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This paper describes methods that can be used to evaluate stand and tree growth response to a single application of fertilization and/or thinning with data collected from multiple installations. Two kinds of methods were proposed: (1) structure analysis which applies covariance analysis in a blocked design with and without sampling units, and (2) multi-step analysis which first fits a control model to control data and then uses it to evaluate treatment response. Ideally, the former method is preferred to the latter method for evaluating the treatment response. However, when the experimental data are large in sampling size and/or complex in their designed structure, structure analysis often can not be performed on most statistical packages, and, therefore, the multi-step analysis is a viable alternative.

The methods were applied in modeling fertilization and thinning effects on Douglas-fir [Pseudotsuga menziesii (Mirb.) Franco] dominant height growth and diameter growth of single trees. Both responses due to improved nutrition from a single application of nitrogen fertilizer were significant (α=0.05) in the first 5-year growth period, and not significant after two 5-year cycles. The response in diameter growth was stronger than that in dominant height growth. Thinning neither increased nor decreased the dominant height growth. It accelerated diameter growth, but the interaction of fertilization with thinning was not significant.

As a comparison, both structure analysis and two-step analysis were used to model the direct effect of fertilization on the gross basal area growth of plots. The results showed that the appropriate variance estimates to test the significance of the parameters in fertilizer response equation were larger when using two-step analysis than when using structure analysis.

Analysis Methods for Modeling Tree and Stand Growth Responses to Fertilization and Thinning

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Chapter 1

Introduction

The application of chemical fertilizers to forests in the Pacific Northwest has generated wide interest in the last two decades. Nitrogen has been found to be the most common limiting nutrient for coniferous tree growth in this region (Gessel et al. 1973). Gessel et al. (1979) reviewed the development of forest tree nutrition research in the Northwest, and concluded that there was little evidence that application of elements other than nitrogen (i.e., phosphorus, potassium, and sulfur) produced an economical response. Addition of nitrogen in the form of urea can result in a rapid acceleration of the stand's nutrient cycle (Cole 1979) and it can improve tree growth of Douglas-fir [Pseudotsuga menziesii (Mirb.) Franco] on a variety of sites in the Pacific Northwest (Miller and Webster 1979, RFNRP 1982, Miller et al. 1986). The rates of application of nitrogen fertilizer

have generally been limited to 400 lbs per acre or less. The biologically and economically optimum dosage of nitrogen fertilizer for a Douglas-fir stand probably lies between 150 and 300 lbs per acre (Miller and Fight 1979). Throughout the region, landowners are now applying nitrogen fertilizer to forest stands to increase growth and improve the economic gain from forestry operations.

The ORegon Growth ANalysis and projectiON system (ORGANON) is a single-tree/distance-independent (Munro 1974) type of growth and yield model. It predicts the structure and composition of the stand in the future through the application of diameter growth (Hann and Larsen 1990), height growth (Hann and Ritchie 1988), height to crown base (Ritchie and Hann 1987), and mortality (Hann and Wang 1990) equations to a representative sample of trees taken from the stand. The southwest Oregon version of ORGANON (SW-ORGANON) (Hester et al. 1989) is applicable to mixed conifer stands with breast height ages from 15 to 120 years. The data set collected to develop the model did not contain stands that had been fertilized, nor did it contain data on type or intensity of cuttings that may have occurred before the start of the five-year growth period that was measured. Therefore, the data could not be used to estimate the effects of fertilizer on tree growth, nor to estimate the "true effect" of thinning. The model does

predict a thinning effect under the assumption that the trees in the stand will immediately and fully respond to reduced density due to thinning. The longer term effect of thinning can be characterized by increases in the crown lengths of the trees, until the stand achieves crown closure, and by continued reduced density. These assumptions, however, should be validated through the analysis of data from thinned stands.

Woollons and Whyte (1988) reviewed the reports on fertilizer research cited in Forestry Abstracts, and found that the large majority of these reports gave no or very sparse details of statistical design and analysis. They concluded that:

> "Fertilizer trials in forest stands do not fit easily into textbook examples of experimental analysis. They are frequently (1) very large, occupying several hectares of forest area, (2) required to be maintained over several decades, and (3) unbalanced with respect to the quanta of initial growing stock and growing conditions in each experimental unit. The first two criteria can produce high levels of residual variation in forest nutrition experiments, while the third consideration can be a source of serious confounding, which unless removed, can produce

badly biased estimates of treatment responses, and low sensitivity in hypothesis testing." (Page 770)

1.1 Objectives

The accurate and precise prediction of the response of stands to fertilization and thinning response is important for making decisions concerning the treatment of stands and the allowable cut of forests. Therefore, the objectives for this study were:

(1) To propose analysis methods for modeling stand and tree growth response to fertilization and thinning.

(2) To develop fertilization response modifier equations for the dominant height growth equation and the diameter growth equation of Douglas-fir in SW-ORGANON.

(3) To develop improved thinning response modifier equations for the dominant height growth equation and the diameter growth equation of Douglas-fir in SW-ORGANON.

Two kinds of analysis methods for modeling stand and tree growth response to treatment are proposed and discussed in Chapter 2. Applications of these methods for modeling the diameter and dominant height growth

response of trees to just fertilization and to both fertilization and thinning are presented in Chapters 3 and 4, respectively. Finally, Chapter 5 compares the results obtained by applying the two different analysis methods to the problem of modeling stand growth response to fertilization.

1.2 Data Source

Two substantial growth and yield data sets have been collected in southwest Oregon. The first was collected to develop the SW-ORGANON model and is composed of temporary plots established in 391 stands covering a wide range in site classes, stand ages, stand structures and species mixes. The second data set is composed of 20 research installations in even-aged Douglas-fir stands that were installed in southwest Oregon as part of several different regional thinning and fertilization studies. Since the first data set has a larger sample size and a wider range in the stand attributes sampled, the existing equations in SW-ORGANON will be used to predict untreated stand response and the second data set will be used to develop fertilizer and thinning response modifiers for SW-ORGANON's existing equations. Unfortunately, the development of the modifier equations is complicated by the fact that the two data sets were

composed of different plot designs. The following is a general description of both plot designs and a detailed description of the thinning and fertilization installations.

1.2.1 The SW-ORGANON Plot Design

The SW-ORGANON plot design is composed of a cluster of 4 to 10 sampling points located at the apices of equilateral triangles spaced 150 feet apart. Three subplots were established at each point: a variable-radius subplot and 2 nested fixed-area subplots. The variable-radius subplot had a basal area factor (BAF) of 20 and was used for measuring trees with diameter at breast height (DBH) > 8.0 inches. One of the fixed area subplots had a radius of 15.56 feet and was used for measuring trees with $4.0 < DBH \leq 8.0$, and the other fixed-area subplot had a radius of 7.78 feet and was used for measuring trees with $DBH \leq 4.0$ inches. More details about this data set can be found in Ritchie and Hann (1987), Hann and Larsen (1990), and Hann and Wang (1990).

1.2.2 The Thinning and Fertilization Data of Southwest Oregon

The thinning and fertilization data set used in this

study was part of a larger data set used by Miller et al. (1988) to develop equations for predicting gross volume growth response to thinning and fertilizing of Douglas-fir stands. All Douglas-fir installations near the study area of SW-ORGANON were visited to determine by visual inspection if the installations had stand structures, species mixes, and soil types similar to the stands found in the SW-ORGANON study area. In addition, each selected installation had to have at least one control plot. Of the 20 installations that met the selection criteria, 16 were established by the Regional Forest Nutrition Research Project (RFNRP).

The number of replications and plot sizes between installations differed because they were installed at different times and by different organizations. Therefore, the 20 installations had a total of 109 fixed-area plots that ranged in size from 0.1 to 0.2 acres per plot. The type of treatments also differed between installations and included:

1. A single application of 200 lbs of nitrogen
2. A single application of 400 lbs of nitrogen
3. Repeated applications of 200 lbs of nitrogen
4. A single application of 400 lbs of nitrogen followed by repeated applications of 200 lbs of nitrogen
5. A single thinning without fertilization

6. Repeated thinnings without fertilization
7. A single thinning with a single application of 200 lbs of nitrogen
8. A single thinning with retreated applications of 200 lbs of nitrogen

In all installations, the treatments were randomly assigned to the plots. Table 1-1 shows the number of installations by the different types of treatments and their replications.

On the fertilized plots, nitrogen was broadcast uniformly by hand within both the plot boundaries and the surrounding buffer zones. On the thinned plots, the intensity of thinning ranged from 17% to 71% of the basal area (BA) removed, and the ratio of quadratic mean diameter for those thinned trees to quadratic mean diameter for trees before thinning (i.e., the d/D ratio) ranged from 0.492 to 0.917. When thinning from below, the d/D should be less than 1.0, otherwise the d/D should be greater than 1.0. Table 1-2 shows the number of plots by their d/D ratio and the BA removed.

The total time over which measurements had been made ranged from 6 to 18 years. Table 1-3 shows the length of and timing of the measurements. The interval between two successive measurements for the RFNRP's data was 2 years. For the other data sets, the interval ranged from 2 to 5 years. At each measurement, DBH was recorded to the

Table 1-1: The number of installations by the different types of treatments and their replications

Number of Installations	Number of Plots	Treatment Codes
1	8	0N 02 2N 2N 2N 22 4N 42
8	6	0N 02 2N 22 4N 42
5	4	0N 0N 2N 2N
1	3	0N 0N 2N
1	2	0N 22
1	9	0N 0N 0N TT TT TT TT TT TT
2	8	0N 0N 2N 2N 0T 0T 2T 2T
1	3	0N TT 3T

Treatment Codes:
- 0N = No fertilizer and no thinning initially
- 2N = 200 lbs N per acre initially with urea fertilizer
- 4N = 400 lbs N per acre initially with urea fertilizer
- 0T = No fertilizer but thinned initially
- 2T = 2N plus thinned initially
- 4T = 4N plus thinned initially
- 02 = 0N plus 200 lbs N per acre after 8 and 12 years with urea fertilizer
- 22 = 2N plus 02
- 42 = 4N plus 02
- 1T = 0T plus 02
- 3T = 2T plus 02
- TT = No fertilizer but thinned every measurement

Table 1-2: The number of plots by their d/D ratio and the basal area removed

d/D	Percentage of BA Removed							
	10% to 19%	20% to 29%	30% to 39%	40% to 49%	50% to 59%	60% to 69%	70% to 79%	Total
	---------- Number of Plots ----------							
.4 to .499	1							1
.5 to .599								
.6 to .699								
.7 to .799			2	4				6
.8 to .899			1	1	4	1		7
.9 to .999			1				1	2
Total	1		4	5	4	1	1	16

d/D ratio: The ratio of quadratic mean diameter for those thinned trees to quadratic mean diameter for trees before thinning

BA removed: The basal area removed

Table 1-3: The length and timing of the measurements by installations

Installation Number	Installation Code	YEAR 1111111111111111111 9999999999999999999 6677777777778888888 8901234567890123456
1	51	-E-R-R-R-R-R-R-R-I-
2	67	--E-R-R-R-R-R-R-R-I
3	92	--E-R-R-R-R-R-R-R-I
4	93	--E-R-R-R-R-R-R-R-I
5	94	--E-R-R-R-D
6	95	--E-R-R-R-R-R-R-R-I
7	105	--E-R-R-R-R-R-R-R-I
8	106	--E-R-R-R-R-R-R-R-I
9	175	-------E-R-R-R-R-R-
10	204	---------E-R-R-I---
11	205	---------E-R-R-I---
12	212	---------E-R-R-R-R-
13	213	---------E-R-R-R-R-
14	215	---------E-R-R-R-R-
15	216	---------E-R-R-R-R-
16	217	---------E-R-R-R-R-
17	310	E----R----R----R---
18	355	ER-R-R-R----R
19	356	ER-R-R-R----R
20	365	---E--R-R---R

E : Established
R : Remeasured
D : Dropped
I : Inactive

nearest 0.1 inch for all trees greater than 1.55 inches in DBH. Total tree heights were measured to the nearest foot on a subsample of from 10 to 20 trees, with about 10 of the trees being Douglas-fir. Finally, crown ratios were measured on a subsample of trees in only one installation.

The Hann and Scrivani's site index for an installation was computed as the mean of the largest ten site index values among all site trees found on the installation. Table 1-4 shows the number of plots by their breast height age and site index. The data were converted into five-year growth periods by linearly interpolating between successive measurements (i.e., if a tree is alive in the sixth year, its fifth year DBH is estimated by the average of its fourth-year DBH and its sixth-year DBH.).

Because of the small sample sizes, all data collected after the application of a second treatment were excluded from the data set. In the end, there were a total of 109 plots in the first 5-year measurement cycle, only 34 plots in the second cycle, and only 21 plots in the third cycle (Table 1-5) and, most of these plots were either control or fertilized plots. The range in site index and breast height age for the thinned plots was narrower than that for unthinned plots (Table 1-5).

Table 1-4: The number of plots by their breast height age and site index

Breast Height Age	Site Index 60 to 69	70 to 79	80 to 89	90 to 99	100 to 109	110 to 119	120 to 129	130 to 139	Total
10-19	3		2		2		6		13
20-29			9	6	2	9	4		30
30-39				7	12		8		27
40-49			4	10	1				15
50-59				7	5	4			16
60-69	3								3
70-79	1		2						3
80-89			2						2
Totals	7	0	19	30	22	13	18	0	109

Table 1-5: The number of plots for each 5-year growth period, and the ranges of site index (SI) and initial breast height age (AGE) by treatments

Treatment	5-Year Growth Period			SI	Initial AGE
	First	Second	Third		
C	39	10	7	66 - 125	11 - 83
F	54	20	14	66 - 125	13 - 81
T	11	2	0	76 - 117	16 - 50
FT	5	2	0	76 - 117	16 - 50
Total	109	34	21		

C : The control plots
F : The fertilized only plots
T : The thinned only plots
FT : The fertilized and thinned plots

Chapter 2

Analysis Methods for Modeling Stand and Tree Growth Response to Fertilization

In fertilizer trials, the experimental unit is usually a fixed area plot of a certain size. This enables the quantitative determination of response to fertilization to be expressed on the basis of a unit of land area, which is the same basis upon which most management decisions are made. These trials can be useful in the analysis of stand and tree growth response to fertilization. Special care, however, should be taken in distinguishing between experimental error and sampling error in analyzing individual tree response to fertilization because a tree is a sampling unit and not an experimental unit. The error variance estimated by ignoring experimental units and using just the sampling units is in general considerably smaller than that estimated from the experimental units (Milliken and Johnson 1984). As a result, incorrectly assuming that the individual tree is an experimental unit will possibly increase the F-statistics normally used to test for significance of fertilization response and, therefore, can lead the experimenter to false conclusions concerning the significance of the fertilization

response.

To evaluate how fertilizer response changes over time, Miller and Tarrant (1983), Auchmoody (1985), and Opalach and Heath (1988) have partitioned long-term fertilizer response into direct and indirect effects. Opalach and Heath (1988) defined the direct effect as "... that part of the response due to improved nutrition...", and the indirect effect as "... the remaining portion of the response due to altered stocking brought on by fertilizer in previous growing seasons." In general, the direct effect is the response that modelers attempt to estimate in the development of fertilizer response equations for growth and yield models. Therefore, this study will deal with the prediction of the direct effect due to fertilization.

