[Please do not distribute this paper. Thanks].

ANALYSIS OF LOCATION AND DISPERSION EFFECTS BASED ON CENSORED DATA FROM UNREPLICATED EXPERIMENTS

Jye-Chyi Lu

Department of Statistics

North Carolina State University

Raleigh, NC 27695-8203

ABSTRACT

A distinctive feature of Japanese quality improvement techniques is running experiments to find the best combination of process variables, which minimizes process variance and appropriately controls the mean at the desired level. In testing durable products for reliability improvement, observations are usually censored or grouped. The incompleteness of data couples with complicated structure of experiments causes difficulties in deciding important control factors. Existing methods such as Taguchi's minute, Hahn-Morgan-Schmee's, Hamada and Wu's methods do not consider dispersion effects and, sometimes, are inadequate and tedious because their variable-selections are performed on the imputed pseudo-complete samples. We develop a censored forward model-selection procedure to select important location and dispersion effects simultaneously based on the original censored data. This method is simple, analytically sounded and is better than Box and Meyer's (graphic) procedure, where dispersion effects are analyzed based on residuals resulted from a fixed mean function. Two real data sets taken from Specht's heat exchanger experiment are analyzed to demonstrate the recommended methodology.

KEY WORDS: Reliability improvement; Censored data; Variable Selection; Dispersion effects; Maximum likelihood; Data analysis.

1. INTRODUCTION

Experimenting process variables to improve quality/reliability of products becomes a routine practice in industries nowadays. In testing durable products, times to failure are usually censored or grouped (c.f. Lawless, 1982; Nelson, 1990). The incompleteness of data couples with complexity of the structure in screening experiments makes variable selections difficult. Traditional methods of model-selection for complete samples cannot be readily applied in this situation. Hamada and Wu (1991) reviewed various existing methods of analyzing censored experimental data and pointed out that Taguchi's (1987) minute accumulating analysis (MAA) and Hahn-Morgan-Schmee's (1981) (HMS) procedure have serious deficiencies, which leads to wrong suggestion of important effects. They proposed an expectation-modeling-maximization (EMM) algorithm, which imputes the incomplete data based on maximum likelihood estimates and performs regular variable selections on pseudo-complete samples.

Other than the traditional emphasis placed on modeling means, one important idea in Japan's quality improvement procedures is the study of factors which affect variances the most and tries to reduce product variation. However, in screening experiments, it is very often that there is no replication for computing dispersion effects. Box and Meyer (1986) proposed a graphic procedure to analyze unreplicated experiments, which first identifies significant location effects and estimates their residuals. Important dispersion effects are then specified relatively by comparing the logarithm of variance-ratios, $\log(\sigma^2_{HA}/\sigma^2_{LA})$, $\log(\sigma^2_{HB}/\sigma^2_{LB})$, and so on, where σ^2_{HA} (or σ^2_{LA}) is computed from observations pooled from the high (or low) level of a particular factor, say A, together. If data is censored, their method is not appropriate because grouping data into smaller blocks introduces heavier censoring and computation of ML estimates becomes much more difficult. Moreover, in Nair and Pregibon's (1988) investigation, which extended Box and Meyer's pooling method to replicated two-level experiment, they suggested that pooling technique is generally biased and is not recommended for model identification. Instead, a maximum likelihood method was introduced to increase efficiency of estimators of dispersion effects.

In analyzing censored data from highly fractionated experiments, none of the aforementioned procedures, including MAA, HMS and EMM analyzes dispersion effects. Moreover, since their procedures perform variable selections based on the pseudo-complete data, the initial model usually dominates the choice of significant factors in the final model. Some of the weakness of the EMM algorithm is presented in Section 3 with examples. In our experience, without working on the censored data itself, important factors in the imputation-modeling procedure could be wrongly specified. The objective of this article is to show how to model location and dispersion effects together based on the censored data and to compare our procedure to the EMM algorithm. Methods of maximum likelihood and likelihood ratio test are utilized to decide the important model terms. Our procedure takes the advantage of the fact that the number of significant factors in screening experiments is usually small (called effect sparsity in Box and Meyer, 1986 pp. 20). Instead of working on imputed data, we can compare various model fitting based on the original censored data and screen through all factors one at a time to decide the best model. See Section 4 for details.

Section 2 reviews background of the problem and describes Specht's (1985) heat exchanger data. Statistical models, Box-Cox (1964) transformation, mean and variance structures and the existence of maximum likelihood estimation are introduced there. Hamada and Wu's EMM procedure is also reviewed. In section 3, we compare contrasts of location effects computed from the censored data for selecting a better initial model to shorten the number of iterations required in the EMM procedure. Several examples are presented for comparing the factors identified from the EMM algorithm and our likelihood approach. Our forward censored regression is presented in Section 4 to analyze location and dispersion effects. Box and Meyer's log variance-ratios are also computed for the comparison purpose. Section 5 gives a brief conclusion of our study.

2. BACKGROUND OF THE PROBLEM AND LITERATURE REVIEW

2.1. The Heat Exchanger Life Data and the Statistical Model

In a study of strategies for improving reliability of a certain type of heat exchanger, Specht (1985) conducted life-testing experiments with a 12-run two-level Plackett-Burnman design. Ten variables including four process variables, A (standard and special), F (no process and process), J (current style and new style), K (extended and standard), two material selection methods, C (special and standard), E (standard and special), and four product design variables, B (style 1 and 2), D (heavy and light), G (sharp and standard), and H (processed and unprocessed) are considered. The design matrix and the interval lifetime (in 100 cycles) until the development of tube corner cracks (TCC) and duct angle cracks (DAC) are listed in Table 1. Note that in both responses 5 out of 12 (41.67%) data points are censored at 164 (× 100) cycles.

