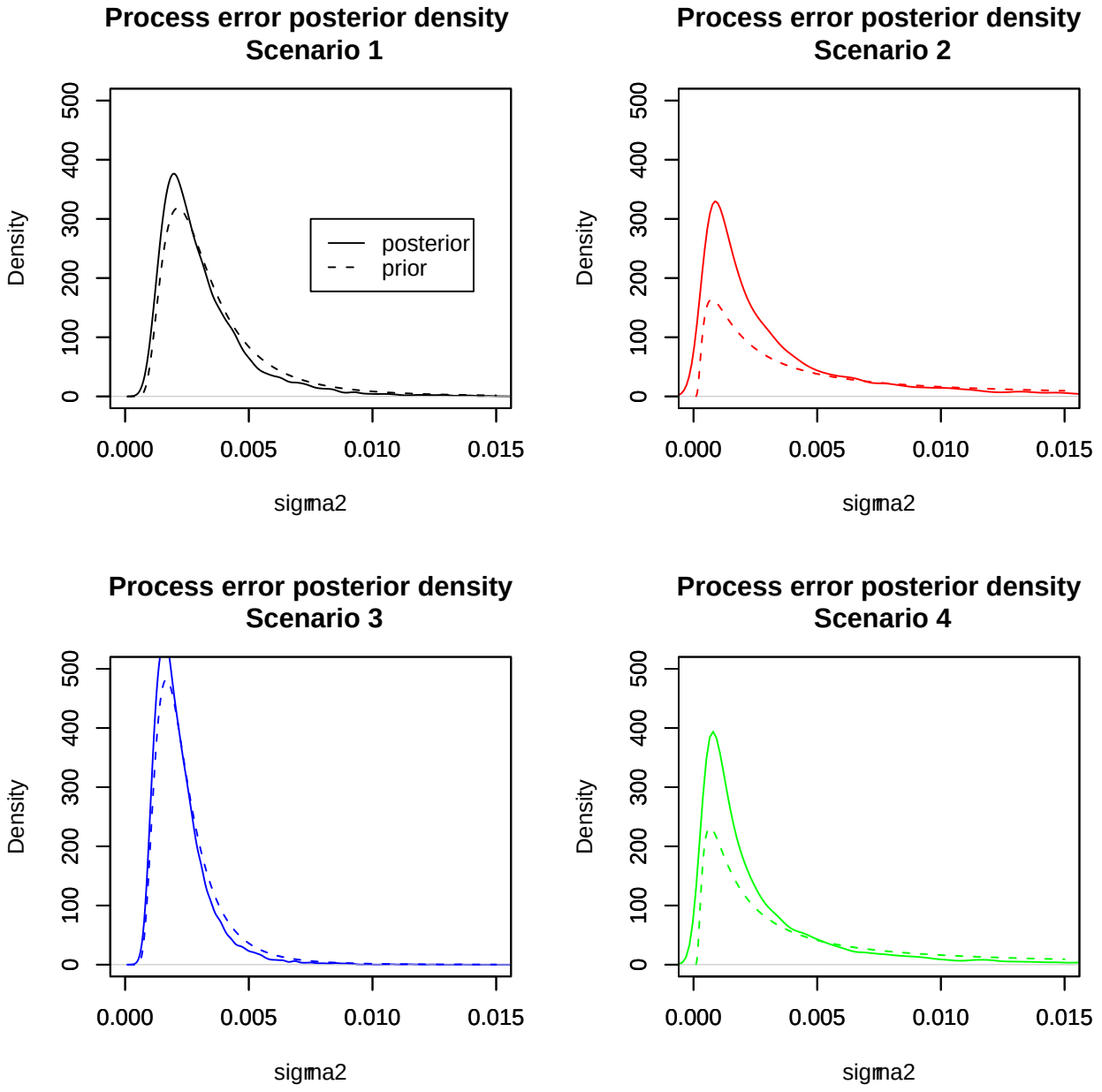
Figure 4.11: These plots show the posterior densities obtained from a change in the σ^2 prior only. Differences between posterior densities for parameters other than σ^2 are all due to the changes in the σ^2 prior and nothing else.



Some interesting conclusions can be drawn from figures 4.2 to 4.5. First of all, the parameters K, r and q seem to be correlated together as a change in the prior of one of these parameters

has an impact on the posterior distribution of all three parameters. Though this impact is not major (see tables 4.6-4.9), the posterior densities for these parameters all change when the prior on one parameter is modified while the posteriors of τ^2 and σ^2 do not move. Second, we see that the posterior distributions of the two error variances (σ^2 and τ^2) are also dependent on the specification of the prior distribution used for these parameters. To further illustrate this fact for σ^2, we have plotted each of its prior with its corresponding posterior in Figure 4.6. Since all four plots use the same scales, it is easy to see that the posterior densities are influenced by the choice of the prior distribution.

Figure 4.12: These four plots represent the four different scenarios for σ^2. The dashed line shows the prior on σ^2 and the solid line, the posterior. For each scenario, we remark that the posterior "follows" the prior.



Interestingly enough, though the posteriors of K and r are sensitive to the choice of priors, the posterior of MSY is quite robust to prior specification.

4.4.2 Correlations

The results from the previous section suggest that estimators of K, q and r might be correlated, which would imply that the data might not contain enough information to "tell them apart". In this section, we present an analysis of the correlation between these parameters. Though there did not seem to be as much correlation between the two variance estimators, we include this pair of parameters in our analysis nonetheless, as one might wonder if it is possible to correctly assign the variability observed in the data to its two sources (process error and measurement error). For each pair of parameters of interest, we used the Meyer and Millar (1999) model, but with vague priors to remove the effect of the prior distributions in the correlations, to simulate 900 observations from the joint posterior distribution of the pair of parameters. We then used these 900 pairs of values to estimate the posterior correlation between the parameters.

Figure 4.13: These plots show scatter plots of 900 pairs of parameters simulated from their joint posterior distribution and give the corresponding estimate of the posterior (Kendall) correlation between the two parameters.