The objective of this chapter is to describe alternative analytical methods that can be used to model the direct response of stands or trees to a single application of fertilizer. Two types of methods are presented: (1) structure analysis, and (2) multi-step analysis. Both of these methods can be useful in estimating either plot or tree response to plot level application of fertilizer, and both methods are well suited for analyzing repeated measurement data collected from multiple installations. Methods appropriate for the analysis of fertilizer effects for a single installation

are discussed by Turnbull and Peterson (1976b), Lipas (1979), Barclay and Brix (1985), Mize and Schultz (1985), and Jozsa and Brix (1989).

In most of the following analytical methods, the parameters can be estimated by either ordinary least squares (OLS) techniques or, if the variances are not homogeneous, by generalized least squares (GLS) techniques. When exceptions occur, they will be discussed under the specific analytical method. Possible complications due to the presence of serial correlation will be ignored for the following reasons:

1. Fertilization data sets are usually composed of many independent growth series that are short in duration and that start in different years. As a result, the effect of serial correlation should be reduced.
2. Parameters estimated by ignoring serial correlation are unbiased, though the variances of the parameters are biased (Kmenta 1986). Gregoire (1987) found that OLS estimation frequently had smaller prediction root mean squared errors and smaller maximum absolute prediction errors than estimation procedures that corrected for serial correlation. He also found that the data set must contain a sufficient number of growth periods in order to accurately estimate the correlation coefficient.
3. The effect of serial correlation can be minimized by

increasing the length of the growth period. For example, Gertner (1985) used diameter growth measurements from increment cores to analyze the effect of growth period length upon the severity of serial correlation. He found that serial correlation was large for annual growth periods but, for periods over four years, the effect was negligible.

4. Because correction for serial correlation can be a difficult problem, especially in some of the more complicated methods to be discussed, the gain from correction should be substantial in order to justify the effort needed to apply the correction.

The following are some common subscriptions that will be used through out the remainder of this thesis:

$i = 1,...,b$ blocks (installations)

$j = 1,...,t$ treatments (j=1 for control)

$k = 1,...,r$ plots (replications)

$l = 1,...,c$ measurement periods (cycles)

$m = 1,...,n_{k,l}$ number of trees on plot "k" and cycle "l"

$p = 1,...,v$ number of plot-level covariates

$q = 1,...,w$ number of tree-level covariates

2.1 Structure Analysis

The use of covariates to analyze split-plot and split-block designs has been previously illustrated by Federer (1955), Hazard and Peterson (1984) and Peterson and Hazard (1990). In the split-plot analysis, the significance of the whole plot covariates are tested using the variance of whole plot error, and the significance of the split-plot covariate(s) are tested using the variance of split-plot error. Applying the same rationale, this study proposes to use covariates in the analysis of a block design with either experimental units (plots) alone or with both experimental units (plots) and sampling units (trees). The mean square of experimental error will be used to test the significance of the plot level covariate(s), and the mean square of sampling error will be used to test for the significance of the tree level covariate(s).

2.1.1 Estimating Plot Response using Structure Analysis

Using structure analysis, the general linear model for estimating periodic stand increment response to fertilization is:

$$Y_{ijkl} = \mu + \Sigma_{i=1}^{b} \beta_i B_i + \Sigma_{l=1}^{c} \tau_{1l} T_{1l} + \Sigma_{j=2}^{t} \Sigma_{l=1}^{c} \tau_{jl} T_{jl} + \Sigma_{l=1}^{c} \Sigma_{p=1}^{v} \alpha_{1lp} X_{ijklp} + \Sigma_{j=2}^{t} \Sigma_{l=1}^{c} \Sigma_{p=1}^{v} \alpha_{jlp} T_{jl} X_{ijklp} + \epsilon_{ijkl}$$

where

Y_{ijkl} = Transformation of G_{ijkl}

G_{ijkl} = periodic increment of period l, replicate k, treatment j, installation i

μ = mean Y

B_i = 1.0 if data from block "i",
= 0.0 otherwise;

T_{jl} = 1.0 if data from treatment "j" at cycle "l",
= 0.0 otherwise;

X = plot-level covariate(s)

τ_{1l}, τ_{jl}, α_{1lp}, α_{jlp} = parameters

β_i and ϵ_{ijkl} are random errors of blocks and plots, respectively

The dependent variable, Y_{ijkl}, is often formed by taking the logarithm of the measured periodic increment, G_{ijkl}, and it assumes that G_{ijkl} is with multiplicative error. This transformation will linearize most of the nonlinear equation forms that are used to characterize stand or tree growth, and the residuals of this transformation often have homogeneous variance and a normal distribution. Several intercept corrections for possible log-bias are available (Flewelling and Pienaar 1981).

However, application of these intercept corrections will not affect the estimated parameters for the direct effect of fertilization (i.e., τ_{j1} and α_{j1p}). Another useful transformation is:

$$Y_{ijkl} = \log(G_{ijkl}) - \log(\hat{G}_{ijkl})$$

where

$\hat{G}_{ijkl}$ = Predicted periodic increment from an existing equation.

This transformation can be used to develop a fertilization response modifier equation for the existing equation, or it can be used to validate the existing equation to the control plots and/or to the fertilized plots.

Since the direct effect is usually the response of interest, this general linear model can be simplified by using a common control equation whose parameters are estimated from data for all growth periods. This can be done by dropping $\Sigma_{l=1}^{c} \tau_{11} T_{11}$ (i.e., set $\tau_{11} = \tau_{12} = \tau_{13} = 0$) and changing $\Sigma_{l=1}^{c} \Sigma_{p=1}^{v} \alpha_{11p} X_{ijklp}$ to $\Sigma_{p=1}^{v} \alpha_{1.p} X_{ijklp}$ (i.e., set $\alpha_{11p} = \alpha_{12p} = \alpha_{13p} = \alpha_{1.p}$). After simplification, the full linear model is as follows:

$$Y_{ijkl} = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} + \epsilon_{ijkl} \qquad [2\text{-}1]$$

where

$\underline{B} = \Sigma_{i=1}^{b} \beta_i B_i$ (block effect)

$\underline{T} = \Sigma_{j=2}^{t}\Sigma_{l=1}^{c} \tau_{jl} T_{jl}$ (treatment effect by cycles)

$\underline{X} = \Sigma_{p=1}^{v} \alpha_{1.p} X_{ijklp}$ (plot-level covariates)

$\underline{TX} = \Sigma_{j=2}^{t}\Sigma_{l=1}^{c}\Sigma_{p=1}^{v} \alpha_{jlp} T_{jl}*X_{ijklp}$
(treatment and plot-level covariate interactions)

In this setting, an installation is treated as a block, and a plot as an experimental unit. The appropriate analysis of variance for equation [2-1] is shown in Table 2-1. In this plot-level analysis, all block, treatment, covariate, and treatment-covariate interaction effects are tested against the experimental error (ϵ_{ijkl}). Woollons and Whyte (1988) have suggested that one should first test the significance of the parameters of the covariates and their interactions with the treatments, dropping all insignificant covariates, and then test the significance of the treatments' main effects, dropping all insignificant parameters (intercepts). The fertilization response for a treated plot from equation [2-1] is predicted by $\underline{T} + \underline{TX}$.

Table 2-1: Analysis of variance for modeling stand growth response to fertilization using structure analysis equation [2-1]

Sources of variance		df	MS	F
Block error	(β)	b-1	MSB	MSB/MSE
Treatment	(τ)	(t-1)c	MST	MST/MSE
Covariate	(X)	p	MSX	MSX/MSE
T*X		(t-1)cp	MSTX	MSTX/MSE
Plot error	(ϵ)	n_ϵ	MSE	
Total		$n_{plot}-1$		

$\underline{X}$: Plot level covariates
(i.e. site index, stand basal area, and stand breast height age)

n_ϵ : n_{plot} - b - (t-1)c - p - (t-1)cp

n_{plot} : The total number of plots

2.1.2 Estimating Tree Response using Structure Analysis

By adding three more terms into equation [2-1], structure analysis can be extended to analysis of individual tree responses:

$$Y_{ijklm} = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} + \underline{E} + \underline{Z} + \underline{TZ} + \delta_{ijklm} \qquad [2\text{-}2]$$

where

$\underline{E} = \Sigma_{i=1}^{b}\Sigma_{j=1}^{t}\Sigma_{k=1}^{r}\Sigma_{l=1}^{c} \epsilon_{ijkl} E_{ijkl}$ (plot effect)

E_{ijkl} = 1.0, if tree comes from block i, treatment j, plot k, cycle l

= 0.0, otherwise

$\underline{Z} = \Sigma_{q=1}^{v} \Gamma_{1.q} Z_{ijklmq}$

Z = tree-level covariate(s)

$\underline{TZ} = \Sigma_{j=2}^{t}\Sigma_{l=1}^{c}\Sigma_{q=1}^{w} \Gamma_{jlq} T_{jl} Z_{ijklmq}$

$\Gamma_{1.q}$, Γ_{jlq} = parameters

$\underline{B}$, $\underline{T}$, $\underline{X}$ and $\underline{TX}$ are as defined in equation [2-1].

In this formulation, an installation is treated as a block, a plot as an experimental unit, and a tree as a sampling unit. Equation [2-2] has three random errors for the block (β_i), plot (ϵ_{ijkl}) , and tree (δ_{ijklm}) levels. It is often assumed that these three errors are mutually independent and that the errors at each level are independent and identically distributed random variables

TABLE 2-2: Analysis of variance for modeling tree growth response to fertilization using structure analysis equation [2-2]

Sources of variance		df	MS	F
Block error	(β)	b-1	MSB	MSB/MSE
Treatment	(τ)	(t-1)c	MST	MST/MSE
Covariate	(X)	p	MSX	MSX/MSE
T*X		(t-1)cp	MSTX	MSTX/MSE
Plot error	(ϵ)	n_ϵ	MSE	
Z		q	MSZ	MSZ/MSS
T*Z		(t-1)cq	MSTZ	MSTZ/MSS
Tree error	(δ)	n_δ	MSS	
Total		n_{tree}-1		

$\underline{X}$: Plot level covariates
(i.e. site index, stand basal area, and stand breast height age)

$\underline{Z}$: Tree level variables
(i.e. diameter at breast height, crown ratio, and basal area for trees larger than the subjective tree)

n_ϵ : n_{plot} - b - (t-1)c - p - (t-1)cp

n_{plot} : The total number of plots

n_δ : n_{tree} - n_{plot} - q - (t-1)cq

n_{tree} : The total number of trees

with a normal distribution of $N(0,\sigma^2_\beta)$, $N(0,\sigma^2_\epsilon)$ and $N(0,\sigma^2_\delta)$ for block, plot and tree, respectively. The analysis of covariance for this model is shown in Table 2-2. The mean square of sampling error (MSS) is used to test whether any of the parameters of the tree level variables are significantly different from 0, and the mean square of experimental error (MSE) is used to test whether any of the parameters of the plot level variables are significant. The response of a tree to fertilization can be predicted by: $\underline{T} + \underline{TX} + \underline{TZ}$.

One consideration in favor of using covariates in Equation [2-2] is that their inclusion usually explains a considerable part of the error sums of squares with a relatively small reduction in the number of degrees of freedom available for testing. However, there are two potential problems with the use of analysis of covariance in Table 2-2. First, one can encounter the same difficulties in making tests of significance of the fixed effects as Federer (1955) experienced when using covariates in split-plot and split-block designs. Both MSZ/MSS and MSTZ/MSS in Table 2-2 are distributed as Snedecor's F no matter whether the experiment is with a balanced design (i.e. the numbers of sampling trees per plot are the same) or not, but MST/MSE, MSX/MSE and MSTX/MSE are not distributed as Snedecor's F even if the experiment is with a balanced design. In order to solve

this problem, an alternative equation using the mean of the dependent variable and independent variables for each plot and cycle can be used. This produces the following equation:

$$M_{ijkl} = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} + \bar{\underline{Z}} + \underline{T\bar{Z}} + e_{ijkl} \qquad [2\text{-}3]$$

where

M_{ijkl} = The mean of Y_{ijklm} for each plot and cycle

$\bar{\underline{Z}}$ = The mean of $\underline{Z}$ for each plot and cycle

All e_{ijkl} are mutually independent from an identical normal distribution with $E(e_{ijkl}) = 0$ and $Var(e_{ijkl}) = \sigma^2_\epsilon + \sigma^2_\delta/n_{ijkl}$. If the number of sampling trees is the same for all plot-cycles, then $Var(e_{ijkl})$ is constant. As a result, equation [2-3] can be fitted by using OLS techniques.

The second problem with using covariates in equation [2-2] is that data sets used to develop tree level growth and yield models are always from unbalanced experimental designs. In order to solve this problem, one can randomly drop sampling units (i.e., trees) such that the number of the remaining trees is the same for all plot-cycles, and then apply OLS to fit equation [2-3]; however, this method can result in the loss of a substantial part of the data set.

Theoretically, another method of solving the second problem, for either equation [2-2] or equation [2-3], is

to use a mixed model form and GLS techniques. Giesbrecht and Burns (1985) mentioned that statisticians have used analysis methods based on a mixed model to deal with data with multi-sources of error and from unbalanced experiments. A mixed model involves two parts, one describing the fixed effects and the other describing the random effects (Milliken and Johnson 1984, Giesbrecht and Burns 1985):

$$\underline{Y} = \underline{W}\,\underline{\beta} + \underline{U}_1\,\underline{e}_1 + \underline{U}_2\,\underline{e}_2 + \underline{U}_3\,\underline{e}_3 \qquad [2\text{-}4]$$

where

$\underline{W}\,\underline{\beta}$ = the fixed part of the model

$\underline{U}_1\,\underline{e}_1 + \underline{U}_2\,\underline{e}_2 + \underline{U}_3\,\underline{e}_3$ = the random part of the model

$\underline{e}_i$ = independent random errors with $N(0,\sigma_i^2)$

If one applies the mixed model form to equation [2-2], then:

$\underline{W}\,\underline{\beta}$ = a matrix of $\mu + \underline{T} + \underline{X} + \underline{TX} + \underline{Z} + \underline{TZ}$

$\underline{U}_1\,\underline{e}_1 + \underline{U}_2\,\underline{e}_2 + \underline{U}_3\,\underline{e}_3$ = a matrix of $\underline{B} + \underline{E} + \delta_{ijklm}$

If one applies the mixed model form to equation [2-3], then:

$\underline{W}\,\underline{\beta}$ = a matrix of $\mu + \underline{T} + \underline{X} + \underline{TX} + \underline{\bar{Z}} + \underline{T\bar{Z}}$

$\underline{U}_1\,\underline{e}_1 + \underline{U}_2\,\underline{e}_2 + \underline{U}_3\,\underline{e}_3$ = a matrix of $\underline{B} + e_{ijkl}$

It follows that $E(\underline{Y}) = \underline{W}\,\underline{\beta}$ and $V(\underline{Y}) = \Sigma\,\underline{U}_i\underline{U}_i'\,\sigma_i^2 = \underline{V}$, is a (n by n) covariance matrix. The best linear unbiased estimate for $\underline{\beta}$ is the GLS estimator.

$$\hat{\underline{\beta}} = (\underline{W}'\underline{V}^{-1}\underline{W})^{-1}\underline{W}'\underline{V}^{-1}\underline{Y}$$

However, a major problem in trying to solve a mixed model is the estimation of σ_i^2 and then the computation of $\underline{V}^{-1}$; the literature gives only asymptotic properties for these estimators (Giesbrecht and Burns 1985). As a result, one should consider the use of mixed model analysis only if the number of sampling trees is quite different from plot to plot and $\underline{V}^{-1}$ is computable.

2.1.3 Advantages and Disadvantages of Structure Analysis

The advantages of estimating plot or tree response due to fertilization using structure analysis are:

(a) It is the statistically correct way to analyze the underlying data structure to predict treatment response.