[Please place Table 1 here]

In this article, the random sample y_i after transformation $h(y_i)$ is assumed to follow a linear model with standard normal error ϵ_i:

$$h(y_i) = \underset{\sim}{x}_i'\underset{\sim}{\beta} + \sigma_i \epsilon_i, \tag{2.1}$$

where $\underset{\sim}{\beta}$ is a vector of a few *important* effects and $\underset{\sim}{x}_i$ is the corresponding vector of explanatory variables, including main effects and interactions. The standard deviation (s.d.) σ_i is a function of one or two *significant* dispersion effects with the following form:

$$\log(\sigma_i) = \log(\sigma_0) + w_{1i}\log(\sigma_{w1}) + \cdots + w_{qi}\log(\sigma_{wq}) = \underset{\sim}{w}_i'\underset{\sim}{\xi}, \tag{2.2}$$

where $\underset{\sim}{\xi} = (\log\sigma_0, \log\sigma_A, \ldots, \log\sigma_K)$, and w_{ji} can be main effects or their interactions. Box-Cox (1964) transformation,

$$h(y_i) = (y_i^\lambda - 1)/\lambda,$$

is employed to transform the data near normality. The transformation parameter λ is usually chosen to maximize the likelihood of the transformed data. The likelihood of a complete sample is $\phi(z_{yi})\,|\partial h(y_i)/\partial y_i|$ and the likelihood of a censored data is $\Phi(z_{bi}) - \Phi(z_{ai})$, where $z_{wi} = [h(y_{wi}) - \mu_i]/\sigma_i$, and $w = a$ or b corresponding to the left- or right-end point of the interval lifetime (y_{ai}, y_{bi}) and $\mu_i = \underset{\sim}{x}_i' \underset{\sim}{\beta}$. In general, the transformation parameter λ is tied with the mean μ_i and s.d. σ_i, which are functions of significant location and dispersion effects, respectively. It is rather difficult to decide them simultaneously, especially in dealing with complicated structure of screening experiments, where ML estimation (MLE) sometimes dose not exist. See Section 2.2 for more detail of the non-existence of MLE. In this article, we fix λ at a value, say -1.0 for DAC and -0.73 for TCC data, for which the ML fitting is the best (when MLE exists) and their dispersion effects are the most representative. Choosing the best transformation parameter and significant location and dispersion effects is under investigation in another of our manuscripts.

2.2. Existence of The Maximum Likelihood Estimation

In dealing with incomplete data, the method of maximum likelihood is commonly employed (c.f. Lawless, 1982) to estimate model parameters. However, in analysis of censored data from screening experiments, there are estimability problems in the ML approach (see Silvapulle and Burridge, 1984; Hamada and Tse, 1988) because the paucity of data. Hamada and Tse (1989a) pointed out that certain design configuration coupled with a special censoring scheme will cause the non-existence of MLE. For example, in the 2^2 experimental plan, corresponding to run #1, #2, #3 and #4, the factors A and B are assigned as (+1, +1, −1, −1) and (+1, −1, +1, −1), respectively. They stated that if left- or right- censored data are contained in the first and the second runs, denoted as 12, then MLE of regression parameters and variance σ^2

do not exist. In fact, if there are two censored data points, ML estimates exist only in cases that censoring occurs at 14 or 23 observations. Hamada and Tse (1989b) thus developed a MLECHK program based on a linear programming algorithm to check whether MLE exists from censored data in a design of experiment. Besides using the MLECHK program, one can detect the non-existence of MLE problem from running LIFEREG in SAS (1991) software, when the warning message of non-negative Hessian matrix is provided (c.f. Hamada and Tse, 1989a, pp. 5). Our experience (c.f. Hamada and Wu, 1991, pp. 37) indicates that in the case where MLE does not exist, the likelihood surface is flat for a range of unbounded parameter values. Even when MLE exists, in some cases, likelihoods can be the same for certain combinations of parameter values (c.f. Lu and Unal 1992a, pp. 6), which makes search for MLE difficult, and thus LIFEREG shows the warning message. In Lu and Unal (1992b), we proposed a Bayesian variable-selection and parameter-estimation procedure following Wei and Tanner's (1990) data augmentation algorithm to overcome the drawback of MLE. However, since Bayesian procedure is rather tedious for engineering usage, in this article, we show how to employ commonly used software to obtain ML estimates for detecting important location and dispersion effects. In next example, considering the corner data, we examine the existence of MLE on models with main effects only.

Example 1 (Main-Effects Model). Both LIFEREG and MLECHK show that MLE does not exist in the model with all ten main effects. Hence, Hamada and Wu's EMM (1991, pp. 33) procedure starting with the main-effects model does not work. One question is then for which part of main-effects model MLE exists and also gives the best likelihood, *i.e.* best ML fitting. Two examples with the transformed TCC data are provided here to show when MLE exists. A simple method, called the quick and dirty (QD) method, of analyzing censored data is to treat the censored times as actual failure times and then analyze them by standard methods applicable for complete data. Using this approach, we order the size of location contrasts as follows:

$$A, K, D, E, G, H, F, B, C, J. \tag{2.3}$$

The MLECHK shows that MLEs exist on the models including the first six terms, *i.e.* up to term H. That is, the MLE does not exist for model (Intercept, A, K, D, E, G, H, F), but does exist for the model without F. The log-likelihood of the model including terms up to H (and G) is obtained using LIFEREG as -10.02338 (and -11.82897).

One can use LIFEREG to estimate location parameters and their contrasts from censored data directly by pooling observations at the same level together (c.f. Box and Meyer, 1986). Specifically, the location parameters of F are estimated as $\hat{\mu}_{FL} = 1.32436$ and $\hat{\mu}_{FH} = 1.33519$ from the top and bottom 6 observations respectively. Hence, the location contrast of F is computed as $\hat{\delta}_F = \hat{\mu}_{FH} - \hat{\mu}_{FL} = .01083$. Similarly, the location contrast $\hat{\delta}_A$ of factor A is estimated as $-.03106$, which is 2.87 times of $\hat{\delta}_F$. Assuming equal variance, comparison of location effects can be easily done by using LIFEREG to regress the censored data *one factor at a time.* For example, for factor A, K, and F, their location contrasts are estimated as $-.01898$, $-.01728$ and .00675, respectively. Clearly, factor A and K have larger location effects than the one for F. For simplicity, one can order the size of location effects by their p-values of estimates provided by LIFEREG. For instance, the order of the 10 main effects and their corresponding p-values are given as follows:

$$\begin{aligned} &A(.0147), K(.0516), D(.2764), E(.3805), G(.4347), F(.4900), B\ (.6044), \\ &\qquad C(.6806), J(.8071) \text{ and } H(.8216)\ . \end{aligned} \tag{2.4}$$

Note that the first five factors are the same as the ones in (2.3) given by QD method. Since only main effects A and K have p-values less than or around 0.05, in latter studies, we select models including the interactions generated from A, K to see if their log-likelihood can be higher than -10.02338 given by (2.3), the main-effects model. □