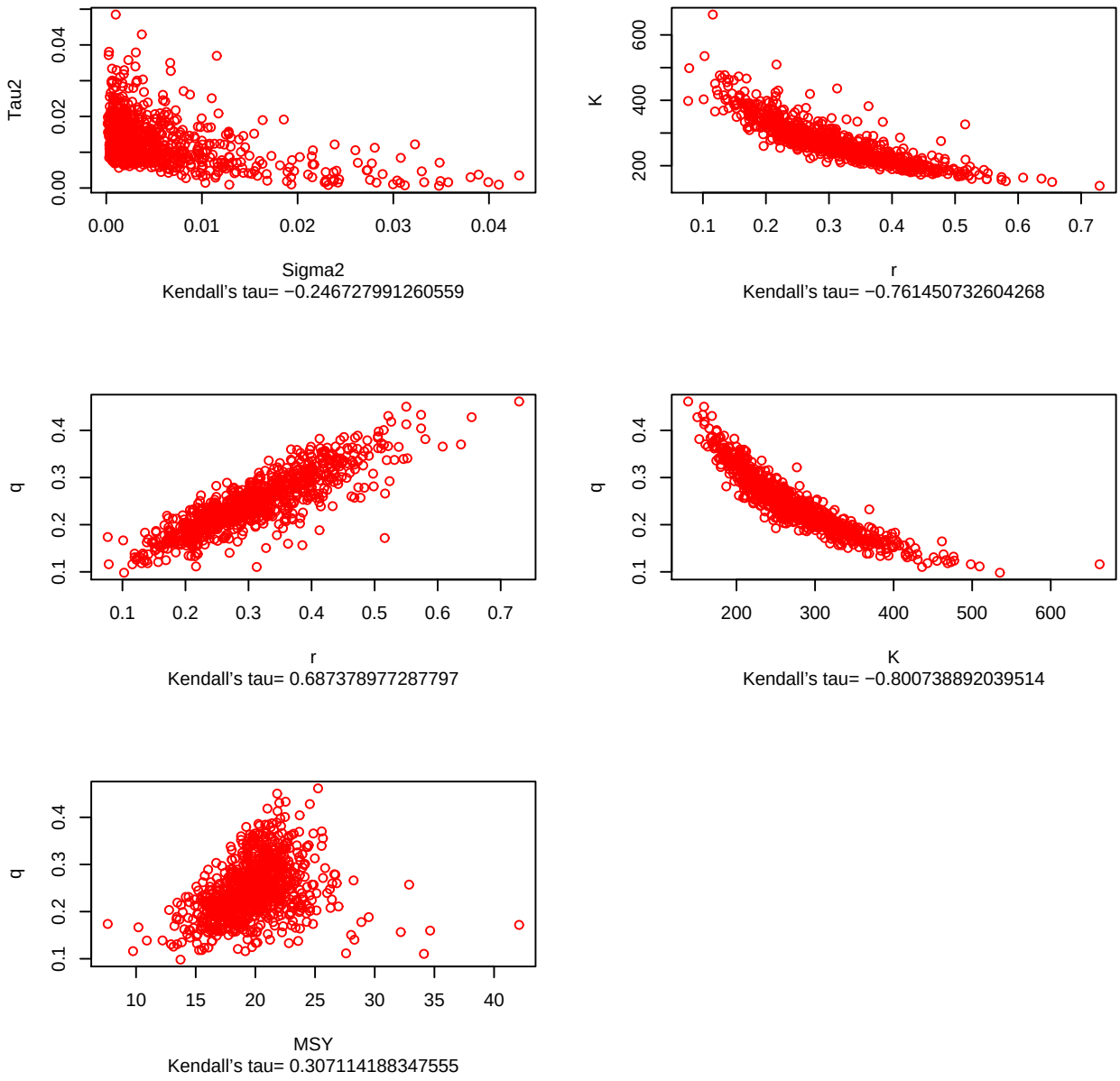


Table 4.10: Posterior correlations between some pairs of parameters.)

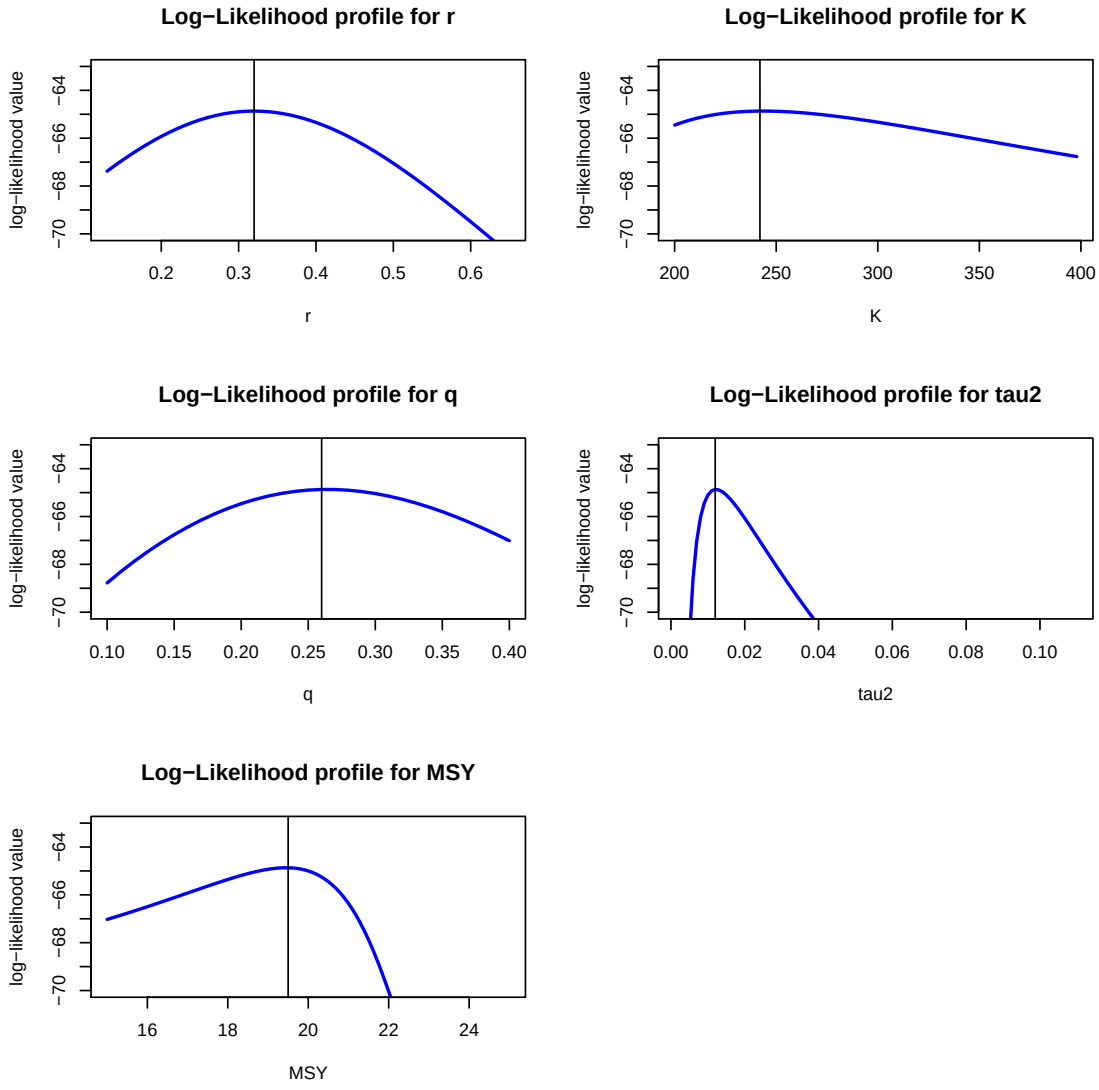
Parameters	Kendall's correlation	Pearson's correlation (95% c.i.)
(σ^2, τ^2)	-0.25	-0.39 (-0.41, -0.37)
(r, K)	-0.76	-0.86 (-0.87, -0.85)
(r, q)	0.69	0.87 (0.86, 0.88)
(q, K)	-0.80	-0.90 (-0.91, -0.89)
(MSY,q)	0.31	0.34 (0.32, 0.36)