(b) It uses all of the available data so that it has the maximum number of degrees of freedom possible to estimate the variances of the random errors.

The disadvantages of this method are:

(a) It may be difficult, if not impossible, to estimate all of the parameters for large problems. For example, if a data set has 50 installations, 3 treatments, 2 plot-level covariates, 2 replications, and 3 measurements, the full linear equation (Equation [2-1]) for analysis of plot response has

70 independent variables. In addition, if the data set has 3 tree-level covariates, the full linear equation (Equation [2-2]) for analysis of tree response has 991 independent variables. While this example assumes a modest number of installations (Miller et al. 1988, for example, had 114 installations), the resulting number of parameters for equation [2-2] could not be estimated on most statistical packages.

(b) This method does not produce a general control plot prediction model. Therefore, it is difficult to predict the response of a control plot that did not come from the modeling data set. The only alternative available is to assign a new control plot to a block that has similar characteristics.

2.1.4 Possible Simplifications to Structure Analysis to Reduce Size of Problem

The following are possible simplifications that have been used in prior studies to reduce the size of the problem when estimating plot response by structure analysis. Some of these simplifications can also be extended to tree level analyses.

(1) If the equation has too many dummy variables for blocks and plots such that it cannot be fit using

standard statistical packages, it may be tempting to simplify either equation [2-1] or equation [2-2] by eliminating all of the dummy variables. For plot level analysis, the block dummy variables can be dropped only if σ_b^2 is equal to zero, which implies that the block effect is not significant (Woollons and Whyte 1988). Similarly, both block and plot dummy variables can be dropped in tree level analysis only if both σ_b^2 and σ_ϵ^2 are equal to zero (i.e. that the block and plot effects are not significant from zero). Unfortunately, to perform these tests requires the fitting of either equation [2-1] or equation [2-2] to the data.

(2) Ignore possible treatment effects upon either the plot-level covariate(s) by dropping $\underline{TX}$ from equation [2-1] (Opalach and Heath 1988) or the tree level covariates by dropping $\underline{TZ}$ from equation [2-2]. This can simplify the analysis but the resulting formulation may be underspecified. If the covariates of $\underline{TX}$ and/or $\underline{TZ}$ are orthogonal to the remaining covariates in the model, the resulting, underspecified, formulation is unbiased, otherwise problems with bias may occur.

(3) Use paired differences between the mean of the control plots and each of the means of the other treatments in each block. The use of paired

differences was previously used by Hazard and Peterson (1984) and Peterson and Hazard (1990) in their analyses of split-plot designs. This method is only applicable to estimate plot level response to treatment in the first growth cycle. One should be careful while applying this method beyond one growth cycle because, if there is a significant treatment response in the first period, some plot level covariates on the treated plots (e.g., BA) will be greater than those on the control plots after the first cycle due to treatment response.

This method eliminate the block effect and it estimates the direct treatment response. However, if there is more than one paired difference in the block (such as different levels of fertilization), the estimation of the variance of the difference by OLS techniques will be biased because the paired differences are correlated with each other. For example, let us only consider the i^{th} instatallation in the first growth period, and there are the average of the periodic growth values in the control plots, $\bar{Y}_{i1.}$, the average in the 200 lb fertilized plots, $\bar{Y}_{i2.}$, and the average in the 400 lb fertilized plots, $\bar{Y}_{i3.}$. The paired differences, $\bar{Y}_{i2.}-\bar{Y}_{i1.}$ and $\bar{Y}_{i3.}-\bar{Y}_{i1.}$, are correlated since they carry over the same random error from $\bar{Y}_{i1.}$. The

problem of the correlation between dependent variables can be eliminated by using GLS techniques. Furthermore, the paired differences among blocks are independent. Therefore, if there are many blocks, the fitting step is not affected very much by the correlation between dependent variables, and, as a result, it might be acceptable to simply ignore the correlation.

If these simplifications are not suitable for the problem, then the use of multi-step analysis procedures may be appropriate.

2.2 Multi-step Analysis

A two-step fitting procedure has seen common usage in the Pacific Northwest of the United States of America as a method to estimate growth response to nitrogen fertilization (Turnbull and Peterson 1976a, Peterson and Gessel 1982, Arney 1985, Miller et al. 1988, and Heath and Chappell 1989). The two-step method separates the data set into two subsets: a control plot subset and a fertilized plot subset. In the first step of the method, a control equation is developed using the control plot subset. In the second step, the difference between the observed dependent variable for the fertilization data set and the predicted dependent variable from the control

equation is fit to the independent variables of the fertilization subset.

In applying traditional two-step analysis, special attention must be given to the procedure used to estimate the variances of the parameters in the treatment response equation. This problem could be very important in Pacific Northwest region, since the most current reports by Miller et al. (1988), and Heath and Chappell (1989) still gave very sparse details of statistical analysis while they applied the procedure of two-step analysis. When data sets are collected from completely randomized designs, the following is an example of how to compute the appropriate variances of the parameters in the treatment response equation when all of the equations are simple linear forms. Computation methods for more complex multiple linear forms are discussed in appendix A.

Let the control equation, treatment equation, response equation, and joint equation be defined as follows:

control equation: $Y_c = a_0 + a_1X$

response equation: $Y_t - \hat{Y}_c = d_0 + d_1X$

treatment equation: $Y_t = b_0 + b_1X$

joint equation: $Y = a_0^* + a_1^*X + d_0^*T + d_1^*TX$

where

Y_c = dependent variable for control data

Y_t = dependent variable for treatment data

$\hat{Y}_c$ = the predicted value by control equation

Y = dependent variable for all data

X = independent variable

T = 1.0, if data from treated plot

= 0.0, otherwise

a_0, a_1, b_0, b_1, d_0, and d_1 = estimated regression parameters

The treatment equation is always defined with the same form as the response equation. The two-step analysis procedure develops only the control equation and the response equation. Application of the structure analysis procedure would result in the development the joint equation and, therefore, its parameter and variance estimates are the correct values for testing the significance of the treatment response. The treatment equation is of concern because, if it is of the same exact form as the control equation, then the estimated parameters for control and response equations are the same as those estimated by the joint equation. If the forms differ, the parameter estimates may also differ.

Although the estimated parameters in the response equation are the same as those in the joint equation (assuming that the control and treatment equations have the same form), the estimated variances of the parameters

in the response equation are not the same as those in the joint equation (in fact they are the same as those in the treatment equation). Therefore, the estimated variances of the response equation parameters derived from fitting the response equation to the data should not be used to test for significance of the estimated response equation parameters.

If the model form for the control equation and the treatment equation are the same, the following statistic can be used to test whether one of the parameter estimates of the response equation is significantly different from zero:

$$(d_i) \;/\; \mathrm{SQRT}[\mathrm{Var}(b_i - a_i)]$$

Since b_i is independent of a_i and, in this case, the variance of b_i equals the variance of d_i, the variance of $b_i - a_i$ is equal to the variance of d_i plus the variance of a_i. In addition, if the control equation and the treatment equation are with common variance, the pooled mean square error (MSE_p) can be computed from mean square error of control equation (MSE_c) and mean square error of treatment equation (MSE_t). Then $\mathrm{Var}(b_i - a_i)$ can be replaced as follows:

$$\mathrm{Var}(b_i - a_i) = [\mathrm{Var}(b_i)/MSE_t + \mathrm{Var}(a_i)/MSE_c] * MSE_p$$

Obviously, if the variance of a_i is small when compared to the variance of d_i, then the variance of a_i can be ignored in this test statistic. This condition may occur

when the control data set is much larger in sample size and has a wider range in the independent variables than the treatment data set. Appendix A presents the appropriate test statistic for the case when the form of the control equation and the treatment equation are not the same.

2.2.1 The General Control Plot Equation

The first step in all of the following multi-step procedures is to either develop a general control equation from the current study's control plots or find an existing equation developed from previous studies. The choice of which approach to use will depend upon the strength of the control plot data set (i.e., its sample size and distribution over the important independent variables) and whether an adequate control model already exists for the population of interest.

For plot level analyses, the general control model takes the from:

$$Y_{con} = \mu + \underline{X} + \epsilon_{ilkl};$$

where $\underline{X}$ is as defined in equation [2-1]

and for tree level analyses, the general control model takes the form:

$$Y_{con} = \mu + \underline{X} + \underline{Z} + \epsilon_{ilklm}$$

where $\underline{X}$ and $\underline{Z}$ are as defined in equation [2-2]

2.2.2 Estimating Plot Response by Traditional Two-step Analysis

Step 1: Develop a new general control equation or use an existing one.

Step 2: Each fertilized plot's response to treatment is estimated by taking the difference between the observed value and the value predicted by the general control equation. These differences are then used to fit the following response equation using all treated plots across all blocks:

$$E(Y_{ijkl} - \hat{Y}_{con}) = \underline{T} + \underline{TX} \quad (\text{for } j \neq 1)$$

where $\underline{X}$ and $\underline{TX}$ are as defined in equation [2-1]

This method has been used by Miller et al. (1988) and Heath and Chappell (1989). It is appropriate for modeling plot growth response to fertilization when data sets are collected from completely randomized designs, but it may not be appropriate when data sets are collected from randomized block designs. The two-step analysis does not consider possible block effects, and, therefore, if the eliminated block variables are significant, then the approach confounds the treatment response with the random block effect and the resulting estimates may not represent just the treatment response. If the block variables are insignificant, then an

advantage of this approach is that the computation of the appropriate variances of the response parameters can be done in a relatively straight forward fashion.

2.2.3 Estimating Plot Response by Three-step Analysis

Step 1: Develop a new general control equation or use an existing one.

Step 2: Calibrate the general control equation to each block's control plots to form the following block-specific control equation. If a new general control equation has been developed or if the existing general control equation was developed using plots of the same design as the fertilization data set, then this calibration takes the form:

$$E(Y_{cal,i}) = E(Y_{i1kl} - \hat{Y}_{con})$$
$$= \beta_i$$

If the existing general control equation was developed from data collected on plots of a design different from the fertilization data set, then the calibration takes the form:

$$E(Y_{cal,i}) = E(Y_{i1kl} - \hat{Y}_{con})$$
$$= \beta_i + \Sigma_{p=1}^{v} \alpha_{p,i} X_{p,i1kl}$$

Because the plot's estimated covariates can vary from one plot design to another (Zumrawi 1990), inclusion of the these covariates in the development

of the calibration equation should help to minimize the effects of differing plot designs. However, application of this full calibration equation requires that the sum of the number of cycles measured on all control plots be at least (v+2) per block to estimate the (v+1) parameters and the variance of the plot level covariates. If fewer control plots exist, then it will be necessary to eliminate all plot level covariates.

Step 3: Each fertilized plot's response to treatment is estimated by taking the difference between the observed value and the value predicted by calibrated, block-specific control equation. These differences are then used to fit the following response equation using all treated plots across all blocks:

$$E(Y_{ijkl} - \hat{Y}_{con} - \hat{Y}_{cal,i}) = \underline{T} + \underline{TX}$$

This method does consider possible block effects. If the block effect is significant, then it can reduce the variance. The disadvantage of this procedure is that computation of the appropriate variances for testing response to fertilization can be quite complex.

2.2.4 Estimating Tree Response by Four-step Analysis

Step 1: Develop a new general control equation or use an

existing one.

Step 2: Calibrate the general tree level control equation to each block's control plots, producing the following block-specific control equations:

$$Y_{cal,i} = Y_{i1klm} - \hat{Y}_{con}$$
$$= \mu_i + \Sigma_{p=1}^{v} \alpha_{i1.p} X_{i1klp}$$
$$+ \Sigma_{q=1}^{w} \Gamma_{i1.q} Z_{i1klq} + \delta_{i1klm}$$

As in the three-step analysis procedure, if a new general control equation is developed or if the plot design for the existing general control equation is the same as the plot design for the fertilization data set, then both the plot level and tree level covariates in the above calibration equation can be eliminated.

Again, application of the full calibration equation, if necessary, requires that the sum of the number of cycles measured on all control plots be at least (v+2) per block to estimate the (v+1) parameters and the variance of the plot level covariates. If fewer control plots exist, then it will be necessary to eliminate all plot level covariates, producing:

$$Y_{cal,i} = Y_{i1klm} - \hat{Y}_{con}$$
$$= \mu_i + \Sigma_{q=1}^{w} \Gamma_{i1.q} Z_{i1klq} + \delta_{i1klm}$$

Step 3: Each tree's response to treatment is estimated by taking the difference between the observed value and

the value predicted by the calibrated, block-specific control equation. These differences are then used to fit, plot by plot, the following plot-specific tree response equation:

$$E(Y_{ijklm} - \hat{Y}_{con} - \hat{Y}_{cal,i}) = \Sigma_{l=1}^{C} \phi_{ijkl} C_l + \Sigma_{l=1}^{C} \Sigma_{q=1}^{W} \theta_{ijklq} Z_{ijklmq}$$

where

C_l = 1.0, if trees come from the l^{th} cycle

= 0.0, otherwise

ϕ_{ijkl}, θ_{ijklq} = regression parameters for plot k, treatment j, installation i

This formulation does not have plot level covariates because, for a given growth cycle, they are constant for all trees on the plot. The formulation uses dummy variables to characterize the number of cycles since treatment and is fitted through the origin. This second step eliminates the block effect and it partitions trees' fertilizer response into that which can be attributed to number of cycles since treatment, and that which can be attributed to the interaction of cycle with tree level covariates.

Step 4: The parameter estimates from step 3 associated with the number of cycles since treatment (i.e., ϕ_{ijkl}) are now used to estimate the fertilization main effect, by cycle, and its interaction with plot level covariates using the following:

$$E(\phi_{ijkl}) = \underline{T} + \underline{TX}$$

where $\underline{X}$ and $\underline{TX}$ are as defined in equation [2-1]. The parameter estimates from step 3 associated with the interaction of cycle with tree level covariates (i.e., θ_{ijklq}) are now used to estimate interaction of the fertilization effect, by cycle, with tree level covariates using the following:

$$E(\theta_{ijklq}) = \Sigma_{j=2}^{t}\Sigma_{l=1}^{c} \Gamma_{jlq}T_{jl}$$

The parameters of both of these equations (i.e., τ_{jl}, α_{jlp} and Γ_{jlq}) can be estimated using varying-parameter (or random coefficient) regression techniques (Biging 1985). In this method, each of the (w+1) equation's parameters are estimated by applying the technique of generalized least squares weighted by the inverse of variance-covariance matrix associated with each dependent variable. A tree's response to fertilization is then predicted from the following:

$$\text{response} = \underline{T} + \underline{TX} + \Sigma_{j=2}^{t}\Sigma_{l=1}^{c}\Sigma_{q=1}^{w} \Gamma_{jlq}T_{jl}Z_{ijklmq}$$
$$= \underline{T} + \underline{TX} + \underline{TZ}$$

2.2.5 Advantages and Disadvantages of Multi-step Analysis

The advantages of multi-step analysis are as following:

(a) It is less affected by size of problem than

structure analysis.

(b) One of the appeals of the multi-step method is that it produces an equation that is useful in predicting the behavior of untreated plots (i.e., control plots). Modelers often have more confidence with fitting a control equation than treatment equations because the form of the control equation has often been well defined in previous studies.

(c) The method can also use an existing control equation. This can be particularly useful if the number of control plots in the fertilization data set is relatively small in size or if they are not well distributed over important plot attributes.

The disadvantages of multi-step analysis are as following:

(a) It has fewer degrees-of-freedom to estimate MSS and MSE than the method of structure analysis.