2.3. Hamada and Wu's Model-Selection Method

The idea of imputation-maximization is commonly used in reliability (c.f. Wei and Tanner, 1990) and biostatistics (c.f. Dempster, Larid and Rubin, 1977). However, in papers other than Hamada and Wu (1991), their concentration is parameter estimation instead of selecting the best model and factor levels. Hamada and Wu's procedure takes the advantage of using the pseudo-complete sample to compare many models simultaneously. Their algorithm consists of the following steps: (A) Model selection phase: (A1) Initial model specification, (A2) Model fitting, (A3) Imputation, (A4) Model selection; repeat steps (A2) to (A4) *until the current model selected is the same as the previous model*; (B) Model assessment phase; repeat (A) and (B) until adequate model(s) are found; (C) Factor-level recommendation. For brevity of reference, Hamada and Wu's paper is denoted as HW later. Details of their procedure in part A are reviewed as follows:

(A1) Initial Model Specification. The experimenter decides the potentially important main effects, interactions and choose $\mu_0 = \underset{\sim}{X}_0 \underset{\sim}{\beta}_0$ (model 0), where $\underset{\sim}{X}_0$ is the matrix of explanatory variables. If no information is provided from the experimenter, they start with the model including all main effects.

(A2) Model Fitting. Fit the current model $\mu_i = \underset{\sim}{X}_i \underset{\sim}{\beta}_i$ using the ML criterion.

(A3) Imputation. Impute the censored data by their conditional expectation,

$$E[\, h(y) \,|\, y \in (a,\, b)]] = \underset{\sim}{X}_i \underset{\sim}{\beta}_i + \sigma_i[\phi(z_a) - \phi(z_b)]/[\Phi(z_b) - \Phi(z_a)]. \tag{2.5}$$

(A4) Model Selection. Informally apply a standard technique to identify significant main effect(s) and then screen out *important interactions between the identified main effect(s) and the other factors.*

In Section 3, we modify their procedure by starting with an initial model which includes significant main effects and interactions identified from the study of their *censored location contrasts* (c.f. Example 1). The improvement of likelihoods from various selected-models is monitored and used as part of our stopping criterion for variable-selection. In Lu and Unal (1992a), instead of restricting our selection within the interactions generated from the significant main effects only, we recommend to consider *all possible interactions in variable selection*, which usually leads to better models.

3. THE MODIFIED EMM PROCEDURE

In this section, we present applications of the EMM algorithm to both TCC and DAC data under a constant-variance model. With the TCC data, since including interactions in the initial model gives a better ML fitting than the model with only part of the main effects, we start our presentation for the model with interactions.

3.1. Starting with A Model Including Main Effects and Interactions for TCC Data

If MLE in the model suggested by experimenter or the model with all main effects does not exist, we suggest to study contrasts of main effects, interactions and pick up a model which fits the censored data best as the initial model. For instance, in Example 1 we show that the main effects A and K have the largest two contrasts and their p-values of estimates are both less than or around 0.05 significance level. Contrasts of the interactions generated from A and K can be computed similarly and ordered according to the size of their p-values as follows:

$$\begin{aligned} &A > K > AH(.1392) > BK = AE(.2764) > AG = DK(.3246) > FK = AC(.3792) \\ &\quad > AD = GK(.3805) > BA = EK(.4347) > AK(.5339) > FA = CK(.6166) \\ &\quad > HK(.7496) > JK(.7370) > AJ(.9564). \end{aligned} \tag{3.1}$$

The MLE exists for the models include the terms up to DK. The Model (Intercept, A, K, AH, BK, AE, AG) gets a log-likelihood -11.69272 from LIFEREG without warning message. However, LIFEREG does not converge for the model including DK and its log-likelihood is 0.0, which is the highest log-likelihood for an interval-censored data set. Since we need a converged ML estimates for initializing the EMM algorithm to perform model selections, Powell's (1964) directional grid search program of computing MLE is used to give the following converged ML estimates:

$$\hat{\beta}_0(1.32856),\ \hat{\beta}_A(-.10717\text{e}-01),\ \hat{\beta}_K(-.15167\text{e}-01),\ \hat{\beta}_{AH}(-.83532\text{e}-02),$$
$$\hat{\beta}_{BK}(.12507\text{e}-01),\ \hat{\beta}_{AE}(.66332\text{e}-02),\ \hat{\beta}_{AG}(-.12913\text{e}-01),$$
$$\hat{\beta}_{DK}(-.10593\text{e}-01),\ \hat{\sigma} = .11957\text{e}-04.$$

The censored data are then imputed at the conditional mean [c.f. Eq. (2.5)] and listed in Table 2. Applying forward regression on the pseudo-complete data, we obtain the following model and their R-Squares:

$$\text{A}(.3859),\ \text{K}(.6720),\ \text{CK}(.8522),\ \text{GK}(.9586),\ \text{AC}(.9886),\ \text{AJ}(.9944),\ \text{FA}(.9994),$$
$$\text{FK}(.9998),\ \text{AG}(1.0), \tag{3.2}$$

where the MLE exists up to the fourth term GK and LIFEREG gives a "floating point zero divide" message during the ML estimation. We thus use the QD method to impute the censored data and get LS estimates for the initial values in using Powell's program to find MLE. After several loops of Powell's program, the ML estimates are obtained and its log-likelihood = -17.77525, which is far less than 0.0 (or -11.69272) from the initial model.

Iterate the "imputation-modeling" procedure three more loops. The selected models are tabulated in Table 3 with the corresponding R-Squares and indications of the term for which MLE exists. In each model, although only a few terms are useful, we list nine terms there for comparison purpose. Their log-likelihoods are calculated as -9.4599, -18.21377, -2.78447. Note that the ML fitting in the fourth model is much better than previous two models. Its imputed data is listed in the fifth column of Table 2. The next model is selected as follows:

A(.5021), K(.8808), CK(.9624), AG(.9989), GK(1.0), AJ(1.0), FK(1.0),
AK(1.0), JK(1.0), (3.3)

where the MLE exists up to the term GK. Note that the fourth model and (3.3) are quite similar and the R-Squares in model (3.3) reaches 1.0 in the fifth term GK. Since the ML estimates from the fourth model and (3.3) are the same, the model selection is terminated and model (3.3) is our final choice.