Figure 4.13 shows scatter plots of pairs of values of the parameters simulated from their joint posterior distribution, while Table 4.10 gives the values of the Kendall and Pearson correlations between the pairs of parameters of interest (to give an idea of the precision in these correlation estimates, confidence intervals for the Pearson correlations are also provided). Since the relationship between the parameters is not linear, the Kendall correlations are more appropriate. They indicate that there two variance parameters are only mildly correlated (-0.25) and, thus, seem to be identifiable from the data. On the other hand, the K, r and q parameters are all strongly correlated (correlations in the 0.7-0.8 range in absolute value), which suggests that the data do not allow a complete identification of each one of them. Although r and K are correlated together and with q, the correlation between MSY$= rK/4$ and q is mild (0.31) and suggests that a reparameterization of the model that would replace (r, K, q) by (MSY,q) could possibly lead to a model that is less sensitive to prior specification. It would be interesting to include the vague priors used in this section in the sensitivity analysis of Section 4.1 to see whether the posterior distributions would be more severely impacted.

4.4.3 Log-likelihood profiles

In order to have an idea of the amount of information about the parameters contained in the data, we can look at the log-likelihood profiles of each parameter. To do this, we fit the SPM using maximum likelihood estimation. For the moment, we can only fit SPMs that only account for observation error with this method, but this should give a first rough idea of how informative the data are.

Figure 4.14: These five plots show the profile log-Likelihoods for the five parameters of the SPM with observation error only fitted to the Meyer and Millar (1999) data. Vertical lines are drawn at the maximum likelihood estimates.



Since 95% likelihood ratio intervals are given by all parameter values that give a profile log-likelihood value greater than or equal to the maximum profile log-likelihood minus roughly 2, a simple way to interpret the plots in Figure 4.14 is to look at all the values of the parameters that satisfy this rule; the flatter the profile log-likelihood, then the wider is the interval and the less informative the data are about the parameter. Using this rules, we see that the data are informative about τ^2, with a quite concave profile log-likelihood yielding a confidence

interval of about (0.01, 0.023), and relatively informative about r, with a curved profile log-likelihood giving a confidence interval of about (0.1,0.47). However, the data seem to contain no information about q and K, for which the profile log-likelihoods are nearly flat and give confidence intervals that almost exceed the range of parameter values used in the plots. On the other hand, the data do contain information about MSY, as its log-likelihood profile is quite concave (especially to the right of the maximum) and a confidence interval for it of approximately (15,21).

4.4.4 Discussion

Our intuition before doing the analysis presented in this chapter was that the data would not be able to clearly identify the two error variance parameters and, thus, inferences about these parameters would rely heavily on the choice of prior distributions. We did observe this phenomenon, but to a lesser extent than anticipated. Though Figure 4.6 shows that the posterior of σ^2 follows closely the prior, the plots if figures 4.2-4.5 as well as the correlation analysis show that these two parameters are not overly correlated or sensitive to the choice of prior, and hence are identifiable from data. However our simulation design is similar to what is used in typical robustness studies and used prior distributions that were not too drastically different. In retrospect, it seems clear that adding more simulations with priors that are much flatter and/or shifted further away from the Meyer and Millar (1999) priors could help in giving a more definite answer to the question of parameter identifiability from data.

On the other hand, the parameters K, q and r proved to be more difficult to identify, especially in the correlation analysis. Furthermore, the profile log-likelihoods for these parameters were very flat, indicating lack of information about these parameters in the data. In spite of these problems with the identifiability of K and r, there seems to be no problem with inferences about MSY. This could be due to the dataset used by Meyer and Millar (1999) for which there is no 2-way trip and/or to an inadequate parameterization of the model; this point should be further investigated.

4.5 Conclusion

The objectives of this report were to assess whether the censored-catch approach to fitting a SPM proposed by HT is efficient, and to see if Bayesian inference within the SPM framework is sensible. As seen in Chapter 3, we can conclude that when landings are truly a lower bound for the true catches, then correcting the inferences according to the HT method improved the inferences in the majority of cases. When there was no misreporting, then correcting for censored catches did not seem to do worse than not correcting. This suggests that safe inferences should consider the possibility of misreported catches. But HT's study as well as that presented in Chapter 3 have two major problems that render them inconclusive: first and foremost, the amount of variability in SPMs with process error is so important that the number of simulations used makes observed differences not statistically significant. Second, all simulations were done with the same priors, which means that differences between methods could be due to inferences being driven by these priors. Hence, to be conclusive an HT-type of study should use many more replications and different sets of prior distributions.

As for the the sensibility of Bayesian inferences, we have seen in Chapter 4 that the SPM might be overparameterized, as the three parameters K, q and r are not identifiable from the data. This suggests that the choice of prior distributions for these parameters may have an influence on their posterior distribution and on the ensuing inferences. But since the initial study presented in this report only considers mild changes in prior distributions, this dependency of inferences on prior specification was rather mild. A follow up study with priors that vary more widely is needed to quantify the implications of the high correlation between model parameters in terms of changes in the posterior distribution. Nonetheless, priors should be chosen carefully; for instance, one should not use identical priors for two series of catches and CPUEs from different species, areas and/or times.

These findings suggest possible avenues for further investigations. Firstly, the studies of Chapter 3 and of Section 4.1 should be expanded so that more definite conclusions can be reached. Secondly, inferences based on maximum likelihood would circumvent the problem of finding appropriate prior distributions. However, maximum likelihood inference for the SPM with both process and measurement error is numerically challenging. It should be investigated

whether inferences by maximum likelihood are robust to misspecification of the error structure (e.g., fit with only observation error when both sources of error are present) and if not, efficient numerical algorithms to fit the SPM with both process and measurement errors should be derived. Thirdly, it would be useful to study possible reparameterizations of the SPM that could help in solving the identifiability issue with the r, q and K parameters. Perhaps there are ways to reduce these parameters from three to two without changing the shape of the biomass time series. For instance, we may be able to take advantage of the fact that MSY= $Kr/4$ is identifiable. Finally, means of incorporating corrections for censored catches in maximum likelihood estimation should be investigated and compared through a well designed simulation study.