(b) It is more complex to compute appropriate variance(s) to test the significance of the parameter(s) in the fertilization response equation (Appendix A and B).

(c) If the independent variables in the control equation are not the same as those in the response equation, then the parameters estimated by multi-step analysis may not be equal to the parameters estimated by

structure analysis using a joint regression model form. In addition, the multi-step equation will have a larger variance than the joint equation.

(d) This method assumes a correct control model which structure analysis does not. If the data set can not develop a good quality general control equation, then the multi-step analysis equation will have a larger variance than the structure analysis equation.

Chapter 3

Modeling Tree Growth Response to Fertilization

The analysis methods discussed in Chapter 2 can be applied to develop fertilizer response modifiers for the Douglas-fir diameter growth and the dominant height growth equations in the SW Oregon version of ORGANON, a single-tree/distance-independent growth and yield simulator (Hester et al. 1989). A set of 18 Douglas-fir fertilization research installations near the ORGANON study area is used to develop the modifier equations. These data are independent of the data set used in construction of the growth and yield equations in ORGANON. The data consists of 35 control and 54 fertilized plots at the first five-year growth cycle, 10 control and 20 fertilized plots at the second five-year cycle, and 7 control and 14 fertilized plots at the third five-year cycle. The plots used in these installations were between 0.1 and 0.2 acres in size. For more information about the plot design of the fertilization data set, see Hazard and Peterson (1984), and Miller et al. (1988).

The plot design used to construct ORGANON consisted of a cluster of between four and ten sampling points.

There were three subplots at each sample point: (1) a 20 basal area factor variable radius subplot for trees greater than 8.0 inches in diameter at breast height (DBH), (2) a fixed area subplot of radius 15.56 feet for trees between 4.1 and 8.0 inches DBH, and (3) a fixed area subplot of radius 7.78 feet for trees less than 4.1 inches DBH. For more information about ORGANON's plot design, see Ritchie and Hann (1987), Hann and Larsen (1990), and Hann and Wang (1990). The ORGANON's data set came from 391 stands in southwest Oregon that covered a wider range of sites, species mixes and stand structures than the fertilization data set. Therefore, the intent of the study was to develop fertilization modifiers for the existing Douglas-fir diameter growth and dominant height growth equations in ORGANON.

3.1 Modeling Dominant Height Growth Response to Fertilization using Structure Analysis

The Douglas-fir height growth equation in ORGANON is composed of a potential component and a vigor and competition modifier (Hann and Ritchie 1988). The potential component is derived from the dominant height growth equations of Hann and Scrivani (1987) and is a function of the stand's site index (SI) and the tree's growth effective age (GEA), which is the age the tree

would be if it were a dominant of the same total height. Therefore, the potential component predicts what the tree's five-year height growth would have been if it were a dominant tree of the same height. The vigor and competition modifier then reduces the potential height growth if the tree is not in a dominant position in the stand. The modifier component is a function of the tree's crown ratio (CR: crown length of the tree divided by the total height of the tree) and the estimated crown closure of the stand at the tree's tip.

The fertilization data set could be used to develop a fertilizer modifier on the potential height growth component only because: (1) CR's had not been measured on any of the 18 fertilization installations, and (2) only about ten Douglas-fir trees were measured for height on each plot and a majority of these were dominant trees. As a result, only the dominant Douglas-fir trees on the plots were used in the following analysis.

Structure analysis equation [2-2] was chosen to model the tree's fertilization modifier to the potential height growth component. Because the potential height growth component for dominant trees is not strongly affected by tree level variables, equation [2-2] was simplified by excluding the tree level covariates:

$$Y_{ijklm} = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} + \underline{E} + \delta_{ijklm}$$

Where,

Y_{ijklm} = $LOG(HG_{ijklm})$ - $LOG(PHG_{ijklm})$

HG_{ijklm} = The observed 5-year dominant height growth of tree m, period l, plot k, treatment j, installation i

PHG_{ijklm} = The predicted 5-year dominant height growth of tree m, period l, plot k, treatment j, installation i from the existing potential height growth equation in ORGANON

LOG = the natural logarithm

This form of the dependent variable was chosen because of the desire to develop a fertilization modifier equation for the potential height growth component. To analyze the fertilization data with this equation would require 17 block and 140 plot-cycle dummy variables. However, because this equation does not have tree level covariates, a further simplification could be done by using the mean of the dependent variable for each plot and cycle and therefore eliminating the need for the 140 plot-cycle dummy variables. This produces the following equation:

$$E(M_{ijkl}) = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} \qquad [3\text{-}1a]$$

Where M_{ijkl} = The mean of Y_{ijklm} for plot k and cycle l.

The equation was not analyzed by the mixed model method because of the difficulty in computing $\underline{V}^{-1}$ ($\underline{V}$ was a 140 by 140 matrix) and because the number of dominant

trees (i.e., sampling units) was similar from plot to plot in this data set.

OLS would have been appropriate to estimate the parameters if the number of trees on a plot had been exactly the same across all plots and cycles. While the number of dominants were similar across plots and cycles, they were not exactly the same. As a compromise, equation [3-1a] was fitted by weighted regression where the weight was the number of dominant trees on each plot and cycle. With such a simplification, the parameters can be estimated by the generalized linear model package -- PC SAS Procedure GLM (SAS/STAT 1985). Using GLM, the following four sets of independent variables were formed, inserted into equation [3-1a] and then fitted to the data:

1. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{X}$ = [SI, A]

   $\underline{XT}$ =[A*$\underline{T}$, SI*$\underline{T}$]

2. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{X}$ = [LOG(SI), A]

   $\underline{XT}$ = [A*$\underline{T}$, LOG(SI)*$\underline{T}$]

3. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{X}$ = [SI, A^{-1}]

$\underline{XT} = [(A^{-1})*\underline{T}, SI*\underline{T}]$

4. $\underline{T} = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]$

$\underline{X} = [LOG(SI), A^{-1}]$

$\underline{XT} = [(A^{-1})*\underline{T}, LOG(SI)*\underline{T}]$

Where,

SI = Hann and Scrivani (1987) site index for the plot.

A = Stand age which should be close, if not equal, to the average of the GEA's for all dominant trees on the plot.

FERT = 1.0 if the plot had been fertilized with either 200 or 400 pounds of nitrogen per acre

= 0.0 otherwise.

F400 = 1.0 if the plot had been fertilized with 400 pounds of nitrogen per acre

= 0.0 otherwise.

C1 = 1.0 if the data was for the first five-year growth cycle after fertilization

= 0.0 otherwise.

C2 = 1.0 if the data was for the second five-year growth cycle after fertilization

= 0.0 otherwise.

C3 = 1.0 if the data was for the third five-year growth cycle after fertilization

= 0.0 otherwise.

In all four regressions, all independent variables involving F400 , C_2, C_3, and the SI and A transformations were not significantly different from zero (α=0.05). Because C_2 and C_3 were not significant, the data for these two cycles were removed and the following final equation was fitted to the remaining dominant height growth data:

$$M = u_1 + \Sigma^{18}_{i=1} a_i B_i + b_1 \text{ FERT*}C_1 \qquad [3\text{-}1b]$$

where

M = the mean value of LOG(HG/PHG) for a plot and cycle

HG = actual 5-year height growth for a dominant tree

PHG = predicted 5-year dominant height growth by the potential height growth equation in ORGANON

B_i = 1, if data come from block "i"

= 0, otherwise.

u, a_1, ..., a_{18}, b1 = regression coefficients

The estimated parameters of equation [3-1b] are presented in Table 3-1, and a plot of the residuals over the predicted dependent variable is presented in Figure 3-1. A check of the residuals by PC SAS Procedure UNIVARIATE (SAS/STAT 1985) showed that they were normally distributed (p=0.1614).

Table 3-1: The estimated parameters of the fertilization response modifier equation [3-1b] for the dominant height growth equation of Douglas-fir in SW-ORGANON

Parameter		Estimate	T for H0: Parameter=0	Pr > |T|	Std Error of Estimate
INTERCEPT		-.1145921851 B	-1.36	0.1782	0.08442818
INCODE	51	-.2282785411 B	-2.11	0.0376	0.10810502
	67	-.2340269750 B	-2.14	0.0355	0.10956014
	92	-.4172606761 B	-3.81	0.0003	0.10950246
	93	-.0898033126 B	-0.82	0.4165	0.10998903
	94	-.2123521664 B	-1.79	0.0773	0.11877773
	95	-.1061676805 B	-0.98	0.3290	0.10816285
	105	0.1038012829 B	0.96	0.3415	0.10853491
	106	-.1515540728 B	-1.38	0.1701	0.10956014
	175	-.0394498743 B	-0.38	0.7081	0.10501197
	204	0.3124376905 B	2.42	0.0178	0.12935627
	205	0.0200220280 B	0.16	0.8744	0.12632108
	212	0.1748331747 B	1.33	0.1862	0.13120631
	213	0.0920378314 B	0.66	0.5105	0.13927607
	215	0.2826772589 B	2.21	0.0296	0.12782821
	216	0.2417206343 B	1.74	0.0861	0.13924666
	217	0.0271498089 B	0.21	0.8323	0.12782821
	355	-.0732230831 B	-0.41	0.6832	0.17885225
	365	0.0000000000 B	.	.	.
FERT*C1		0.0915088524	2.35	0.0210	0.03894100

Root MSE	0.472611	R-square	0.526933
Dep Mean	-0.127500	Adj R-sq	0.429058
Observation	106.000000		

NOTE: The X'X matrix has been found to be singular and a generalized inverse was used to solve the normal equations. Estimates followed by the letter 'B' are biased, and are not unique estimators of the parameters.

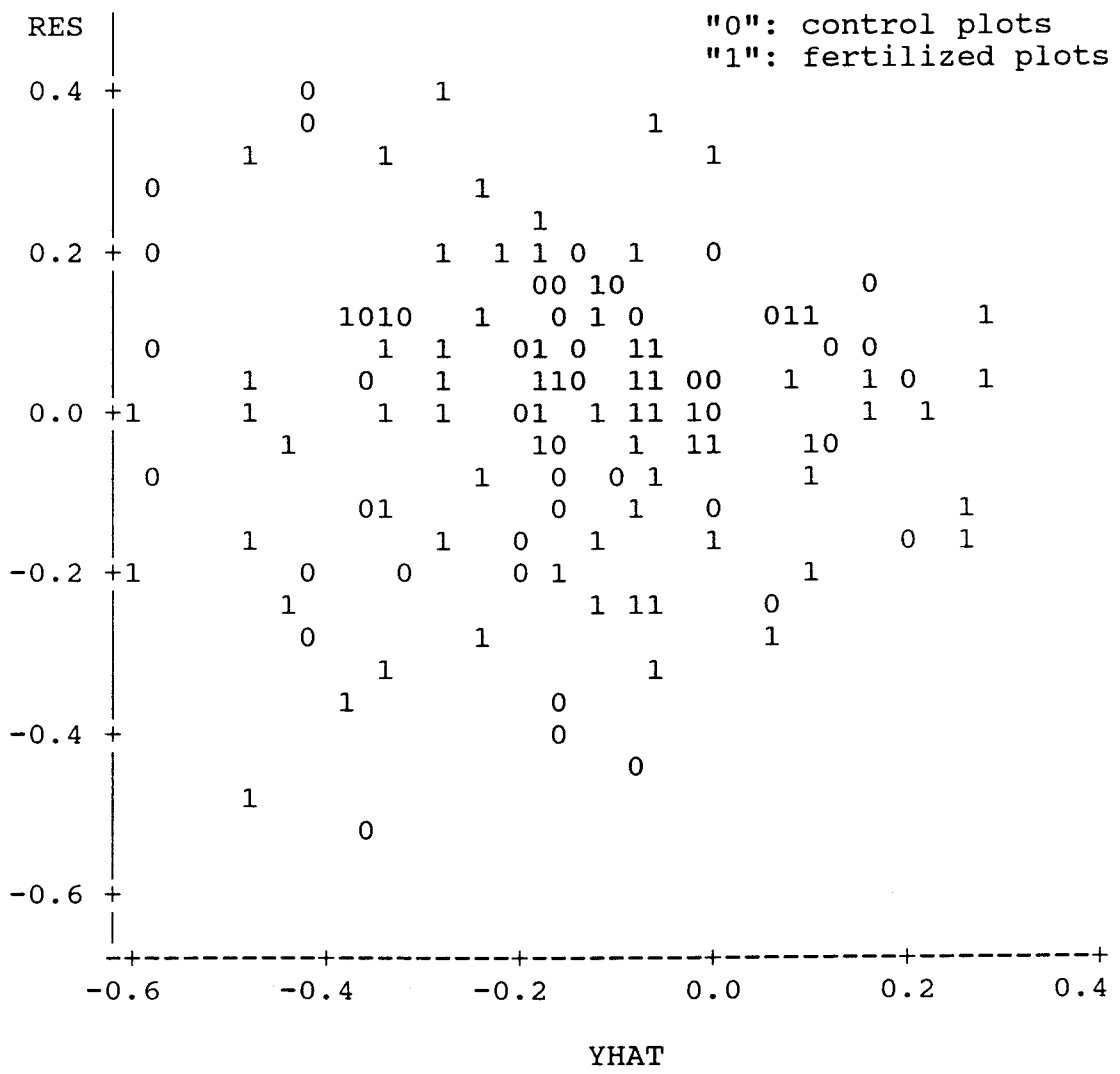

Figure 3-1: Plotting of residuals (RES) on predicted Y (YHAT) from the fertilization response modifier equation [3-1b] for the dominant height growth equation of Douglas-fir in SW-ORGANON.

3.2 Modeling Diameter Growth Response to Fertilization using Four-step Analysis

The Douglas-fir diameter growth equation (Hann and Larsen 1990) in ORGANON is a function of the plot's SI and BA and the tree's DBH, CR, and stand basal area in trees with DBH's larger than the subject tree's DBH (BAL). As a result, structure analysis equation [2-2] can not be simplified by dropping tree level covariates as was done in the height growth analysis. Therefore, fitting Equation [2-2] would require the use of 17 block dummy and 140 plot-cycle dummy variables. Since PC - SAS could not solve a problem of this size, this analysis used the following four-step method to model the tree's fertilization response modifier to the ORGANON Douglas-fir diameter growth equation:

Step 1: The existing diameter growth equation in ORGANON was used to form the general control equation.