Denote $\hat{\rho}_{12}$ as the product-moment estimate of correlation between the first and the second imputed data. From the correlations, $(\hat{\rho}_{12}, \hat{\rho}_{23}, \hat{\rho}_{34}, \hat{\rho}_{45})$ = (.844, .975, .981, .989), between the imputed data, one can see that the match of imputed data is improved and the R-Squares increase as the EMM algorithm proceeds. However, the imputed data given here does not match that well with the imputed data given in next section (c.f. Table 3) for another initial model. For example, the observations 9 and 10 are imputed as 1.3848 and 1.3603 here, but are imputed as 1.3588 and 1.3623 in Section 3.2. The sizes are reversed in these two censored data. Hence, the selected models are very different in these two sections.

[Please place Table 2 and 3 here]

3.2. Starting with A Model Including Only Main Effects for TCC Data

Comparing the main-effects models (2.3) and (2.4), since (2.3) gives a better likelihood, we consider (Intercept, A, K, D, E, G, H) as our initial model. Their regression parameters are estimated from LIFEREG as follows:

$$\hat{\beta}_0(1.32444),\ \hat{\beta}_A(-.14207\text{e}-01),\ \hat{\beta}_K(-.12153\text{e}-01),\ \hat{\beta}_D(-.79638\text{e}-02),$$
$$\hat{\beta}_E(.36203\text{e}-02),\ \hat{\beta}_G(.31543\text{e}-02),\ \hat{\beta}_H(-.37740\text{e}-02),\ \hat{\sigma} = .39882\text{e}-02,$$

with a log-likelihood -10.02338. The censored data are imputed at their conditional mean and tabulated in the first column of Table 3. The model selected from forward regression is given as follows:

A(.4450), K(.7689), FA(.8769), AK(.9270), AJ(.9519), GK(.9719), HK(.9855), BK(.9950), AC(.9990), EK(1.0), (3.4)

where the MLE exists up to the third term FA only. Going through the "imputation-modeling" procedure again, we obtain the next model:

A(.4831), K(.8622), FA(.9480), AJ(.9621), GK(.9781), HK(.9909), AE(.9975), EK(.9992), AK(.9996), CK(1.0), (3.5)

where the MLE exists up to the fifth term GK. The log-likelihood given by Powell's program reaches 0.0 for the converged ML estimates:

$$\hat{\beta}_0(1.32846),\ \hat{\beta}_A(-.19708e-01),\ \hat{\beta}_K(-.21279e-01),\ \hat{\beta}_{FA}(.88835e-02),$$
$$\hat{\beta}_{AJ}(-.69994e-02),\ \hat{\beta}_{GK}(-.52604e-02),\ \hat{\sigma} = .12321e-04.$$

With the newly imputed data (c.f. column 3 of Table 3), we select another model:

A(.4985), K(.8937), FA(.9437), AJ(.9742), GK(1.0), AG(1.0), CK(1.0), (3.6)

where the MLE exists up to the fifth term GK again. Since we reaches the same ML estimates, the model-selection is terminated and model (3.6) is our final choice in this study. Note that model (3.6) and (3.5) are quite similar except the last two terms, which are insignificant.

In models (3.6) and (3.3) selected with different initial models, only GK and AG interactions are the same. There is no FA in model (3.3), but it is the most important interaction term in model (3.4) to (3.6).

[Pleas put Table 4 here]

3.3. Analysis of Duct Angle (DAC) Data with the EMM Algorithm

Example 2 (Case with An Initial Model of Main Effects). Since MLE of the model with all main effects does not exist in fitting censored DAC data, we order censored location contrasts and consider the following initial model:

Intercept, J, A, B, K, C.

This model includes the most significant main effects and its MLE exists. The DAC censored data is imputed and tabulated in the first column of Table 5. The model selected from a regular forward regression is listed in Table 6 along with their R-Squares. MLE exists for this new model including the first 4 terms, J, A, AE and AC, and its log-likelihood is estimated as -9.18467. Getting ML estimates and using them to impute the data, we obtain a better-fitting model given in the second column of Table 6. Its MLE exists up to the sixth term, J, A, AE, AC, AH and AG. LIFEREG does not converge but Powell's algorithm gives the following converged ML estimates with 0.0 log-likelihood.

$$\hat{\beta}_0(.99104),\ \hat{\beta}_J(.49244\text{e}-02),\ \hat{\beta}_A(-.41902\text{e}-02),\ \hat{\beta}_{AE}(.28621\text{e}-02),$$
$$\hat{\beta}_{AC}(.22606\text{e}-02),\ \hat{\beta}_{AH}(-.12659\text{e}-02),\ \hat{\beta}_{AG}(-.17561\text{e}-02),\ \hat{\sigma}=.16406\text{e}-04.$$

From the imputed data given in the second column of Table 5, we select another model and list it in the third column of Table 6. Note that this new model,

Intercept, J, A, AE, AC, AG, AH, GJ, EJ, AJ (3.7)

agrees to previous model up to GJ. Since the MLE exists for the terms up to AG and AH only which is the case in previous model, we conclude that the selected models are converged and model (3.7) is our final choice. □

[Please place Table 5 and 6 here]

Example 3 (Case with An Initial Model Including Main Effects and Interactions). Including the censored contrasts of interactions in consideration, we are able to find the following model for which MLE exists:

Intercept, J, A, AC, JK, AH, DJ.

Although its log-likelihood converges to zero in Powell's program, we take its final estimates and impute the censored data for model selection. The imputed data and the selected model are listed in Table 5 and Table 7, respectively. The MLE exists for the model includes J, A, AE, AC, FJ, CJ and its log-likelihood is -4.37633 from Powell's program. We continue data imputation and model selection for two more loops. The selected models are listed in Table 7. From Table 7 we note that the final two models are very similar and their MLE exists up to AK with a log-likelihood -4.33777. Hence, we conclude the selection is terminated and the final model is

$$\text{Intercept, J, A, AE, AC, FJ, CJ, AK, GJ, AJ, BA.} \quad (3.8)$$

□

[Please place Table 7 here]

From these examples, we see that the initial model dominates the selection in the EMM algorithm. Models selected from different initial models can be rather distinct. For instance, models (3.7) and (3.8) agree in the first four terms, J, A, AE and AC only and its log-likelihood is -9.18467, which is very low compared to -1.38631 given from the model (Intercept, J, A, AE, GJ) selected from our censored forward regression given in next section. Note that the models (3.7) and (3.8) suggested by the EMM algorithm did not include GJ until the seventh or eighth term. Because there are only a few interactions generated from the main effects A and K, one should be able to work on the original censored data and include interactions into the model one factor at a time for comparing their likelihoods. This approach avoids troubles of data imputation and gives the basis of using likelihood ratio tests to check significance of the selected model. Hence, unless the number of interactions are too many for doing a forward censored regression, we recommend to work on the censored data directly. Details are given in the next section.