Bibliography

[1] Cadigan, N.G. and Farrell, P.J. 2005. *Local Influence Diagnostics for the Retrospective Problem in Sequential Population Analysis*. ICES Journal of Marine Science, **62**: 256-265.

[2] Hammond, T. R., and Trenkel, V. M. 2005. *Censored-catch data in fisheries stock assessment*. ICES Journal of Marine Science, **62**: 1118–1130.

[3] Lapointe, M. F., Peterman, R. M., and A. D. MacCall. 1989. *Trends in fishing mortality rate along with errors in natural mortality rate can cause spurious time trends in fish stock abundances estimated by virtual population analysis (VPA)*. Canadian Journal of Fisheries and Aquatic Sciences. **46**: 2129-2139.

[4] Megrey, B.A. 1989. *Review and comparison of age-structured stock assessment models from theoretical and applied points of view*. Amer. Fish. Soc. Symp. **6**: 8-48.

[5] Meyer, R. and Millar, R. B. 1999. *BUGS in Bayesian stock assessments*. Can. J. Fish. Aquat. Sci. **56**: 1078—1086.

[6] Mohn, R. 1999. *The retrospective problem in sequential population analysis: An investigation using cod fishery and simulated data*. ICES Journal of Marine Science, **56**: 473-488.

[7] The BUGS Project *http://www.mrc-bsu.cam.ac.uk/bugs/*

[8] Rivard, D. 1989. *Overview of the systematic, structural, and sampling errors in cohort analysis*. Amer. Fish. Soc. Symp. **6**: 49-65.

[9] Robert, P.R, Casella, G. *Monte Carlo Statistical Methods*. Springer Texts in Statistics, Springer, New York (2004)

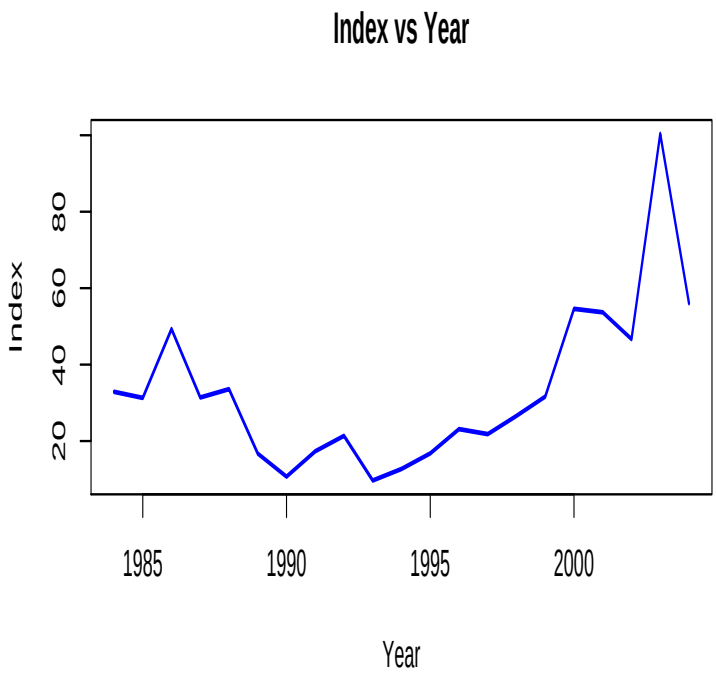
Part 5

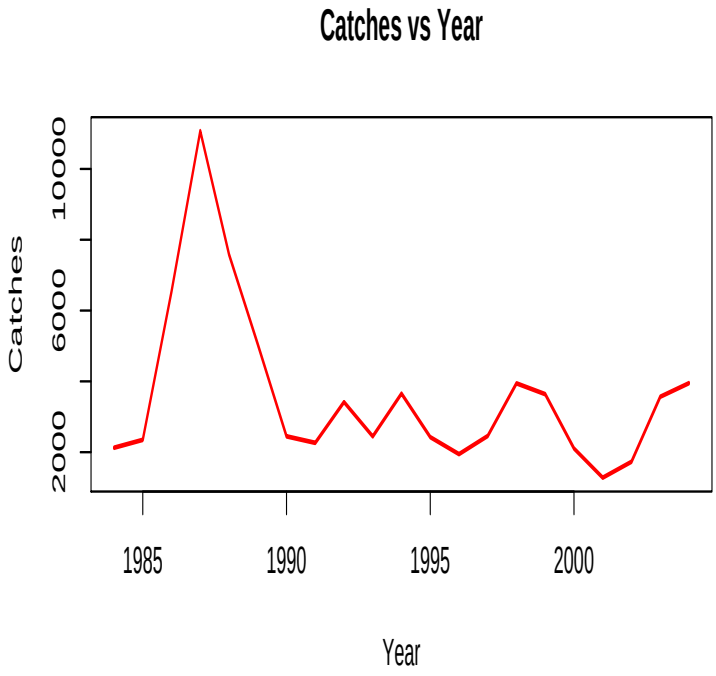
Application to St. Lawrence Gulf Turbot data

In this section we will present the results of fitting an SPM to a real dataset using MLEO and MLEP. The observations used here are those of the St. Lawrence Gulf Turbot from 1984 to 2004 (N=21). In this case, the abundance index is a combined (and standardized) index that is expressed as the quantity (in kg) of Turbot per haul in surveys. Finally, the catches used are the landings reported in tonnes (1000 kg). The data are presented in table 5.1

Table 5.1: This table shows the St-Lawrence Gulf Turbot data used in this section.

Year	Index (Kg per haul)	Catches (tonnes)
1984	32.883	2126
1985	31.288	2349
1986	49.325	6537
1987	31.399	11069
1988	33.576	7585
1989	16.72	5049
1990	10.69	2448
1991	17.323	2264
1992	21.358	3417
1993	9.686	2445
1994	12.703	3655
1995	16.767	2426
1996	23.122	1945
1997	21.815	2459
1998	26.591	3945
1999	31.627	3638
2000	54.59	2105
2001	53.688	1280
2002	46.671	1730
2003	100.367	3565
2004	56.058	3950





We can observe in table (5.1) a great curve in the abundance index, indicating a two-way trip in the population biomass, and hence some hope that at least the SPM with observation error only can be fitted to these data with reasonable accuracy in the inferences. Also, we can note the large catches made during years 1986 to 1989 leading to a significant decrease in the population abundance index for the corresponding years. Finally, we can see on the index plot that the population seems to have been harvested before 1984 since the abundance index is higher for the years 2000 to 2004 than it was in 1984.