Step 2: The general diameter growth equation was calibrated to each block's control plots, producing the following block-specific control equation:

$$\hat{Y}_{cal,i} = E(LOG(DG_{ijklm}) - LOG(PDG_{ijklm}))$$
$$= b_{0,i} + b_{1,i}*LOG(DBH+1.0)$$
$$+ b_{2,i}*BAL^2/LOG(DBH+1.0) \quad [3\text{-}2a]$$

where

$\hat{Y}_{cal,i}$ = the calibrated, block-specific control equation of installation i

DG_{ijklm} = the observed 5-year diameter growth

PDG_{ijklm} = the predicted 5-year diameter growth by the general control equation

$$= EXP\{ - 3.50204 + 0.361294 * LOG(DBH+1.0) - 0.000413140 * DBH^2 + 1.34888 * [(CR+0.2)/1.2] + 0.765801 * LOG(SI) - 0.0000425385 * [BAL^2/LOG(DBH+1.0)] - 0.0127359 * SQRT(BA) \}$$

SQRT = function of square root

Since the plot design of ORGANON's data set is different with that of the fertilization data set, ideally the calibration equations should have included all of the plot level and tree independent variables used in ORGANON's Douglas-fir diameter growth equation. The independent variable involving the plot's SI could be excluded from the calibration equation because it was constant for all plots in an installation. The remaining plot level independent variable involving BA was dropped for two reasons: (1) one of installations had only one control plot and one growth cycle making it impossible to estimate the parameter and variance for the

Table 3-2a: The estimated parameters of the calibrated, block-specific control equations [3-2a] for modeling the diameter growth response to fertilization

INCODE	N	MSE	Adj.R^2	b_0	b_1	b_2
051	391	.2656	.2120	-2.8279450 **	1.0102810 **	.38412149E-04**
			SE : (	.50466852) (	.21126783) (	.51953429E-05)
067	128	.3235	.2731	-3.3811109 **	1.0848726 **	.32358479E-04**
			SE : (	.41085235) (	.15458870) (	.84282476E-05)
092	213	.3311	.3042	-2.2287862 **	.71198058 **	-.92983219E-05
			SE : (	.46028850) (	.18616966) (	.13204141E-04)
093	293	.3131	.0046	-.32972398	.20789985	.89683881E-05
			SE : (	.45718552) (	.18797925) (	.55841996E-05)
094	62	.3001	.2636	1.8884203	-.76798511	-.82249397E-04*
			SE : (	2.2112687) (	.75097105) (	.39338143E-04)
095	437	.2486	.2813	-1.1615974 **	.57945341 **	-.14849704E-04**
			SE : (	.23808265) (	.11168558) (	.47406381E-05)
105	190	.2236	.4759	-1.4453309 **	.80528754 **	-.10986727E-04
			SE : (	.26777041) (	.11507180) (	.10522289E-04)
106	106	.2521	.0597	-.24089853	.18583077	-.10726770E-04
			SE : (	.33160999) (	.13245724) (	.19088799E-04)
163	37	.5304E-01	.2355	-1.7647744 **	1.4345036 **	.58818742E-03*
			SE : (	.46341793) (	.39841027) (	.24215276E-03)
175	146	.3661	.3506	-2.9239562 **	1.0947165 **	.39066172E-05
			SE : (	.88026323) (	.36489359) (	.25124502E-04)
204	200	.3111	.1824	-4.2058630 **	1.7713599 **	.47108515E-04**
			SE : (	.94160621) (	.39318529) (	.16075898E-04)
205	116	.3984	.2562	-4.5211606 **	1.5839223 **	.42280855E-04**
			SE : (	.84146048) (	.27764304) (	.65581419E-05)
212	123	.4135	.0623	-2.8000369 **	1.0483742 **	.29481134E-04**
			SE : (	.85081404) (	.34850717) (	.94790383E-05)
213	79	.3839	.2156	-1.7611098	.61334330	-.29077421E-04
			SE : (	1.1086082) (	.44748363) (	.25837162E-04)
215	128	.3279	.3415	1.8082328	-.76979178	-.15175121E-03**
			SE : (	1.8281313) (	.74451543) (	.52203625E-04)
216	73	.4527E-01	.1108	-1.7564961 **	.96418607 **	.18119534E-03*
			SE : (	.64392047) (	.31277068) (	.74675233E-04)
217	99	.3390	.0318	-1.7601678	.62450308	.19912328E-04#
			SE : (	1.2949733) (	.42647611) (	.10092928E-04)

Table 3-2a: (Continued)

INCODE	N	MSE	Adj.R^2	b_0	b_1	b_2
355	290	.4018		.1890 -1.0596837	** .62296999	** -.48244707E-04**
				SE : (.31554451	) (.19331631	) (.14084083E-04)
365	697	.3051		.0712 -1.1063452	** .53329343	** .21381722E-05
				SE : (.18123423	) (.98377341E-01)	(.33652883E-05)

** significant at a = 0.01, * at a = 0.05, # at a = 0.10

INCODE: Installation code

N: The number of trees

MSE: Mean square error

adj.R^2: Adjusted R-square

SE: The standard error of the estimated parameter

independent variable involving BA and, (2) the independent variable did not strongly affect predicted diameter growth for Douglas-fir (Hann and Larsen 1990). Finally, the CR and DBH^2 independent variables were excluded because: (1) the CR's in the fertilization data set had to be predicted by the ORGANON model, and (2) DBH^2 is highly correlated with LOG(DBH+1.0) and, for most installations, LOG(DBH+1.0) was a stronger independent variable in the calibration equations than DBH^2. Table 3-2a shows the resulting 18 block-specific control equations.

Step 3: Each tree's diameter growth response to fertilization is estimated by taking the difference between the tree's observed diameter growth and the diameter growth predicted by the calibrated, block specific diameter growth equation determined in step 2. These differences are then used to fit, plot by plot, the following plot-specific tree response equation:

$$E(R_{ijk}) = E(LOG(DG_{ijklm}) - LOG(PDG_{ijklm}) - \hat{Y}_{cal,i})$$
$$= \Sigma_{l=1}^{3} \phi_{ijkl} C_l + \Sigma_{l=1}^{3} \Theta_{ijkl1} C_l * LOG(DBH+1.0)$$
$$+ \Sigma_{l=1}^{3} \Theta_{ijkl2} C_l * BAL^2/LOG(DBH+1.0)$$

where

C_l = 1, if trees come from the l^{th} period,

= 0, otherwise

ϕ_{ijkl}, θ_{ijkl1}, θ_{ijkl2} = regression parameters of plot k, treatment j, installation i

To apply the varying-parameter (or random coefficient) regression procedures in the next step, it is necessary that each of the plot-specific response equations have the same form. Fits of the above full response equation to all plots resulted in a large number of insignificant parameters and parameters that changed sign from plot to plot. Therefore, simpler formulations of the response equation were examined in order to find one that had both significant parameters and consistent signs across the most number of plots. The response equation which best met these objectives was:

$$E(R_{ijk}) = \Sigma_{l=1}^{3} \phi_{ijkl} C_l \qquad [3\text{-}2b]$$

Table 3-2b presents the estimated parameters of these plot-specific response equations.

Table 3-2b: The estimated parameters of the plot-specific response equations [3-2b] for modeling the diameter growth response to fertilization

INCODE	PLOT	N	MSE	Adj.R^2	$\hat{\phi}_1$		$\hat{\phi}_2$		$\hat{\phi}_3$	
051	1303	399	.2883	.0198	.48375282	**	.29319194	**	.33362675	**
					SE : (.68650564E-01)		(.61123645E-01)		(.76644635E-01)	
051	1304	261	.3627	.0014	.24708575	**	.14827894		.11191260	
					SE : (.68396637E-01)		(.87072958E-01)		(.11741380)	
051	1305	122	.3465	.0000	.21966136	**				
					SE : (.83581697E-01)					
051	1306	81	.2765	.0000	.63797444	**				
					SE : (.89846536E-01)					
067	1398	36	.3111	.0000	.36344194	**				
					SE : (.11195088)					
067	1399	139	.2959	.0431	.63190854	**	.44133034	**	.31119600	*
					SE : (.10109402)		(.10661613)		(.12703936)	
067	1400	81	.3197	.0000	.78440756	**				
					SE : (.10294659)					
067	1401	94	.3421	.0860	.57109398	**	.30698296	**	.84842630E-01	
					SE : (.11903361)		(.11432847)		(.12169223)	
092	1548	43	.3116	.0000	.57692033	**				
					SE : (.10753139)					
092	1549	141	.3067	.0882	.40888259	**	.15595873		-.42847075E-01	
					SE : (.11053959)		(.10211758)		(.11562872)	
092	1550	110	.2777	.0451	.25311214	#	.12353806		-.83371237E-01	
					SE : (.13110301)		(.11625403)		(.12319497)	
092	1551	47	.1867	.0000	.48383644	**				
					SE : (.11696581)					
093	1553	188	.3926	-.0013	.68278476E-02		.51590400E-02		.13677847	
					SE : (.99223485E-01)		(.81611274E-01)		(.88863941E-01)	
093	1555	60	.3346	.0000	.68336107E-01					
					SE : (.87417962E-01)					
093	1557	29	.3960	.0000	.16036990					
					SE : (.11517378)					
093	1558	120	.2907	-.0003	.27008453E-01		-.13926031		-.81605718E-01	
					SE : (.13663821)		(.11323869)		(.99633830E-01)	
094	1559	31	.5869	.0000	.72679949	**				
					SE : (.19704822)					
094	1560	38	.3718	.0000	.59032798	**				
					SE : (.15855598)					
094	1562	36	.4261	.0000	.71630746	**				
					SE : (.20031226)					
094	1563	26	.3778	.0000	.11891369					
					SE : (.19337011)					

Table 3-2b: (Continued)

INCODE	PLOT	N	MSE	Adj.R^2	$\hat{\tau}_1$	$\hat{\tau}_2$	$\hat{\tau}_3$
095	1566	317	.2390	-.0004	.17005634 **	.22868218 **	.26223731 **
					SE : (.59321160E-01)	(.65241091E-01)	(.92355834E-01)
095	1567	204	.3223	.0287	.11816547E-02	-.45284782E-01	-.27690881 **
					SE : (.80938866E-01)	(.75108588E-01)	(.96131681E-01)
095	1569	71	.3280	.0000	.14387494 #		
					SE : (.78823220E-01)		
095	1570	61	.3714	.0000	-.82703181E-01		
					SE : (.91296221E-01)		
105	1625	65	.5504	.0000	.18449336 *		
					SE : (.86716204E-01)		
105	1627	66	.2725	.0000	.39174506 **		
					SE : (.10042410)		
105	1628	156	.2611	.0458	.28099856 *	.39816421E-01	-.20631060E-02
					SE : (.11299115)	(.94192887E-01)	(.11985408)
105	1629	174	.3056	-.0037	.43470851 **	.33092093 **	.43336591 *
					SE : (.88625053E-01)	(.12525574)	(.21975668)
106	1631	135	.3997	.0063	-.25600952 *	-.41088927 *	-.18946145
					SE : (.11565898)	(.18520259)	(.26584206)
106	1632	81	.4281	.0000	.21943805		
					SE : (.21441082)		
106	1634	139	.2765	.0257	.48142192 **	.58627594 *	.73903698 *
					SE : (.15660460)	(.23749947)	(.34247628)
106	1635	26	.0831	.0000	-.75742520E-01		
					SE : (.13022289)		
175	2266	95	.3029	.0350	.38292882 **	.14541773	
					SE : (.11883181)	(.14404860)	
175	2267	54	.4217	.0000	.25658506 *		
					SE : (.11267209)		
175	2269	142	.3007	.0287	.37858206 *	.16884312	
					SE : (.17502000)	(.10722406)	
175	2270	113	.4774	.0167	.96906567 **	.74732715 **	
					SE : (.12539139)	(.27388136)	
175	2271	62	.3966	.0000	.48226473 **		
					SE : (.10720075)		
175	2272	93	.3556	.1192	.85529351 **	.40142676 #	
					SE : (.17662389)	(.23604449)	
204	2509	72	.2797	.0000	.10350462		
					SE : (.12790622)		
204	2512	110	.4463	.0000	.30383334 **		
					SE : (.11597845)		

Table 3-2b: (Continued)

INCODE	PLOT	N	MSE	Adj.R^2	$\hat{T}_1$	$\hat{T}_2$	$\hat{T}_3$
205	2513	45	.2090	.0000	-.23557061E-01		
				SE : (	.15455420)		
205	2515	52	.5454	.0000	-.27274379 *		
				SE : (	.11336666)		
212	2549	39	.2693	.0000	.36291385 **		
				SE : (	.13018064)		
212	2551	55	.6703	.0000	.15010244		
				SE : (	.12118993)		
213	2559	44	.3371	.0000	-.25895588E-01		
				SE : (	.13901439)		
213	2560	47	.5288	.0000	.27098078		
				SE : (	.16586440)		
215	2565	69	.2865	.0000	-.70491865E-01		
				SE : (	.10305338)		
215	2568	58	.4889	.0000	.65115738 **		
				SE : (	.24330228)		
216	2570	38	.0328	.0000	.36171147 **		
				SE : (	.63787146E-01)		
217	2574	56	.4911	.0000	.23068431 *		
				SE : (	.10653638)		
217	2576	75	.3808	.0000	.11476761E-01		
				SE : (	.22420526)		
355	0014	149	.2342	.0000	.51842886 **		
				SE : (	.64751062E-01)		
365	0026	389	.3510	.0055	.83359219E-01	-.23497652E-01	
				SE : (	.51353676E-01)	(.58864251E-01)	
365	0032	412	.6046	.0090	.12918890 *	-.37655711E-01	
				SE : (	.60819405E-01)	(.50027992E-01)	

** significant at a = 0.01, * at a = 0.05, # at a = 0.10

INCODE: Installation code

N: The number of trees

MSE: Mean square error

adj.R^2: Adjusted R-square

SE: The standard error of the estimated parameter

Step 4: The parameter estimates from step 3 (i.e. ϕ_{ijkl}) are now used to estimate the fertilization main effect, by cycle, and possibly its interaction with plot level covariates. The following three sets of independent variables were formed:

1. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{XT}$ = [SI*$\underline{T}$, SI^{-2}*$\underline{T}$, RD*$\underline{T}$, LOG(RD)*$\underline{T}$]

2. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{XT}$ = [LOG(SI)*$\underline{T}$, RD*$\underline{T}$, LOG(RD)*$\underline{T}$]

3. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

   $\underline{XT}$ = [LOG(SI)*$\underline{T}$, $(BA^{1/2})$*$\underline{T}$]

Where,

RD = Reineke's (1933) stand density index (SDI) of the plot divided by the maximum SDI for the species

= $[N(QMD/10.0)^{1.605}]/530$

N = Number of trees per acre on the plot

QMD = $\{BA/[0.005454154(N)]\}^{1/2}$

The SI and RD transformations of set 1 are basically the same as those used by Miller et al. (1988) and the SI and BA transformations of set 3 are those used by Hann and Larsen (1990).

These three sets of independent variables were then fit to the data set and their parameters estimated using varying-parameter (or random coefficient) regression techniques (Biging 1985). In all three regressions, all independent variables involving F400, and the SI, RD and BA transformations were not significantly different from zero (α=0.05) for all cycles. Of the three remaining independent variables, FERT*C_1, FERT*C_2 and FERT*C_3, only FERT*C_1 was significantly different from zero (α=0.05). However, all three variables were included in the final equation because: (1) the variances of the parameters of FERT*C_2 and FERT*C_3 are influenced (i.e., increased) by the reduced sample sizes for these cycles, and (2) the monotonic reduction in the size of the parameters with increasing number of cycles since fertilization followed expected behavior. Therefore, the final fertilization response modifier equation for the Douglas-fir diameter growth equation in ORGANON is:

$$\begin{aligned} LOG(DGFM_1) &= E(\hat{\phi}_{ijkl}) \\ &= \Sigma_{l=1}^{3} b_l C_l \end{aligned} \qquad [3\text{-}2c]$$

Where,

$DGFM_1$ = Diameter growth fertilization response modifier for the l^{th} cycle

b_1, b_2, b_3 = estimated parameters

Because each observation is weighted by the variance-covariance matrix for ϕ_{ijkl} that was estimated in step 3, the following was used to calculate the weighted residuals:

$$\underline{f} = \underline{P}^{-1} (\underline{Y} - \hat{Y}) \quad \text{(Draper and Smith 1981)}$$

where

$\underline{f}$ = the column matrix of weighted residuals

$\underline{P}^{-1}$ = the inverse matrix of $\underline{P}$

$\underline{P}$ = a unique nonsingular symmetric matrix

$= \underline{E}\ \underline{D}_{SQRT(z)}\ \underline{E}^{-1}$ (Selby 1974)

such that $\underline{P}^2 = \underline{V}$, (the weighted matrix)

$\underline{E}$: eigen vectors of $\underline{V}$

z : the eigen values of $\underline{V}$

$\underline{D}_{SQRT(z)}$: a diagonal matrix with square root of eigen values as its diagonal elements

$\underline{Y}$ = the observed value of dependent variable

$\hat{Y}$ = the predicted value

The estimated parameters of equation [3-2c] are presented in Table 3-2c, and a plot of the weighted residuals over the predicted weighted dependent variable is presented in Figure 3-2. A check of the weighted residuals by PC SAS Procedure UNIVARIATE (SAS/STAT 1985) showed that they were normally distributed (p=0.6067).