4. THE PROPOSED PROCEDURE – A FORWARD CENSORED REGRESSION

4.1. Model with Constant Variance

Example 4 (Analysis of TCC Data). LIFEREG gives a -16.35830 log-likelihood for the model with intercept, and two main effects A and K. Entering the interactions, FA, BA, AC, ..., one factor at a time and comparing their log-likelihoods, we obtain the best three-term model (Intercept, A, K, CK) with log-likelihood = -11.15440, which is significant at $\alpha = 0.01$ compared to the model with A and K only. Other log-likelihoods for models including an extra factor in (Intercept, A, K) are listed in the size of their likelihoods as follows:

$$\text{FK}(-13.14787),\ \text{AH}(-14.73027),\ \text{AJ}(-15.14202),\ \text{AE}(-15.69969),\ \ldots \tag{4.1}$$

Note that only interactions involve either A or K can be entered as a candidate model term. *Because this effect heredity (c.f. Hamada and Wu, 1993), the model-selection is better to be done in the forwarding fashion. If one can afford to proceed more searches, he/she can pick up a few top models and perform a (partial) fowarding all-subsets selection to select a better model (see Lu, Liu and Unal, 1993 for details).*

Including CK in the model, we enter another interaction term one factor at a time again and obtain their log-likelihoods:

$$\text{AG}(-4.96770),\ \text{HK}(-9.45996),\ \text{DK}(-9.79690),\ \text{JK}(-10.09590),\ \text{etc.} \tag{4.2}$$

Note that FK, AH and AJ does not appear this time. With more interactions added into the model (Intercept, A, K, CK, AG), LIFEREG starts to produce warning messages. The best converged ML estimate provided by LIFEREG is given as follows:

$$\begin{aligned}&\hat{\beta}_0(1.32837),\ \hat{\beta}_A(-.21093\text{e}-01),\ \hat{\beta}_K(-.13430\text{e}-01),\ \hat{\beta}_{CK}(-.96889\text{e}-02),\\ &\quad \hat{\beta}_{AG}(.54804\text{e}-02),\ \hat{\beta}_{GK}(-.88450\text{e}-03),\ \hat{\sigma} = .16350\text{e}-03,\end{aligned} \tag{4.3}$$

with a log-likelihood -2.78447. Changing GK to any interactions from FA, AH, FK, EK, JK, BA, DK and AJ will give near 0.0 log-likelihoods and their estimates have to be obtained from many iterations of Powell's program. We thus take GK as the final model for presenting procedures of detecting possible dispersion effects. In summary, the selected terms and their log-likelihoods are listed as follows:

Intercept(-24.19004), A(-21.27824), K(-16.35830), CK(-11.15440),

AG(-4.96770), GK(-2.78447). (4.4)

A series of likelihood ratio tests (LRT) can be conducted to see the significance of our selected factors. For example, for testing the necessity of including the last term GK, the LRT statistic is 4.36645 and its p-value from χ^2_1 distribution is 0.03665, which is significant at 0.05 level. Adding AG into the model (Intercept, A, K, CK) gives a big LRT statistic 12.37341 with p-value = 0.43550e-03. And, comparing our final model to the model with intercept only, the LRT statistic is calculated as 42.81113 and its p-value is 0.40355e-07 from χ^2_5 distribution. Hence, from our approach we can test significance of each term being added into the model based on the original censored data, which is the missing part in the EMM and other traditional procedures reviewed in HW's paper . □

Example 5. When we choose the third factor in Example 4, the interaction CK gave the best ML fitting with a log-likelihood -11.34123 and its final model (4.3) agrees to the model (3.3) selected from the EMM algorithm with an initial model including interactions. Since the second best ML fitting in the third factor is FA, which agrees to model (3.6) selected from another initial model including main effects only, in this example, we proceed the forward censored regression to see if more terms in (3.6) such as AJ and GK or AG will be matched to our selection here.

Starting with the model (Intercept, A, K, FA), forward censored regression is applied to tube corner data and the following model is selected:

Intercept, A, K, FA(-13.14787), AJ(-9.84343), GK(0.0). (4.5)

After fixing FA, interaction AJ indeed is the most important term, which agrees with the selection in (3.6). LIFEREG did not converge in the model with GK and Powell's program gives a converged result but its log-likelihood reaches 0.0. Changing the factor GK to AG, we obtain converged ML estimates from Powell's program and its log-likelihood is $-.74672e\text{-}04$, which is very good as well. Our model (4.5) matches perfectly to the model (3.6) selected in Section 3.2. □

In next example, we show a case that *the EMM algorithm and forward censored regression produce different selections and our procedure gives a better model.*

Example 6 (Analysis of DAC Data). Going through a series of ML fitting to the censored DAC data, we obtain the final model along with their log-likelihoods:

$$\text{Intercept}(-24.14369),\ \text{J}(-21.98314),\ \text{A}(-18.60972),\ \text{AE}(-9.78729),$$
$$\text{GJ}(-1.38631),\ \text{AK}(0.0). \tag{4.6}$$

Since LIFEREG does not converge for models including GJ and AK, Powell's algorithm is used to get converged ML estimates. For the model with AK, LIFEREG gives $-0.13945e\text{-}04$ log-likelihood, which is close to 0.0. Likelihood ratio tests show that it is significant for every term being added into the model, except the last term AK, which has a p-value 0.09589 from the χ_1^2 distribution for testing $\beta_{AK} = 0$. □

The final model (4.6) selected here does not agree to the models (3.7) and (3.8) selected from the EMM algorithm. Interactions such as AC, FJ or AG in the model (3.7), (3.8) did not show up in here at all. From all these examples, we feel that the forward censored regression is easier to use and it is more analytically sounded than the EMM algorithm.

4.2. Models for the TCC Data with Possible Dispersion Effect(s)

To reduce the product variability, one usually adjusts the controllable variables to the design levels which gives smaller variances. *In both articles of Box and Meyer (1986), and Nair and Pregibon (1988), the mean functions are all fixed at a known structure for studying dispersions.* In Section 4.2.1, Box and Meyer's log-variance contrasts are computed under the mean function (4.3). Our forward censored regression is extended to detect possible dispersion effect(s) in Section 4.2.2.