5.1 Results

This section section only presents tables and plots related to the data analysis of the St. Lawrence Gulf Turbot, the discussion can be read in section 5.2.

Table 5.2: This plot shows the results from fitting the SPM using the MLEO and MLEP. The dashed line represents the Index data and the red and blue lines are for the MLEO and MLEP index estimates, respectively. We can see that the MLEO is a lot smoother than the MLEP. This arises from the fact that the MLEO's biomass estimates are based only on the r and K estimates, whereas the MLEP used the I_{t-1} value to predict I_t for every t.

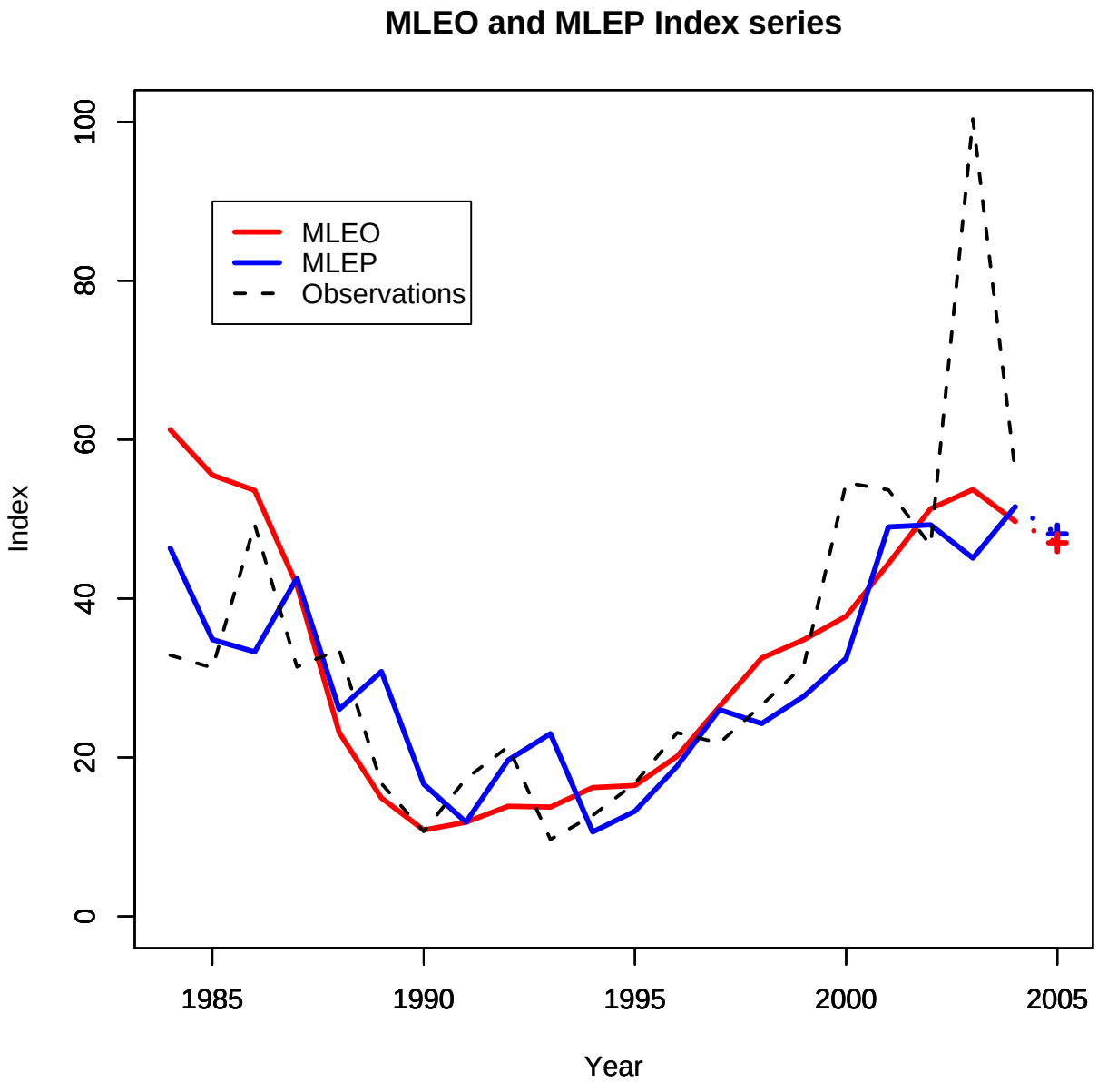


Table 5.3: This table presents the parameter estimates for the two methods. We can notice that although r and K estimates are quite different, the MSY estimates are similar. Standard errors are between parenthesis. They are obtained from the observed information matrix.

Method	$\hat{r}$	$\hat{K}$	$\hat{q}$	$\hat{\sigma}^2$	$\hat{\tau}^2$	$\widehat{MSY}$
MLEO	0.849(0.044)	22722(636)	0.00270(2.9e-4)	—	0.103(0.032)	4821(109)
MLEP	0.392(0.27)	55084(4.9e4)	0.000842(9.7e-4)	0.144(0.044)	—	5395(2637)

Table 5.4: These two plots present the estimated biomasses and the exploitation rates (C_t/B_t) under the two models, MLEO and MLEP. Although the two series of estimated I_t were very similar, the estimated biomass trajectories are very different. The principal reason for this difference comes from the distance between the MLEO and MLEP estimates.