Table 3-2c: The estimated parameters of the fertilization response modifier equation [3-2c] for the diameter growth equation of Douglas-fir in ORGANON

VARIABLE	COEFFICIENT	S.E.	T-VALUE	TEST
C1	.26588788	.37849400E-01	7.025	P < 0.01
C2	.75117715E-01	.49117870E-01	1.529	P > 0.10
C3	.46983624E-01	.71954360E-01	.653	P > 0.10

SSE = 478.09121
DF = 85
MSE = 5.6246025
Wt. MEAN of Y= .19244134
Wt. VAR(Y) = 6.4613520
Wt. Adj-Rsq. = .12950068

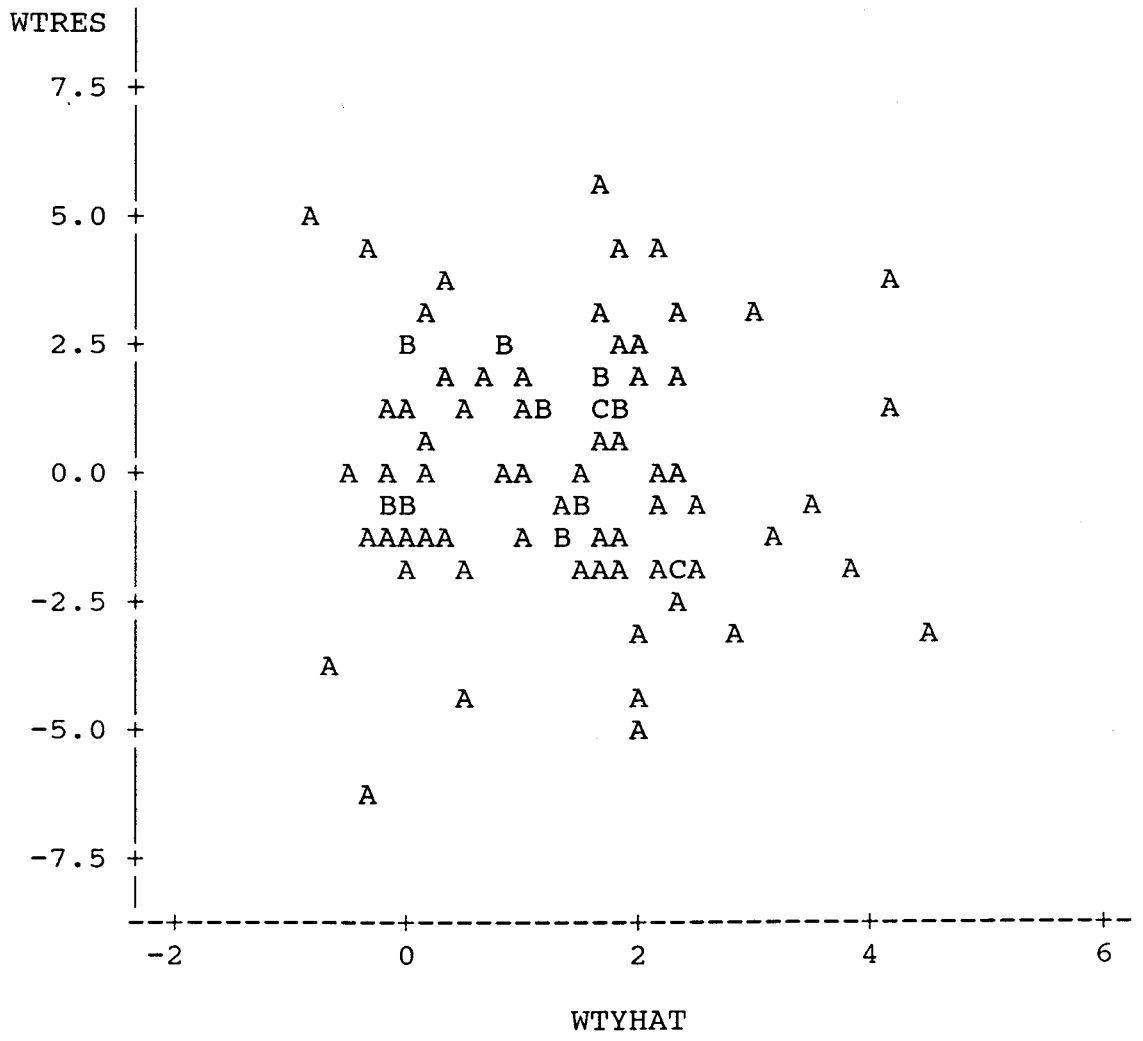

Figure 3-2: Plotting of weighted residuals (WTRES) on weighted predicted Y (WTYHAT) from the fertilization response modifier equation [3-2c] for the diameter growth equation of Douglas-fir in ORGANON

3.3 Discussion

Given equation [3-1] and its parameter estimates in table 3-1, the direct response of dominant height growth to fertilization in the first five years after fertilization can be predicted by:

$$HGFM = EXP(0.09029)$$
$$= 1.09450$$

Where,

HGFM = Dominant height growth fertilization modifier for the first five-year cycle since fertilization.

Similarly, given equation 3-2c and its estimated parameters in table 3-2c, the direct response of diameter growth to fertilization in the C_1 cycle since fertilization can be predicted by:

$$DGFM_1 = EXP(0.26589)$$
$$= 1.30459$$
$$DGFM_2 = EXP(0.07512)$$
$$= 1.07801$$
$$DGFM_3 = EXP(0.04698)$$
$$= 1.04810$$

Therefore, these equations predict a 9 percent increase in dominant height growth and a 30 percent increase in diameter growth in the first five-years after fertilization. For dominant height growth, there does

not appear to be any evidence that the direct effect of fertilization lasts any longer than one five-year cycle. For diameter growth, the results found in this study seem to agree with prior findings that the direct effect may last for ten years. Though the direct effect is not significant from zero in the second and third five-year cycles, the effect does decline in the same monotonic fashion as has been found previously. For example, Stegemoeller and Chappell (1989) reported that, for unthinned Douglas-fir, direct gross stand basal area growth response to a single application of fertilizer "...decreases to non-significant levels between years 10 and 12 (page 5)."

The lack of significance of the stand level independent variables involving A, SI, BA and/or RD for predicting direct response to fertilization in Douglas-fir contradicts the findings of Miller et al. (1988) and Heath and Chappell (1989). However, in a summary of the findings of Regional Forest Nutrition Research Project, Stegemoeller et al. (1989) reported that, for Douglas-fir, "Neither stand age, site index, nor initial stems/acre were statistically significant variables in explaining response variability for unthinned stands in regional analyses (page 1.19)."

This study also could not detect a significant difference between the application of 200 pounds of

nitrogen and the application of 400 pounds. The size of the data set for the 400 pound application was small in relation to the 200 pound application and the data were concentrated in the first five-year cycle since fertilization. Examination of the data presented in Stegemoeller and Chappell (1989) indicates a non-significant (α=0.05) difference in gross stand basal area growth for the first four years after fertilization, a significant difference in the next four years, and, finally, a non-significant difference after eight years. Therefore, the lack of significance in the first five-year cycle seems to agree with the data of Stegemoeller and Chappell (1989). The data was probably too limited to detect a possible significant difference in the second five-year cycle.

Chapter 4

Modeling Tree Growth Response to Fertilization and Thinning

The analysis methods discussed in chapter 2 can be applied not only in the fertilization trials but also in the thinning trials. The examples used in Chapter 3 will be extended to include direct thinning response in the modifiers for the Douglas-fir diameter growth and the dominant height growth equations in SW-ORGANON. The data used to develop these modifiers includes all 20 installations described in Tables (1-1) through (1-5).

4.1 Modeling Dominant Height Growth Response to Fertilization and Thinning using Structure Analysis

The simplified tree's structure analysis equation [3-1] in Chapter 3 can be extended to develop the fertilization and thinning response modifier for the dominant height growth equation in ORGANON. This produces the following equation:

$$E(M_{ijkl}) = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} \qquad [4\text{-}1]$$

Where,

M_{ijkl} = the mean of Y_{ijklm} for each plot and

cycle

Y_{ijklm} = $LOG(HG_{ijklm})$ - $LOG(PHG_{ijklm})$

HG_{ijklm} = The observed 5-year dominant height growth of tree m, period l, plot k, treatment j, installation i

PHG_{ijklm} = The predicted 5-year dominant height growth of tree m, period l, plot k, treatment j, installation i from the existing potential height growth equation in ORGANON

LOG = the natural logarithm

Again, this equation must be fitted by weighted regression where the weight is the number of dominant trees on each plot and cycle. Also, the parameters can be estimated by the generalized linear model package -- PC SAS Procedure GLM (SAS/STAT 1985). Using GLM, the following four sets of independent variables were formed, inserted into equation [4-1] and then fitted to the data:

1. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*$_{C2}$, THIN*FERT*C_1, THIN*FERT*C_2]

   $\underline{X}$ = [SI, A]

   $\underline{XT}$ =[A*$\underline{T}$, SI*$\underline{T}$]

2. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*$_{C2}$, THIN*FERT*C_1, THIN*FERT*C_2]

$\underline{X}$ = [LOG(SI), A]

$\underline{XT}$ = [A*$\underline{T}$, LOG(SI)*$\underline{T}$]

3. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*$_{C2}$, THIN*FERT*C_1, THIN*FERT*C_2]

$\underline{X}$ = [SI, A^{-1}]

$\underline{XT}$ = [(A^{-1})*$\underline{T}$, SI*$\underline{T}$]

4. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*$_{C2}$, THIN*FERT*C_1, THIN*FERT*C_2]

$\underline{X}$ = [LOG(SI), A^{-1}]

$\underline{XT}$ = [(A^{-1})*$\underline{T}$, LOG(SI)*$\underline{T}$]

Where,

THIN = 1.0 if the plot had been thinned

= 0.0 otherwise.

SI, A, FERT, F400, C_1, C_2 and C_3 have defined in equation [3-1]

In all four regressions, all independent variables involving F400, THIN, C_2, C_3, and the SI and A transformations were not significantly different from zero (α=0.05). Because C_2, C_3 and THIN were not significant, the data for these two cycles and for the thinnings were removed for final estimation of the parameters. As a result, the final equation is the same as equation [3-1b] in Chapter 3.

4.2 Modeling Diameter Growth Response to Fertilization and Thinning using Four-step Analysis

The four-step analysis equations [3-2a], [3-2b], and [3-2c] in Chapter 3 can be extended to develop the fertilization and thinning response modifier for the diameter growth equation in ORGANON:

Step 1: Again, the existing diameter growth equation in ORGANON was used to form the general control equation.

Step 2: The general diameter growth equation was calibrated to each block's control plots, producing 20 block-specific control equations [3-2a]. In addition to the 18 block-specific control equations which have already been presented in Chapter 3, Table 4-1 shows the remaining 2 block-specific control equations.

Step 3: Each tree's diameter growth response to fertilization is estimated by taking the difference between the tree's observed diameter growth and the diameter growth predicted by the calibrated, block-specific diameter growth equation determined in step 2. These differences are then used to fit the plot-specific tree response equation [3-2b] (plot by plot). In addition to those plot-specific response

Table 4-1: The estimated parameters of the additional calibrated, block-specific control equations [3-2a] for modeling the diameter growth response to fertilization and thinning

INCODE	N	MSE	Adj.-Rsq.	b_0	b_1	b_2
310	468	.3911	.3800	-4.2089520 **	1.8700881 **	.61429651E-04**
			SE : (	.59268997) (	.27424622) (	.23101563E-04)
356	447	.1589	.0144	-.30335662 *	.19148116 #	-.56945560E-05
			SE : (	.14055310) (	.10396899) (	.84993068E-05)

** significant at $\alpha = 0.01$, * at $\alpha = 0.05$, # at $\alpha = 0.10$

INCODE: Installation code

N: The number of trees

MSE: Mean square error

adj.R^2: Adjusted R-square

SE: The standard error of the estimated parameter

Table 4-2: The estimated parameters of the additional plot-specific response equations [3-2b] for modeling the diameter growth response to fertilization and thinning

INCODE	PLOT	N	MSE	Adj.R^2	$\hat{\phi}_1$	$\hat{\phi}_2$	$\hat{\phi}_3$
212	2553	30	.2545	.0000	1.2169265 **		
					SE : (.18413039)		
212	2554	18	.2357	.0000	.83546728 **		
					SE : (.16107452)		
212	2555	16	.2333	.0000	.78578395 **		
					SE : (.16865942)		
212	2556	28	.1353	.0000	.86457473 **		
					SE : (.14380542)		
310	0051	59	.0873	.0000	.50265342 **		
					SE : (.80413929E-01)		
310	0062	54	.2860	.0000	.37803769 **		
					SE : (.82617189E-01)		
310	0103	58	.1699	.0000	.48335499 **		
					SE : (.81562246E-01)		
310	0106	57	.1524	.0000	.43133765 **		
					SE : (.81583699E-01)		
310	0107	54	.1350	.0000	.38558584 **		
					SE : (.83413428E-01)		
310	0121	55	.1280	.0000	.48241219 **		
					SE : (.82454836E-01)		
356	0021	96	.8300	.0000	-.22921748 **		
					SE : (.73330076E-01)		
356	0022	50	1.279	.0000	-.46630421 **		
					SE : (.96047384E-01)		
365	0025	83	.0875	.3510	.41447788 **	-.22938512E-01	
					SE : (.97483845E-01)	(.97971935E-01)	
365	0028	74	.1280	.0800	.36425751 **	.13875955	
					SE : (.10102475)	(.10428327)	
365	0030	77	.0578	.1117	.18043569 #	.24831516E-02	
					SE : (.10000000)	(.10194606)	
365	0031	84	.1529	.0955	.59682578 **	.33026722 **	
					SE : (.95656155E-01)	(.10202941)	

** significant at $\alpha = 0.01$, * at $\alpha = 0.05$, # at $\alpha = 0.10$

equations which have already been presented in Chapter 3, Table 4-2 shows the estimated parameters of the remaining 16 plot-specific response equations.