4.2.1. Box and Meyer's Procedure Based on Contrasts of Residuals

Box and Meyer (1986) recommended to work on residuals for computing variances to eliminate location effects. In our case, the residual for interval censored data is defined similar to the usual definition of residuals, namely, $e = y - \hat{y}$, as follows:

$$(e_L, e_R) = (y_L, y_R) - \hat{y}, \qquad (4.7)$$

where $\hat{y}$ is the prediction from a mean function. The predictions and the residuals from model (4.3) are listed in Table 8. For example, since the first two observations are right censored, the right-end points of the first two residuals are equal to infinities. From these residuals, one can use the *pooling technique* given by Box and Meyer (1986) to compute log-contrasts of dispersion effects. For instance, applying LIFEREG on the first 6 residuals, which are all from the low level of F, we obtain the ML estimate of σ_{FL} as .10587e-03. Similarly, from the bottom 6 residuals, $\hat{\sigma}_{FH}$ is calculated as .43952e-03. This gives a contrast of log-variances for F as $\log(\sigma^2_{FH}/\sigma^2_{FL}) = 2.84694$. Going through these contrasts of log-variances, one can identify significant dispersion effects. However, since there are only 6 observations in a group and, sometimes, the residuals are heavily right-censored. LIFEREG does not perform well and, in many cases, produces warning messages. We thus loop Powell's program a few times to get converged ML estimates of dispersion effects. The estimates of scale parameters and the dispersion effects are all tabulated in Table 9. From Table 9, we note that factor C has the largest dispersion effect, but the worst likelihood. In this case, the size of the estimated dispersion effects and the log-likelihood of the ML fitting are not consistent.

[Please put Table 8 and 9 here]

4.2.2. Modeling with Mean and Variance Functions

In this section, the forward censored model-selection idea is extended to detecting possible important dispersion effects. The underlying mean and variance structures are as stated in (2.1-2) and (4.8). Because it is easier to explain our idea with examples, the TCC data is analyzed here to illustrate our procedure. First, we start with the search of the best one-term model. This term can be in the mean or in the standard deviation (s.d.) function. For the constant variance model, comparing the fitting of all 10 main effects, factor A fits the best and its log-likelihood is -21.278. Consider the following one-term s.d.-model,

$$h(y_i) = \beta_0 + \sigma_i \epsilon_i, \text{ and } \log(\sigma_i) = \log(\sigma_0) + \mathrm{w}_i \log(\sigma_{\mathrm{w}}), \tag{4.8}$$

where the factor w_i can be any main effect. By fitting the 10 main effects in the $\log(\sigma_i)$ function one by one, the best one-term s.d.-model is with factor B and its log-likelihood is -20.471, which is better than the log-likelihood -21.278 from the best one-term mean model. Hence, our best one-term model is the one-term s.d.-model with factor B.

Proceeding the same procedures, we obtained the best two-term model as follows:

$$h(y_i) = \beta_0 + \beta_1 A_i + \sigma_i \epsilon_i, \text{ and } \log(\sigma_i) = \log(\sigma_0) + B_i \log(\sigma_1), \tag{4.9}$$

which is the 1-mean-and-1-s.d.-model, and its log-likelihood is -17.914. The best 2-term s.d.-model,

$$h(y_i) = \beta_0 + \sigma_i \epsilon_i, \text{ and } \log(\sigma_i) = \log(\sigma_0) + B_i \log(\sigma_1) + F_i \log(\sigma_2),$$

has a log-likelihood -18.088 larger than the log-likelihood -17.914 of model (4.9). Note that when the main effect B is entered in the s.d. function, the interactions BF, BA, ..., can then be considered as candidate terms in the model. Hamada and Wu (1992) called this requirement of the sequence of terms entering the model the "effect heredity."

The next step is to find the best three-term model based on the 1-mean-and-1-s.d.-model (4.9). After a series of model fittings, the best 2-mean-and-1-s.d.-model is with factors A and K in the mean function and B in the s.d. function, and its log-likelihood is -12.270. The best 1-mean-and-2-s.d.-model is with the mean factor A and s.d. factors B and H, and its log-likelihood is -16.371, which is not as good as -12.270. Hence, the best three-term model is the 2-mean-and-1-s.d.-model. The best four-term model is the 3-mean-and-1-s.d.-model with the log-likelihood -5.784. The best 2-mean-and-2-s.d.-model has a log-likelihood -6.024, which is not as good as -5.784. The best five-term model is the 3-mean-and-2-s.d.-model with the log-likelihood -3.617 with factors A, K, D in the mean function and factors B, BJ in the s.d. function. The best 4-mean-and-1-s.d.-model has a log-likelihood -4.333, which is worse than -3.617. Because there are only 12 data points in the TCC data set, we do not consider the s.d. model with more than two factors. Hence, the only six-term model is the 4-mean-and-2-s.d.-model. However, because the log-likelihood of the best 4-mean-and-2-s.d.-model is very close to the log-likelihood of the best 3-mean-and-2-s.d.-model, we stop our model-selection here. Note that the improvement of the log-likelihood in the best one-, two-, to five-term models are justified by the likelihood ratio tests (at the 0.05 significance level).

5. CONCLUSION

Hamada and Wu's (1991) expectation-modeling-maximization algorithm and our forward censored regression are applied to Specht's (1985) censored failure times from tube corner and duct angle cracks for detecting significant location effects. Our variable selection utilizes maximum likelihood method and works on the original censored data to avoid the ambiguity of the initial modeling, and the repetitions of imputation-modeling routines in the EMM algorithm. Significance of the model terms is checked sequentially and the stopping criterion for further model-selection is determined from likelihood ratio (LR) tests. Instead of using the large sample χ^2 approximation to find the critical values of the LR tests, the bootstrap idea can be utilized to find a better set of LR test critical values. In the last section, our procedure is extended to identify important dispersion effects. The forward censored model-selection idea can also be generalized to the all-subsets selection by incorporating more candidate models in the search.

REFERENCES

Box, G. E. P., and Cox, D. R. (1964), "An Analysis of Transformations" (with discussion), *Journal of the Royal Statistical Society*, B, 26, 211-252.

Box, G. E. P., and Meyer, R. D. (1986), "Dispersion Effects From Fractional Designs," *Technometrics*, 28, 19-27.