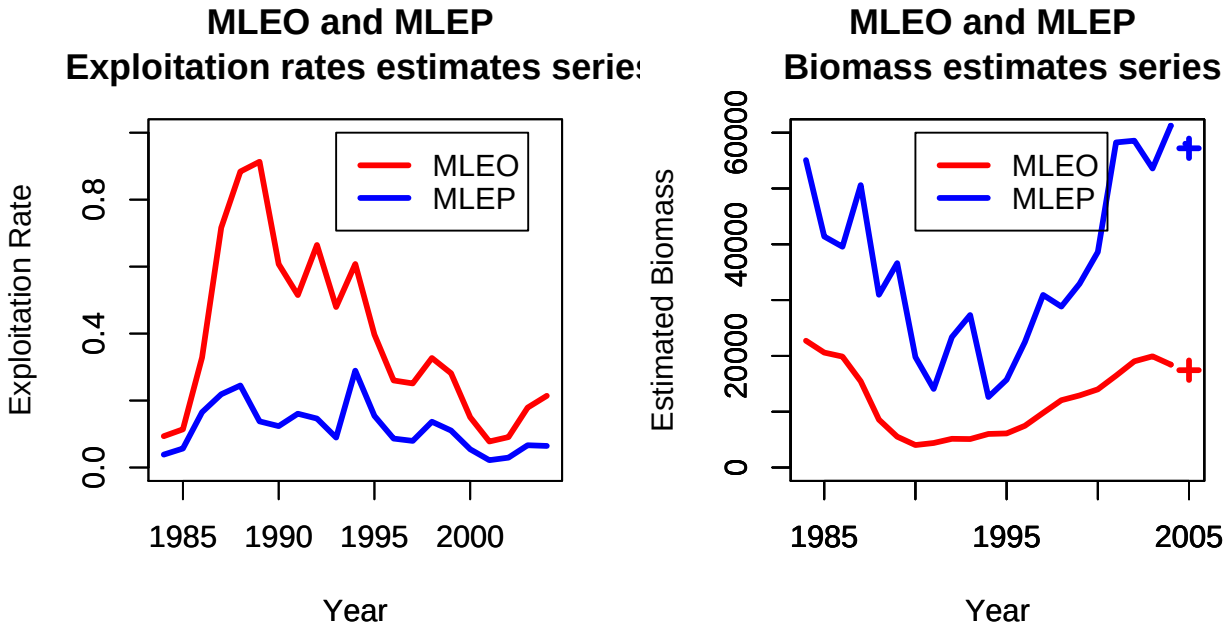


Table 5.5: These plots verify the normality assumption for the error terms. For both MLEO and MLEP, normality seems reasonable.

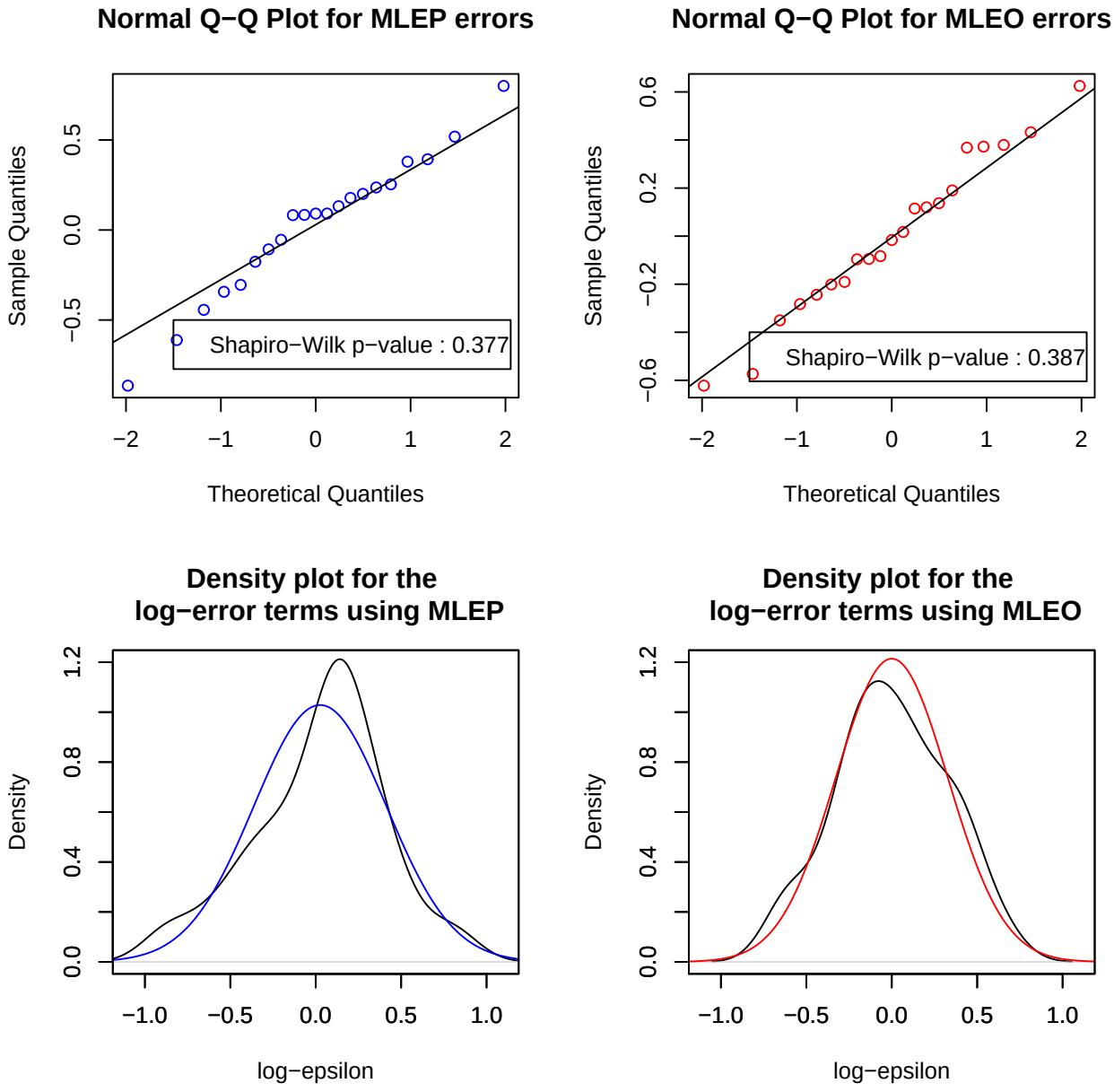


Table 5.6: These four plots show the likelihood profiles for r, K, q and MSY. In each case, the data seems more informative for the MLEO than MLEP. The vertical dashed lines represent the 2 estimates (the maximum of the function) while the horizontal doted lines are used to get the likelihood ratio confidence intervals.