Step 4: The parameter estimates from step 3 are now used to estimate the fertilization and thinning main effects, by cycle, and possibly their interaction with plot level covariates. The following three sets of independent variables were formed:

1. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*C_2, THIN*FERT*C_1, THIN*FERT*C_2]

   $\underline{XT}$ = [SI*$\underline{T}$, SI^{-2}*$\underline{T}$, RD*$\underline{T}$, LOG(RD)*$\underline{T}$, THIN*{RATE/EXP[$(d/D)^2$]}*C_1, THIN*FERT*{RATE/EXP[$(d/D)^2$]}*C_1]

2. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*C_2, THIN*FERT*C_1, THIN*FERT*C_2]

   $\underline{XT}$ = [LOG(SI)*$\underline{T}$, RD*$\underline{T}$, LOG(RD)*$\underline{T}$, THIN*{RATE/EXP[$(d/D)^2$]}*C_1, THIN*FERT*{RATE/EXP[$(d/D)^2$]}*C_1]

3. $\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3, THIN*C_1, THIN*C_2, THIN*FERT*C_1, THIN*FERT*C_2]

   $\underline{XT}$ = [LOG(SI)*$\underline{T}$, ($BA^{-1/2}$)*$\underline{T}$, THIN*{RATE/EXP[$(d/D)^2$]}*C_1,

$$THIN*FERT*\{RATE/EXP[(d/D)^2]\}*C_1]$$

Where,

RATE = ratio of removal BA to BA before thinning

d/D = ratio of QMD for the removal trees to QMD for the trees before thinning

These three sets of independent variables were then fit to the data set and their parameters estimated using varying-parameter (or random coefficient) regression techniques (Biging 1985). In all three regressions, all independent variables involving F400, THIN by itself, the interaction of THIN with FERT, and the SI, RD and BA transformations were not significantly different from zero (α=0.05) for all cycles. Of the four remaining independent variables (i.e., $FERT*C_1$, $FERT*C_2$, $FERT*C_3$, and $THIN*\{RATE/EXP[(d/D)^2]\}*C_1$) both $FERT*C_2$ and $FERT*C_3$ were not significantly different from zero (α=0.05). However, all four variables were included in the final equation because: (1) the variances of the parameters of $FERT*C_2$ and $FERT*C_3$ are influenced (i.e., increased) by the reduced sample sizes for these cycles, and (2) the monotonic reduction in the size of the parameters with increasing number of cycles since fertilization followed expected behavior. The resulting fertilization and thinning response modifier equation is:

$$LOG(DGM) = E(\hat{\phi}_{ijkl})$$
$$= a_1\ FERT*C_1 + a_2\ FERT*C_2 + a_3\ FERT*C_3$$
$$+ a_4\ THIN*\{RATE/EXP[(d/D)^2]\}*C_1 \qquad [4\text{-}2]$$

Where,

DGM = Diameter growth fertilization and thinning response modifier

a_1, a_2, a_3, a_4 = estimated parameters

The direct response of diameter growth to fertilization and/or thinning can be predicted by:

$$DGM = EXP[a_1\ FERT*C_1 + a_2\ FERT*C_2 + a_3\ FERT*C_3$$
$$+ a_4\ THIN*\{RATE/EXP[(d/D)^2]\}*C_1]. \qquad [4\text{-}3]$$

4.3 Results and Discussion

Thinning does not affect dominant height growth, but application of nitrogen fertilizer does increase it in the first five-year cycle after treatment. Both thinning and fertilization affects diameter growth, but the interaction of thinning with fertilization is not significant (α=0.05). Equation [4-2] indicates that the diameter growth thinning response is significant in only the first five-year growth cycle since thinning. Because the sample size was small for the second five-year cycle since thinning, all of the second cycle data was removed and equation [4-2] was refitted to the reduced data set. The resulting parameter estimates of equation [4-2] are

presented in Table 4-3. A check of the weighted residuals by PC SAS Procedure UNIVARIATE (SAS/STAT 1985) showed that they were normally distributed ($p=0.1635$).

These results indicate that the diameter growth response to thinning currently built into SW-ORGANON is inadequate for at least the first 5-year growth cycle since thinning. Unfortunately, this study did not have enough data to test the thinning response in subsequent cycles. Table 4-4 shows the thinning component of the diameter growth modifier (equation [4-3]). The magnitude of the departure in the first 5-year period increases both as the amount of stand basal area removed increases and as the d/D ratio decreases. The Douglas-fir diameter growth equation in SW-ORGANON is more sensitive to BAL than to BA (Hann and Larsen 1990). As a result, the current equation would predict little response to thinning from below. The findings of this study indicate that, when thinning from below (i.e., small d/D ratios), the current SW-ORGANON's diameter equation may underestimates the thinning response.

Table 4-3: The estimated parameters of the modifier equation [4-2] for modeling the diameter growth response to fertilization and thinning

VARIABLE	COEFFICIENT	S.E.	T-VALUE	TEST
FERT*C1	.24280603	.37768500E-01	6.429	P < 0.01
FERT*C2	.70398241E-01	.50319900E-01	1.399	P > 0.10
FERT*C3	.44045434E-01	.75999710E-01	.580	P > 0.10
RATE/EXP[(d/D)^2]	1.1535114	.32762540	3.521	P < 0.01

SSE = 644.66620
DF = 102
MSE = 6.3202569
Wt. MEAN of Y= .20495213
Wt. VAR(Y) = 7.0832744
Wt. Adj-Rsq. = .10772101

Table 4-4: The thinning component of the diameter growth modifier in Equation [4-3]

	BA Removal								
d/D	.1000	.2000	.3000	.4000	.5000	.6000	.7000	.8000	.9000
.4	1.1033	-	-	-	-	-	-	-	-
.5	1.0940	1.1968	-	-	-	-	-	-	-
.6	1.0838	1.1746	1.2731	-	-	-	-	-	-
.7	1.0732	1.1518	1.2361	1.3267	-	-	-	-	-
.8	1.0627	1.1294	1.2002	1.2754	1.3554	1.4404	-	-	-
.9	1.0527	1.1081	1.1664	1.2278	1.2925	1.3606	1.4322	-	-
1.0	1.0433	1.0886	1.1358	1.1850	1.2364	1.2900	1.3459	1.4042	1.4651
1.1	1.0350	1.0712	1.1087	1.1475	1.1877	1.2292	1.2722	1.3168	1.3628
1.2	1.0277	1.0562	1.0854	1.1155	1.1464	1.1782	1.2108	1.2444	1.2789
1.3	1.0215	1.0435	1.0659	1.0889	1.1123	1.1362	1.1607	1.1856	1.2111
1.4	1.0164	1.0330	1.0500	1.0672	1.0846	1.1024	1.1205	1.1388	1.1575
1.5	1.0122	1.0246	1.0371	1.0498	1.0627	1.0757	1.0888	1.1022	1.1156

Chapter 5

Modeling Stand Growth Response to Fertilization

The analysis methods discussed in chapter 2 can be applied to evaluate the direct effect of fertilizer on stand gross basal area growth. The emphasis of this chapter is upon how fertilizer response changes over time, and the similarities and differences between the estimates derived from structure analysis and those derived from the traditional two-step analysis. These analyses were conducted using the remeasurement data from 18 fertilization research installations established in unthinned Douglas-fir stands near the study area of ORGANON. Chapter 1 contains a detailed description of these installations. The availability of more recent plot level data on five installations (numbers 212 through 217) allowed the addition of 19 more second cycle measurements to the data set described in chapter 1. Each installation has at least one control plot, and the fertilized plots were treated with either 200 or 400 lbs of nitrogen per acre. In the following analyses, an installation is treated as a block, and a plot is an experimental unit.

5.1 Estimating Stand Gross Basal Area Growth Response using Structure Analysis

The general linear model form used for analyzing stand gross basal area growth using structure analysis is:

$$Y_{ijkl} = \mu + \underline{B} + \underline{T} + \underline{X} + \underline{TX} + \epsilon_{ijkl} \qquad [5\text{-}1]$$

where

Y_{ijkl} = natural logarithm of 5-year stand gross basal area growth at cycle l, plot k, treatment j, installation i

μ = mean Y

$\underline{B} = \Sigma_{i=1}^{b} \beta_i B_i$

β_i = block effect of installation i

B_i = 1.0, if data come from installation i

= 0.0, otherwise

$\underline{T} = \Sigma_{j=2}^{t} \Sigma_{l=1}^{c} \tau_{jl} T_{jl}$

τ_{jl} = main effect of treatment j at cycle l

T_{jl} = 1.0, if data come from treatment j at cycle l

= 0.0, otherwise

$\underline{X} = \Sigma_{p=1}^{v} \alpha_{1.p} X_{ijklp}$

$\alpha_{1.p}$ = the slope parameter of the p^{th} covariate for the control plots

X_p = the p^{th} covariates

$\underline{TX} = \Sigma_{j=2}^{t} \Sigma_{l=1}^{c} \Sigma_{p=1}^{v} \alpha_{jlp} T_{jl} X_{ijklp}$

α_{jlp} = the slope parameter of the interaction of

covariate p with treatment j at cycle l

All treatment effects are fixed. The independent variables tested in this equation were:

$\underline{T}$ = [FERT*C_1, FERT*C_2, FERT*C_3, F400*C_1, F400*C_2, F400*C_3]

$\underline{X}$ = [SI, LOG(SI), SI^{-2}, SI^{-1}, A, A^{-1}, A^2, RD, LOG(RD), BA, BA/A, BA/$(A)^2$, $(BA)^2/(A)^2$,

$\underline{XT}$ = $\underline{X}$ * $\underline{T}$

Errors were assumed to have a normal distribution with mean zero and a constant variance. The generalized linear model package, PC SAS Procedure GLM (1985) was used the estimate the parameters of equation [5-1]. All independent variables involving F400, and SI, RD, were not significantly different from zero (α=0.05) for all cycles. The final fertilization response equation using structure analysis for the Douglas-fir five-year stand gross basal area growth is as follows:

$$\hat{Y} = u + \Sigma_{i=1}^{18} a_i B_i + \Sigma_{l=1}^{3} b_l \text{ FERT*}C_l + c \text{ BA/A} \qquad [5\text{-}2]$$

This equation shows that gross stand basal area growth experienced a direct response to fertilization. The estimated parameters of equation [5-2] are presented in Table 5-1.

Table 5-1: The estimated parameters in equation [5-2] using structure analysis for modeling stand gross basal area response to fertilization

Parameter		Estimate	T for H0: Parameter=0	Pr > |T|	Std Error of Estimate
INTERCEPT		3.010856749 B	29.03	0.0001	0.10373261
INCODE	51	-0.309668787 B	-5.33	0.0001	0.05805303
	67	-0.318176538 B	-5.41	0.0001	0.05876791
	92	-0.409246905 B	-6.21	0.0001	0.06594011
	93	-0.023987913 B	-0.41	0.6849	0.05898191
	94	-0.615213236 B	-7.96	0.0001	0.07731783
	95	-0.035509389 B	-0.64	0.5258	0.05582233
	105	0.207710480 B	3.34	0.0011	0.06217511
	106	-0.025863921 B	-0.40	0.6917	0.06509313
	175	-0.220185294 B	-3.51	0.0006	0.06274067
	204	-0.007439502 B	-0.09	0.9269	0.08088819
	205	-0.201070943 B	-2.59	0.0106	0.07764157
	212	-0.231831633 B	-3.37	0.0010	0.06872807
	213	-0.493620293 B	-6.79	0.0001	0.07266836
	215	-0.706038807 B	-7.98	0.0001	0.08852110
	216	0.057973061 B	0.71	0.4814	0.08211165
	217	-0.383119941 B	-5.08	0.0001	0.07546957
	355	0.102862605 B	1.07	0.2880	0.09644306
	365	0.000000000 B	.	.	.
BA/A		0.098502021	7.63	0.0001	0.01290515
FERT*C1		0.266879092	11.73	0.0001	0.02275019
FERT*C2		0.132268765	4.86	0.0001	0.02723701
FERT*C3		0.062592318	1.69	0.0926	0.03695992

Root MSE	0.11912	R-square	0.9119
Dep Mean	3.42613	Adj R-sq	0.8984
Observation	159.00000		

NOTE: The X'X matrix has been found to be singular and a generalized inverse was used to solve the normal equations. Estimates followed by the letter 'B' are biased, and are not unique estimators of the parameters.

5.2 Estimating Stand Gross Basal Area Growth Response using Two-step Analysis

Step 1: The following general control equation without block dummy variables was developed from the fertilization installation's control data:

$$E(Y_{ilkl}) = \mu + \underline{X}$$

After an initial screening of the independent variables by PC SAS procedure REG (SAS/STAT 1985), it was found that the estimated parameters for all of the SI transformations, while significantly different from zero, had negative signs. Because it was expected that stand gross basal area growth should increase with increasing SI, all the SI transformations were dropped from $\underline{X}$. The remaining independent variables were screened again, resulting in the following final control equation:

$$\hat{Y} = b_0 + b_1 A^{-1} + b_2 BA/A + b_3 BA/(A*A) \qquad [5\text{-}3]$$

where Y is LOG(BAG). Table 5-2 shows the estimated parameters of equation [5-3]

Table 5-2: The estimated parameters in the general control equation [5-3] using two-step analysis for modeling stand gross basal area growth response to fertilization

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > |T|
INTERCEPT	1	1.832484	0.19911699	9.203	0.0001
1/A	1	29.073167	6.19772750	4.691	0.0001
BA/A	1	0.225488	0.03895914	5.788	0.0001
BA/(A*A)	1	-3.227366	0.99974277	-3.228	0.0021

Root MSE	0.21684	R-square	0.6875
Dep Mean	3.29475	Adj R-sq	0.6713
Observation	62.00000		

Covariance of Estimates

COVB	INTERCEP	1/A	BA/A	BA/(A*A)
INTERCEP	0.039647575	-1.066358858	-0.00720656	0.1785501853
1/A	-1.066358858	38.41182612	0.1705442923	-5.729165817
BA/A	-0.00720656	0.1705442923	0.0015178146	-0.033894013
BA/(A*A)	0.1785501853	-5.729165817	-0.033894013	0.9994856078

Step 2: Each fertilized plot's direct response to treatment is estimated by taking the difference between the observed value and the value predicted by the general control equation. These differences are then used to fit the following fertilization response equation using all treated plots:

$$E(Y_{ijkl} - \hat{Y}_{con}) = \underline{T} + \underline{TX}$$

The appropriate estimated variances to test the significance of the parameters in the fertilizer response equation were computed using the techniques described in Appendix A. After screening the same independent variables as was used in the final control equation, the resulting direct fertilizer response equation was:

$$\begin{aligned} LOG(BAFM) &= E(Y_{ijkl} - \hat{Y}_{con}) \\ &= \Sigma_{l=1}^{3} a_l \, FERT*C_l \end{aligned} \qquad [5\text{-}4]$$

where

BAFM = Stand gross basal area growth fertilization response modifier

a_1, a_2 and a_3 = estimated parameters

Table 5-3 presents the estimated parameters in equation [5-4].

Table 5-3: The estimated parameters in the response equation [5-4] using two-step analysis for modeling the gross basal area growth response to fertilization

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > |T|
FERT*C1	1	0.237315	0.05679842	4.178	P < 0.01
FERT*C2	1	0.149913	0.06875638	2.180	P < 0.05
FERT*C3	1	0.127327	0.09445454	1.348	P > 0.10

The total number of observations = 97

5.3 Results and Discussion

Both structure analysis and two-step analysis show that the direct fertilization response on gross stand basal area growth declines over time, and that the interaction of fertilization with any other covariates are not significant. The appropriate estimated variances to test the significance of the parameters in fertilizer response equation [5-4], estimated using two-step analysis, are larger than the estimated variances to test the significance of the fertilizer response parameters in equation [5-2], estimated using the structure analysis.

A potential problem in the two step-analysis is that the data set may be too small to develop a good quality general control equation. In order to check this problem, a control equation with block dummy variables was fitted to the control plot data and the resulting parameter estimates and associated statistics are presented in Table 5-4. If this equation is used instead of equation [5-3], the adjusted R^2 changes from 0.6713 to 0.9239. Therefore, the additional covariates in equation [5-3] (i.e. A^{-1} and BA/A^2) explained only a small part of the variation due to the block effect. Because the control equation [5-3] does not adequately explain the block effect, the block effect is carried into the second step

of the analysis. In the second step, this block effect may increase the error about the equation if the block effect is orthogonal to the fertilization independent variables, or the block effect may change the parameter estimates of the fertilization independent variables. Therefore, it is recommended that structure analysis should be used to estimate direct stand growth response to fertilization in the case where small data sets preclude the estimation of a good quality control equation.