Dempter, A. P., Larid, N. M., and Rubin, D. B. (1977), "Maximum Likelihood From Incomplete Data via the EM Algorithm" (with discussion), *Journal of the Royal Statistical Society*, B, 39, 1-18.

Hahn, G. J., Morgan, C. B., and Schmee, J. (1981), "The Analysis of A Fractional Factorial Experiment With Censored Data Using Iterative Least Squares," *Technometrics*, 23, 33-36.

Hamada, M., and Tse, S. K. (1988), "A Note on the Existence of Maximum Likelihood Estimates in Linear Regression Models Using Interval-Censored Data," *Journal of the Royal Statistical Society*, Ser. B, 50, 293-296.

Hamada, M., and Tse, S. K. (1989a), "When Do Estimates Exist From Censored Data in Industrial Experiments?" Research Report 89-03, University of Waterloo, Institute for Improvement in Quality and Productivity.

Hamada, M., and Tse, S. K. (1989b), "MLECHK: A FORTRAN Program for Checking The Existence of Maximum Likelihood Estimates From Censored, Grouped, Ordinal and Binary Data From Designed Experiments," Research Report 89-09, University of Waterloo, Institute for Improvement in Quality and Productivity.

Hamada, M., and Wu, C. F. J. (1991), "Analysis of Censored Data From Highly Fractionated Experiments," *Technometrics*, 33, 25-38.

Hamada, M., and Wu, C. F. J. (1992), "Analysis of Designed Experiments with Complex Aliasing," *Journal of Quality Technology*, 24(3), 130-137.

Lawless, J. F. (1982), *Statistical Models and Methods for Lifetime Data*, NY: Wiley.

Lu, J. C., and Unal C. (1992a), "Process Characterization and Optimization Based On Censored Data From Highly Fractionated Experiments," to be published in *IEEE Transactions on Reliability.*

Lu, J. C., and Unal C. (1992b), "Bayesian Analysis of Censored From Highly Fractionated Experiments," Technical Report #2212, the Department of Statistics, North Carolina State University.

Lu, J. C., Liu, S., and Unal C. (1993), "Lowflow Regression Modeling with Bivariate Censored Data," revised for *Water Resources Research.*

Nair, V. N., and Pregibon, D. (1988), "Analyzing Dispersion Effects From Replicated Factorial Experiments," *Technometrics*, 30, 247-257.

Nelson, W. (1990), *Accelerated Testing. Statistical Models, Test Plans, and Data Analysis*, NY: Wiley.

Powell, M, J, D. (1964), "An Efficient Method for Finding the Minimum of a Function of Several Variables Without Calculating Derivatives," *Computer Journal*, 7, 155 -162.

SAS (version 6.03, 1991), a statistical software package marketed by the SAS institute Inc., SAS Campus Drive, Cary, NC 27513.

Silvapulle, M. J., and Burridge, J. (1984), "Existence of Maximum Likelihood Estimates in Regression Models for Grouped and Ungrouped Data," *Journal of the Royal Statistical Society*, B, 46, 100-106.

Specht, N. (1985), "Heat Exchanger Product Design via Taguchi Methods," in *Third Symposium on Taguchi Methods*, Romulus, MI: American Supplier Institute, Inc., pp. 302-318.

Taguchi, G. (1987), *System of Experimental Design*, White Plains, NY: Unipub/Kraus International.

Wei, G. C. F., and Tanner, M. A. (1990), "Posterior Computations for Censored Regression Data," *Journal of the American Statistical Association*, 85, 829-839.

Table 1. Design and Data for the Heat Exchanger Experiment

	Factor										Time to Failure	
Run	F	B	A	C	D	E	G	H	J	K	TCC*	DAC**
1	1	1	1	1	1	1	1	1	1	1	(164, ∞)	(128, 140)
2	1	1	1	1	1	2	2	2	2	2	(164, ∞)	(164, ∞)
3	1	1	2	2	2	1	1	2	2	2	(0, 42)	(116, 128)
4	1	2	1	2	2	2	2	1	1	2	(93.5, 105)	(56.5, 71)
5	1	2	2	1	2	1	2	1	2	1	(82, 93.5)	(71, 82)
6	1	2	2	2	1	2	1	2	1	1	(93.5, 105)	(71, 82)
7	2	1	2	2	1	2	2	1	2	1	(164, ∞)	(164, ∞)
8	2	1	2	1	2	2	1	1	1	2	(56.5, 71)	(56.5, 71)
9	2	1	1	2	2	1	2	2	1	1	(164, ∞)	(164, ∞)
10	2	2	2	1	1	1	2	2	1	2	(56.5, 71)	(0, 42)
11	2	2	1	2	1	1	1	1	2	2	(128, 140)	(164, ∞)
12	2	2	1	1	2	2	1	2	2	1	(164, ∞)	(164, ∞)

*: Tube Corner Cracks; **: Duct Angle Cracks.

Table 2. Imputed Tube Corner Data for Models in Section 3.1

*First**	*Second*	*Third*	*Fourth*	*Fifth*	*Original***
1.3417	1.3707	1.3659	1.3677	1.3603	893.06
1.3368	1.3613	1.3591	1.3403	1.3463	261.81
1.2775	1.2865	1.2755	1.2825	1.2756	39.11
1.3240	1.3220	1.3226	1.3228	1.3220	98.89
1.3199	1.3175	1.3166	1.3159	1.3167	85.67
1.3211	1.3220	1.3227	1.3236	1.3233	102.87
1.3370	1.3586	1.3397	1.3379	1.3396	185.68
1.3075	1.3033	1.3024	1.2990	1.3009	59.97
1.4054	1.3802	1.3923	1.3773	1.3848	∞
1.2979	1.3033	1.3024	1.3053	1.3009	59.97
1.3326	1.3315	1.3315	1.3313	1.3310	131.68
1.3413	1.3707	1.3659	1.3528	1.3603	893.06

*: Data is given in the transformed scale with $\lambda = -0.73$ in Box-Cox Transformation

$$y^{(\lambda)} = (y^{\lambda} - 1)/\lambda.$$

**: The fifth imputation is transformed back to the original scale.

Table 3. Selected Models in Section 3.1 for TCC Data

Second		*Third*		*Fourth*	
Model	*R-Square*	*Model*	*R-Square*	*Model*	*R-Square*
A	.4613	A	.5333	A	.5042
K	.8057	K	.8368	K	.8609
CK	.9134	CK	.9764	CK	.9781
HK*	.9493	AH*	.9861	GK	.9897
BA	.9912	HK	.9928	AG*	.9976
DK	.9949	AG	.9959	EK	.9988
AD	.9983	GK	.9986	FK	.9998
AG	.9995	AK	.9996	AK	.9999
AE	1.0	BA	1.0	AE	1.0

*: The MLE exists up to this term.