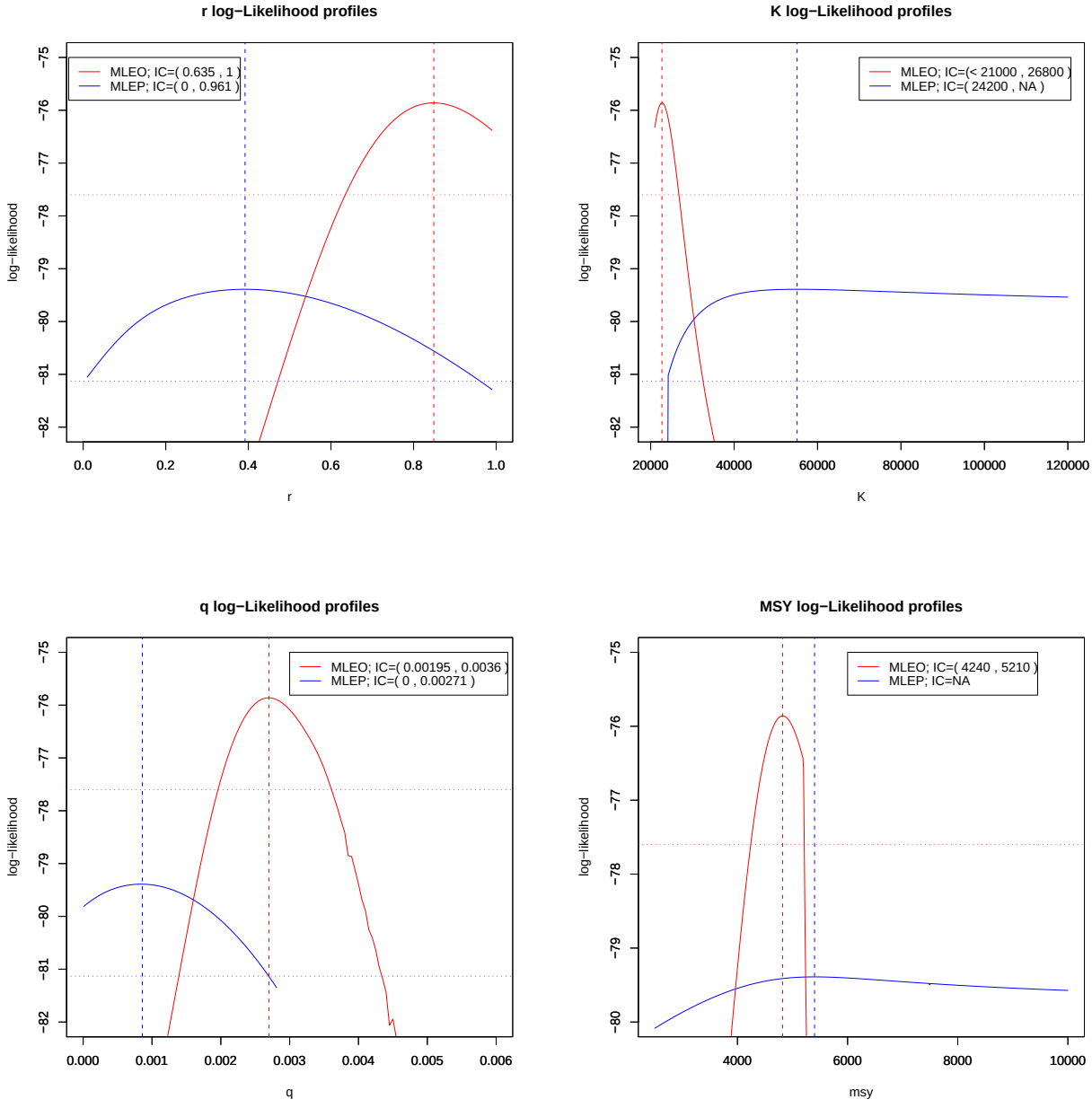
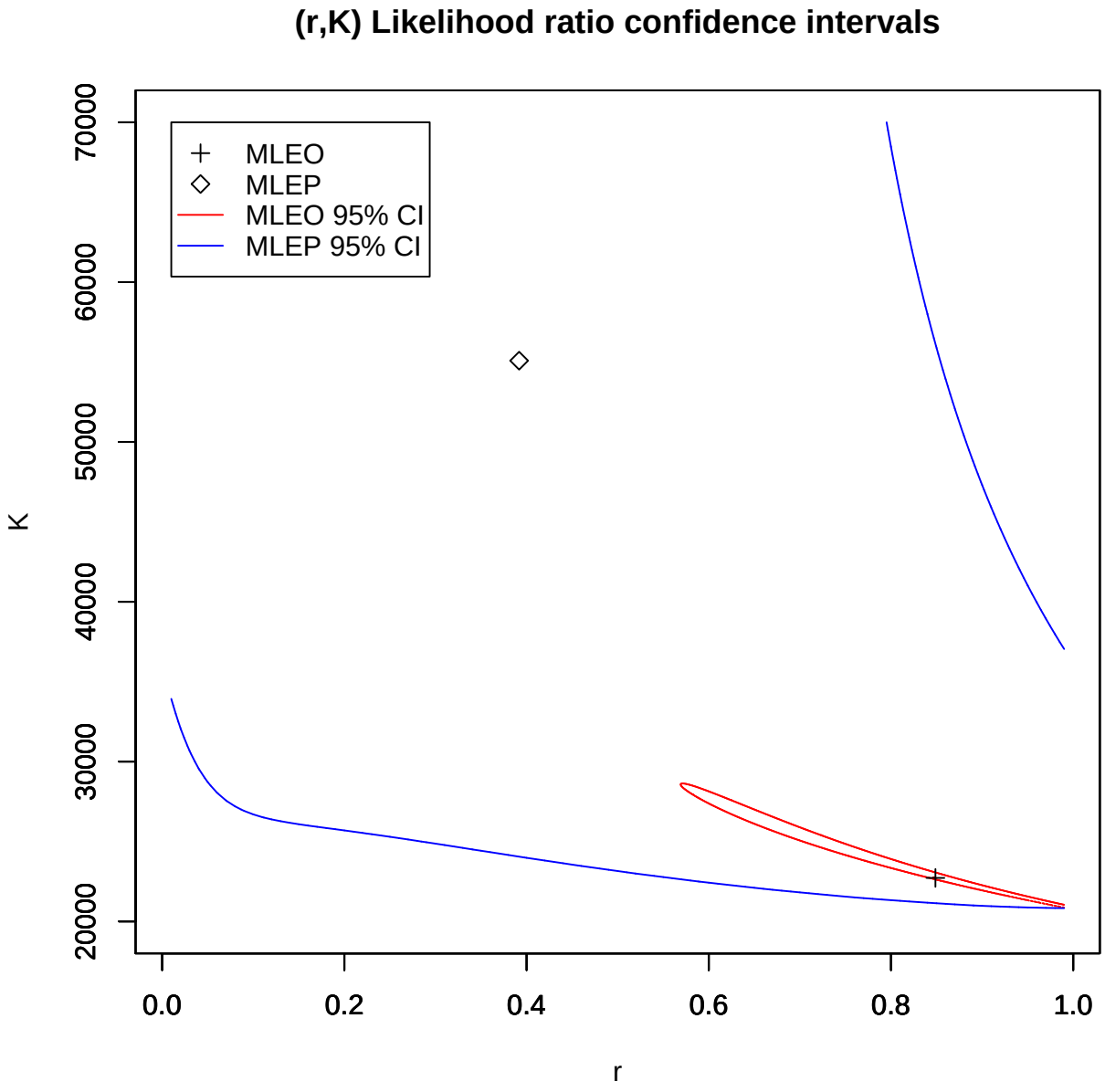


Table 5.7: This contour plot presents the MLEO and MLEP for r and K with their respective likelihood profile confidence intervals. Clearly, the joint confidence interval for the MLEP is a lot wider than for MLEO. This suggests that MLEO is more informative than MLEP.