Table 5-4: The estimated parameters of the alternative control equation with dummy variables for block effects in the two-step analysis

Parameter		Estimate	T for H0: Parameter=0	Pr > |T|	Std Error of Estimate
INTERCEPT		3.124042550 B	13.26	0.0001	0.23557088
INCODE	51	-0.476891690 B	-5.08	0.0001	0.09391370
	67	-0.568910276 B	-6.81	0.0001	0.08352748
	92	-0.477435419 B	-4.33	0.0001	0.11021152
	93	-0.075910266 B	-0.95	0.3497	0.08028527
	94	-0.751312665 B	-5.37	0.0001	0.13979798
	95	-0.153281745 B	-1.73	0.0902	0.08843990
	105	0.120768915 B	1.15	0.2573	0.10519285
	106	-0.097781883 B	-0.73	0.4706	0.13432699
	175	-0.478193105 B	-4.06	0.0002	0.11772215
	204	-0.080523178 B	-0.60	0.5509	0.13395248
	205	-0.129657980 B	-1.30	0.1996	0.09951745
	212	-0.276311158 B	-2.36	0.0229	0.11707779
	213	-0.587523001 B	-4.55	0.0001	0.12922268
	215	-0.766230425 B	-4.30	0.0001	0.17812954
	216	-0.040598919 B	-0.29	0.7757	0.14156595
	217	-0.481156352 B	-3.68	0.0007	0.13086143
	355	0.079645789 B	0.68	0.4995	0.11695306
	365	0.000000000 B	.	.	.
BA/A		0.094931701	3.01	0.0043	0.03148977

Root MSE	0.10437	R-square	0.9463
Dep Mean	3.29475	Adj R-sq	0.9239
Observation	62.00000		

NOTE: The X'X matrix has been found to be singular and a generalized inverse was used to solve the normal equations. Estimates followed by the letter 'B' are biased, and are not unique estimators of the parameters.

Chapter 6

Summary and Conclusions

Landowners in the Pacific Northwest of United States are now applying nitrogen fertilizer to either thinned or unthinned forest stands to increase growth and therefore improve the economic gain from forest operations. As a result, it is very important for a growth and yield model to be able to make an accurate and precise prediction of the fertilization and thinning response of stands.

Fertilization studies are always more complex in experimental design and analysis than those examples commonly presented in the textbooks because a forest ecosystem is more complex than a soy bean experiment, and the large majority of the reports on fertilization give little or no details concerning their statistical design and analysis (Woollons and Whyte 1988). Therefore, the primary objective of this study was to present general analysis methods for modeling direct stand and tree growth response to fertilization and thinning. Two methods were proposed:

(1) Structure analysis:

This method applies covariance analysis to blocked designs with either experimental units (plots) alone or with both experimental units

(plots) and sampling units (trees). The mean square of experimental error is used to test the significance of the plot level covariate(s), and the mean square of sampling error is used to test the significance of the tree level covariate(s).

There are two potential problems with the use of structure analysis for modeling tree growth response to fertilization and thinning. First, MSB/MSE, MST/MSE, MSX/MSE AND MSTX/MSE are not distributed as Snedecor's F. In order to solve this problem, an alternative equation using the mean of the dependent variable and independent variables for each plot and cycle can be used if the experiment has a balanced design. Second, if the data sets used to develop tree level growth and yield models are from unbalanced experimental designs (the usual case), then one must either randomly drop sampling trees such that the number of the remaining trees is the same for all plot-cycles or one must use a mixed model form and GLM techniques.

(2) Multi-step analysis:

In the first step of this method, either a general control equation is developed from the study's control plot data or an existing general control equation developed from a previous study is found and used. This general control equation is

then used to evaluate direct treatment response using the fertilized and/or thinned plots. Estimation of variances in multi-step analysis is more difficult than in structure analysis.

A potential problem with the use of traditional two-step analysis for modeling stand growth response to fertilization is that past users of the method have underestimated the appropriate variance for testing treatment response. This study suggests that the appropriate variance to test the significance of a parameter in the treatment response equation can be computed by adding the variance of the parameter from the control equation to the variance of the parameter from the treatment response equation.

Ideally, structure analysis is preferred to multi-step analysis for evaluating direct treatment response because structure analysis pools all the data together in a joint regression and, therefore, it has more degrees of freedom to estimate variances. However, when the experimental data are large in sampling size and complex in their designed structure, structure analysis often can not be performed on most statistical packages, and therefore multi-step analysis is a viable alternative. Although the multi-step equation will have a larger variance than the joint equation, the multi-step analysis enables one

to either use an existing or to develop a new general control equation which is useful when building growth and yield models.

The analysis methods were applied in modeling direct fertilization and thinning effects on the diameter growth and the dominant height growth of single trees. Both dominant height growth and diameter growth responses due to improved nutrition were significant (α=0.05) in the first 5-year growth period, and not significant after two 5-year cycles. The response in tree's diameter growth was larger than that in tree's dominant height growth.

Thinning neither increased nor decreased the dominant height growth. It accelerated the diameter growth, but the interaction of fertilization with thinning was not significant. The diameter growth response to thinning departs from that predicted by SW-ORGANON in the first 5-year growth period after thinning. The magnitude of this departure increases both as stand basal area removed increases and as the d/D ratio decreases. This indicates that SW-ORGANON may underestimate the tree growth response in stands with heavy thinning from below.

As a comparison, both structure analysis and two-step analysis were used to model the direct fertilization effect on the gross basal area growth of plots. The results showed that both methods produced predictions of

the direct fertilization responses that declined over time and that were significantly different from zero in the first and second 5-year growth cycles. The appropriate variance estimates to test the significance of the parameters in fertilizer response equation were larger when using two-step analysis than when using structure analysis. Therefore, it is recommended that structure analysis should be used to estimate direct growth response to fertilization in the situation when data sets are small enough to allow the application of the method.

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Appendices

Appendix A

Computation of the Appropriate Variances to Test the Significance of the Parameters in the Treatment Response Equation of the Traditional Two-step Analysis Method

In the general multiple regression case, the independent variables of the response equation can be different from those of the control equation. However, the treatment equation must be defined with the same independent variables as the response equation. For example:

control equation: $\underline{Y}_c = \underline{X}_c \underline{a}$

treatment equation: $\underline{Y}_t = \underline{Z}_t \underline{b}$

response equation: $\underline{Y}_t - \hat{\underline{Y}}_c = \underline{Z}_t \underline{d}$

join equation: $\underline{Y} = \underline{X} \underline{a}^* + \underline{TZ} \underline{d}^*$

where

$\underline{Y}_c$ = dependent variable for control data

$\underline{Y}_t$ = dependent variable for treatment data

$\hat{\underline{Y}}_c$ = the predicted values by control equation using treatment data

$\underline{Y}$ = dependent variable for all data

$\underline{X}_c$ = independent variables for control equation

$\underline{Z}_t$ = common independent variables for treatment and response equations

TZ = Z if data comes from treated plot

= 0.0 otherwise

$\underline{a}$, $\underline{b}$, $\underline{d}$, $\underline{a}^*$, and $\underline{d}^*$ = estimated parameters

In this case, the appropriate variance to test the significance of the parameters in the response equation should be computed as follows:

$$\underline{d} = (\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t (\underline{Y}_t - \hat{\underline{Y}}_c)$$

$$= (\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t (\underline{Y}_t - \underline{X}_t\underline{a})$$

$$\text{Var}(\underline{d}) = \text{Var}[(\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t (\underline{Y}_t - \underline{X}_t\underline{a})]$$

$$= \text{Var}[(\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t\underline{Y}_t - (\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t\underline{X}_t\underline{a})]$$

$$= \text{Var}[\underline{b} - (\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t\underline{X}_t\underline{a})]$$

$$= \text{Var}(\underline{b}) + \text{Var}[(\underline{Z}'_t \underline{Z}_t)^{-1}\underline{Z}'_t\underline{X}_t\underline{a})]$$

{since $\underline{b}$ is independent with $\underline{a}$}

where $\underline{X}_t$ is the matrix of independent variables of control equation applied to the treatment data. In general, the response equation variances computed directly by the two-step analysis procedure will underestimate the appropriate variances to test the significance of the parameters in the response equation.

In the special case where $\underline{Z}$ is the same as $\underline{X}$, the Var($\underline{d}$) is computed by:

$$\text{Var}(\underline{d}) = \text{Var}(\underline{b}) + \text{Var}(\underline{a}).$$

In this case, $\underline{d}$ is the same as the estimated parameters of a joint equation using the structure analysis. If $\underline{Z}$ is not the same as $\underline{X}$, the estimated parameters of the

control equation and the response equation using the two-step analysis are no longer the same as the estimated parameters of the joint equation using structure analysis. The latter method uses both control and treatment data to estimate the common slope(s), but the former method uses only one of them. The greater the difference in the independent variables between the control and the response equations, the greater the risk that the estimated parameters using the former method will depart from those using the latter method.

Appendix B

Computation of the Variance-Covariance Matrix of the Dependent Variable for the Fourth Fitting Step using Four-step Analysis

It is necessary to compute the variance-covariance matrix of the dependent variable when the varying-parameter model (Biging 1985) is used to estimate the parameters of the following equation in four-step analysis:

$$\phi_{ijkl} = \underline{T} + \underline{TX} + \epsilon^{*}_{ijkl} \qquad [A\text{-}1]$$

where

$j \neq 1$;

ϕ_{ijkl} = estimated intercept for cycle "1" of the ijk^{th} plot-specific response equation

$\underline{T}$ = The treatment effect

$\underline{TX}$ = The interactions of treatments with plot level covariate(s) by cycles

ϵ^{*}_{ijkl} = error term

Among blocks, the ϕ_{ijkl} is independent of $\phi_{i'j'k'l'}$ (for $i \neq i'$); however, within a block, the ϕ_{ijkl} is correlated with $\phi_{ij'k'l'}$ because they use the prediction from the same control equation. The variance-covariance matrix of

$\underline{\phi}$ is as follows:

$$\begin{matrix} \underline{V}_1 & O & \cdots & O & \cdots & O \\ O & \underline{V}_2 & \cdots & O & \cdots & O \\ \vdots & \vdots & & \vdots & & \vdots \\ O & O & \cdots & \underline{V}_i & \cdots & O \\ \vdots & \vdots & & \vdots & & \vdots \\ O & O & \cdots & O & \cdots & \underline{V}_b \end{matrix}$$

where

$\underline{O}$ = zero matrix

$\underline{V}_i$ = the covariance matrix of ϕ for the i^{th} block, which is a symmetric matrix

$$= \begin{matrix} \mathrm{Var}(\phi_{i211}) & \mathrm{COV}(\phi_{i211},\phi_{i212}) & \cdots & \mathrm{COV}(\phi_{i211},\phi_{ijkl}) \\ & \mathrm{Var}(\phi_{i212}) & \cdots & \mathrm{COV}(\phi_{i212},\phi_{ijkl}) \\ & & & \vdots \\ & & & \mathrm{Var}(\phi_{ijkl}) \end{matrix}$$

In order to compute the appropriate variances (see Appendix A), the coefficients of response equations are expressed in matrix notation as $\underline{d} = [\phi\ \theta_1 \ \ldots\ \theta_w]'$. The $\mathrm{Var}(\phi_{ijkl})$ and $\mathrm{COV}(\phi_{ijkl},\phi_{ij'k'l'})$ are equal to the first diagonal elements of $\mathrm{Var}(\underline{d}_{ijkl})$ and $\mathrm{COV}(\underline{d}_{ijkl},\underline{d}_{ij'k'l'})$, respectively. The variance and covariance of $\underline{d}$ can be computed as following:

$$\begin{aligned} &\mathrm{Var}(\underline{d}_{ijkl}) \quad \text{for } j \neq 1 \\ &= \mathrm{Var}[(\underline{Z}'_{ijkl}\underline{Z}_{ijkl})^{-1}\underline{Z}'_{ijkl}(\underline{Y}_{ijkl}-\underline{Z}^{o}_{ijkl}\,\underline{c}_{i1})] \\ &= \mathrm{Var}(\underline{t}_{ijkl}) + \mathrm{Var}[(\underline{Z}'_{ijkl}\underline{Z}_{ijkl})^{-1}\underline{Z}'_{ijkl}\underline{Z}^{o}_{ijkl}\,\underline{c}_{i1})] \end{aligned}$$

and

$$\begin{aligned}
&\mathrm{COV}(\underline{d}_{ijkl}, \underline{d}_{ij'k'l'}) \quad \text{for } j \neq 1 \text{ and } jkl \neq j'k'l' \\
&= \mathrm{COV}[(\underline{Z}'_{ijkl}\underline{Z}_{ijkl})^{-1}\underline{Z}'_{ijkl}(\underline{Y}_{ijkl} - \underline{Z}^{o}_{ijkl}\,\underline{c}_{i1})), \\
&\quad (\underline{Z}'_{ij'k'l'}\underline{Z}_{ij'k'l'})^{-1}\underline{Z}'_{ij'k'l'}(\underline{Y}_{ij'k'l'} - \underline{Z}^{o}_{ij'k'l'}\,\underline{c}_{i1})] \\
&= \mathrm{COV}((\underline{Z}'_{ijkl}\underline{Z}_{ijkl})^{-1}\underline{Z}'_{ijkl}\underline{Z}^{o}_{ijkl}\underline{c}_{i1}, \\
&\qquad (\underline{Z}'_{ij'k'l'}\underline{Z}_{ij'k'l'})^{-1}\underline{Z}'_{ij'k'l'}\underline{Z}^{o}_{ijkl}\underline{c}_{i1})
\end{aligned}$$

where

$\underline{d}$ = coefficients of plot-specific response equation

$\underline{c}$ = coefficients of block-specific control equation

$\underline{t}$ = coefficients of plot-specific treatment equation

$\mathrm{Var}(\underline{d}_{ijk})$ = the suggested variance of coefficients in the ijk^{th} plot-specific response equation

$\mathrm{Var}(\underline{c}_{i1})$ = the variance of the coefficients of the i^{th} block-specific control equation

$\mathrm{Var}(\underline{t}_{ijk})$ = the variance of the coefficients of the ijk^{th} plot-specific treatment equation

$\underline{Z}$ = variables used in the plot-specific response equation

$\underline{Z}^{o}$ = variables used in the block-specific equation

In a special case, when the control equation and the response equation have the same independent variables, the variance-covariance matrix of the i^{th} block, V_i, can be simplified to:

$$\begin{matrix} Var(t_{i211})+Var(c_{i1}) & Var(c_{i1}) & \cdots & Var(c_{i1}) \\ Var(c_{i1}) & Var(t_{i212})+Var(c_{i1}) & \cdots & Var(c_{i1}) \\ & & \vdots & \\ Var(c_{i1}) & Var(c_{i1}) & Var(t_{ijkl})+Var(c_{i1}) & \end{matrix}$$

The diagonal elements of the variance-covariance matrix are the sum of the estimated variances of the parameters in the plot-specific treatment equations and the estimated variances of the parameters in the block-specific control equation. The covariances within a block are the estimated variances of the parameters in the block-specific control equation. All the covariances among blocks are zero. Therefore, if there are many blocks, the forth fitting step is not affected very much by the correlation between dependent variables, and, as a result, it might be acceptable to simply ignore the correlation.