Table 4. Imputed Tube Corner Data for Models in Section 3.2

First Imputation		*Second Imputation*		*Third Imputation*	
Original	*Transformed*	*Original*	*Transformed*	*Original*	*Transformed*
527.74	1.3358	∞	1.3808	3195.66	1.3361
190.62	1.3402	236.60	1.3445	169.23	1.3375
41.51	1.2796	42.00	1.2804	39.83	1.2769
100.57	1.3226	99.85	1.3223	103.42	1.3235
87.50	1.3175	87.72	1.3176	92.07	1.3194
100.13	1.3224	98.96	1.3220	101.54	1.3229
207.49	1.3420	248.24	1.3454	166.85	1.3371
58.94	1.3000	62.37	1.3028	70.60	1.3086
195.11	1.3407	1143.25	1.3618	738.64	1.3588
62.07	1.3026	62.37	1.3028	56.81	1.2981
133.77	1.3315	133.39	1.3314	128.28	1.3303
199.53	1.3412	1143.25	1.3618	1240.81	1.3623

Table 5. Imputed Data from the EMM Algorithm for DAC Data

Example 5 First	Example 5 Third	Example 6 First	Example 6 Third
133.65	131.62	133.73	136.91
208.48	43307.90	17335.51	5077.06
121.76	119.89	122.90	118.69
66.52	69.78	62.27	57.13
77.20	72.24	72.82	80.92
73.99	80.22	76.74	75.21
287.05	227.98	173.26	169.66
59.15	69.18	62.32	58.13
244.45	164.69	212.19	169.68
40.50	38.13	41.34	41.14
185.32	440.56	185.72	298.51
198.16	1062.62	357.21	5077.06

Table 6. Selected Models in Example 2 for DAC Data

First		*Second*		*Third*	
Model	*R-Square*	*Model*	*R-Square*	*Model*	*R-Square*
J	.3106	J	.4155	J	.3647
A	.5658	A	.6594	A	.6700
AE	.7940	AE	.9127	AE	.8510
AC*	.8624	AC	.9584	AC	.9288
AJ	.9272	AH	.9752	AG	.9755
AG	.9572	AG*	.9861	AH*	.9948
EJ	.9771	GJ	.9934	GJ	.9967
FA	.9949	AJ	.9992	EJ	.9999
JA	.9994	HJ	.9999	AJ	1.0
AH	1.0	DJ	1.0		

*: The MLE exists up to this term.

Table 7. Selected Models in Example 3 for DAC Data

First		*Second*		*Third*	
Model	*R-Square*	*Model*	*R-Square*	*Model*	*R-Square*
J	.3306	J	.4083	J	.4160
A	.6439	A	.7021	A	.7194
AE	.7816	AE	.8442	AE	.8439
AC	.8876	AC	.9273	AC	.9296
FJ	.9557	FJ	.9729	FJ	.9659
CJ*	.9813	CJ	.9939	CJ	.9873
BA	.9924	AK*	.9978	AK*	.9994
AJ	.9974	AJ	.9991	GJ	.9997
HJ	.9998	GJ	.9999	AJ	.9999
AG	1.0	EJ	1.0	BA	1.0

*: The MLE exists up to this term.

Table 8. Prediction and Residual for Constant Variance Model (4.3)

Prediction		Transformed Data**		Residual	
*Transformed**	*Original*	*Left*	*Right*	*Left*	*Right*
1.35780	653.6897	1.33676	1.36956	$-2.10380e-02$	$1.17563e-02$
1.33936	183.4059	1.33676	1.36956	$-2.59499e-03$	$3.01993e-02$
1.27956	41.4752	$-\infty$	1.28039	$-\infty$	$8.25103e-04$
1.31998	93.5074	1.31998	1.32403	$-2.87339e-06$	$4.04758e-03$
1.31738	87.2292	1.31496	1.31998	$-2.42260e-03$	$2.59333e-03$
1.32403	105.0133	1.31998	1.32403	$-4.05467e-03$	$-4.22280e-06$
1.33676	163.9918	1.33676	1.36956	$1.21244e-06$	$3.27955e-02$
1.29894	57.7422	1.29781	1.30887	$-1.13492e-03$	$9.93303e-03$
1.36799	8359.9767	1.33676	1.36956	$-3.12240e-02$	$1.57034e-03$
1.30813	69.8348	1.29781	1.30887	$-1.03267e-02$	$7.41226e-04$
1.33271	139.9991	1.33020	1.33271	$-2.51157e-03$	$1.76494e-07$
1.35780	653.6897	1.33676	1.36956	$-2.10380e-02$	$1.17563e-02$

*: Box-Cox Transformation $y^{(\lambda)} = (y^\lambda - 1)/\lambda$ and $\lambda = -0.73$.

**: The right censored data are changed to 99999 and 1.36956 in the orginal and the transformed scales, respectively, for better presentation.

Table 9. Maximum Likelihood Estimates of Scale Parameters and Dispersion Effects

	Factor				
	E	*H*	*F*	*A*	*G*
$\widehat{\sigma}_H$	.99856e − 07	.80774e − 04	.20660e − 06	.32891e − 03	.71002e − 07
$\widehat{\sigma}_L$	.92337e − 04	.94191e − 07	.30643e − 03	.70218e − 07	.21742e − 04
dispersion*	− 13.65894	13.50817	− 14.60392	16.90387	− 11.44859
log-likelihood	− .74158	− .74863	− 1.42318	− 1.48888	− 1.59903

	Factor				
	B	*D*	*J*	*K*	*C*
$\widehat{\sigma}_H$	.40609e − 03	.19152e − 06	.13275e − 06	.30089e − 06	.64475e − 03
$\widehat{\sigma}_L$	.58151e − 07	.86050e − 04	.96950e − 09	.10358e − 07	.22867e − 07
dispersion	17.70257	− 12.21538	9.83889	6.73799	20.49385
log-likelihood	− 2.09132	− 2.11359	− 2.30259	− 2.30259	− 2.77575

*dispersion effect $= \log(\widehat{\sigma}^2_H/\widehat{\sigma}^2_L)$.