5.2 Discussion

The results from this application of the SPM to real data suggests that a lot of improvement can be done. The difference from this part and the previous ones is that the results are now based on a real life situation and reveal problems that simulation studies cannot detect. In the following paragraphs, we will try to outline some of the more important conclusions that can be made from this study of the SPM applied to the St. Lawrence Gulf Turbot.

The first observation made is that the assumption of normality, which is easy to forget, is clearly verified with both MLEO and MLEP methods. This means that our simulations were made from a reasonable pattern since at least one species verifies the normality assumption. However, even if the MLEP normality assumption is verified, the MLEO seems to have better results for the tail of the normal distribution (see table 5.5).

Another conclusion that can be drawn is that the MLEO and MLEP estimations of the I_t's are really similar, except for the fact that the MLEO series is a lot smoother than MLEP (see table 5.2) . At first, this seems a good property from the SPM : whatever source of error you use, you will get approximately the same I_t's estimations. However, it is clearly not the case. In fact, MLEO and MLEP produce very different estimations of r and K (see table 5.3). This is then clearly reflected in the B_t estimates (see table 5.4). The source of this discordance between the two models is probably the difficulty of the model to find the right scale for the data. Because the data are basically the I_t (the B_t's aren't observed), both models estimate the same shape (or pattern) for the biomass dynamic (which are the predicted I_t's), but cannot precisely estimate the scale of the B_t's (which are predicted by the K and q parameters). This is an example of what has not been observed from the simulations studies, because our interest then was primarily the parameters estimates.

When we have a look at the standard error estimates for MLEO and MLEP, we also find an interesting problem. Actually, the estimates from MLEP are very imprecise. The standard error estimates are sometimes as big as the parameter estimate value (see K and q estimates in table 5.3). This suggest that MLEP estimates, as they are defined, should be used with caution. However, even if the MLEO produces more precise estimates, the associated standard errors are clearly too small, which means that confidence intervals under MLEO should be used with care.

Nevertheless, we may have found a source for the imprecision problem of the MLEP method. Let us suppose for a moment that the normal distribution is used for process error instead of the log-normal distribution that we used. In this case, the maximum likelihood estimates of r, K and q would rely on the multidimensionality of the I_t, I_t^2 and C_t series. Unfortunately, these variables are suffering from a multicollinearity problem when we consider the St. Lawrence Gulf data. It is well known that multicollinearity is often associated with a precision problem, which would explain the results obtained.

An encouraging observation is that the MSY estimates seem to be quite similar with values of 4821 tonnes for MLEO and 5395 tonnes for MLEP, respectively. Although the MLEP estimate for MSY is not included in the confidence interval obtained using MLEO (this may be caused by the impressive and improbable precision of the MLEO method), the two methods lead to reasonable MSY estimates. This fact puts forward the idea that the SPM may be overparameterized. Actually, the simulation study was leading in the same direction : there is a high correlation between r and K, which in turn implies that they may not be distinguishable. This conclusion leads unfortunately to a problem at another level : is the SPM a good model for data analysis to begin with?

A last conclusion that can be drawn from this analysis is that the assumption made about the virginity of the population ($B_0 = K$) is clearly not reasonable for the St. Lawrence Gulf data. Actually, since the I_t's are supposed to be proportional to the B_t's, the assumption that $B_0 = K$ means that the first year of data is the greatest observation. However, this is clearly not verified in our case. This particular dataset would request the introduction of a new parameter (B_0), but the addition of a new parameter is anything but encouraging since the model seems to suffer from overparametrisation.

Finally, this analysis of the St. Lawrence Gulf Turbot data is revealing some more interesting facts that should be taken into account in further studies of the SPM, such as the use of censored data for catches and the MLEPO implementation.

Part 6

Conclusion

The results reported in this work are all pointing in the same direction : the process error, as defined, may not be the appropriate way to express the fact that SPM dynamic is not deterministic (non random). Actually, it is a common assumption that there is both observation and process errors in reality. However, modeling the process error is delicate because some parameter estimates are biased and imprecise even when there is no observation error. Our last study about the MLEP has shown that even in the rare cases where MLEP does good (always in cases with no observation errors), the introduction of a small amount of observation error is leading to large bias and larger variance. As we noted in part 5, the imprecision of the MLEP parameter and scale estimates are also an issue . Our analysis of the St. Lawrence Gulf Turbot data brought to our mind the idea that it is probably related to a multicollinearity problem in the data or to catch and index data being not sufficiently informative to support MLEP estimation.

Our simulation studies and observation study about the MLEO and MLEP have pointed out that process error is a key problem to be solved before considering the MLEPO method. Actually, the solution may reside in the definition of the process error itself. It could be interesting to see the effect of applying the process error to the production function only instead of the biomass dynamic function (see equation 1.2). Another idea may be to introduce the process error on the r parameter only. These ideas are coming from the fact that the form $B_{t+1} = B_t + f(B_t) - C_t$ is intuitively reasonable so that the errors are more probably in the

$f(B_t)$ function itself. It may also be interesting to investigate wether or not the process error is coherent with the model, that is to study the stochastic proprieties of the model in presence of process error.

Also, a common conclusion to both Bayesian and maximum likelihood analysis is the correlation between the parameter estimates. For example, in the Bayesian study, although we were starting with independent priors for the model parameters, we obtained highly correlated posterior densities. This correlation, which is significantly high even when we are estimating exactly from the simulation model, is indicating the incapacity of the model to distinguish the parameters. One of the interesting correlation patterns was between r and K because its shape is really similar to the $MSY = rK/4$ relation. This may mean that the data are only informative about combinations of parameters, such as the MSY, instead of individual parameters. This phenomenon suggests to investigate a possible reparametrization of the model, a task that may not be easy because the SPM is already a parsimonious model if we think of the complexity of the fish population dynamic.

To continue this analysis of the SPM, these two problems have to be solved. If they cannot be, another model should be investigated if we wish to apply the idea of reported catches vs true catches. A kind of model that could be used is Virtual Population Analysis (VPA). One interesting thing with VPA is that it clusters fish in age classes and estimates the number of fish in these classes instead of the global biomass of the stock. An advantage of using an age-based approach is that it can take advantage of richer, more informative database with catch-at-age data.