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Implications of Random Variation in the Stand Prognosis Model

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ABSTRACT

Although the Stand Prognosis Model has several stochastic components, features have been included in the model in an attempt to minimize run-to-run variation attributable to these stochastic components. This has led many users to assume that comparisons of management alternatives could be made based on a single run of the model for each alternative. Recent analyses have demonstrated that this assumption may often be incorrect. Several possible solutions are given, and *the author recommends that in almost all applications of the Stand Prognosis Model it would be wise to make at least two or three projections for each alternative. The number of replications required for any specific application must be determined by evaluating the tradeoff between the added costs of additional replications and the need for additional precision based on intended uses of model output.*

KEYWORDS: growth projection, management planning,modeling

Stage (1987) pointed out that growth is a deviation-amplifying process characterized by positive feedback of both random and deterministic effects. This aspect of the growth process is represented in the Stand Prognosis Model by several stochastic components. The effect of including the stochastic components is that faster growing trees grow faster and slower growing trees grow slower than they do when the stochastic components are suppressed. The impact on stand development of suppressing the stochastic components is that estimates of total volume are much lower than those observed in nature.

THE PROBLEM

Typically, the Stand Prognosis Model (Stage 1973) is thought of as a deterministic rather than a stochastic model of stand development. Two features have been included in the model to attempt to provide "almost" deterministic output: (1) record tripling, which results in internal replication of tree records, and (2) a means by which the sequence of random numbers used in the model's few stochastic components may be replicated in successive runs of the model. Many users of the model have felt that these features eliminate random variation as a problem when comparing alternative strategies and permit them to make such comparisons with a single run of the model for each alternative. Recent analyses based on the Inland Empire variant of the Stand Prognosis Model show that this practice can produce comparisons of alternatives that, although unbiased, are subject to large random variation. Thus, decisions based on comparisons of single model runs may be wrong.

The problem became apparent during an analysis designed to estimate differences attributable to genetically improved stock of ponderosa pine in stand volume at age 100. Fourteen years of data were available to estimate genetic gain in individual tree height and diameter growth rates. Multipliers in the Stand Prognosis Model were used to simulate how these increased individual tree growth rates would translate into stand volume at age 100. In some of the simulations, as the multipliers were increased to simulate the difference between a low and a moderate level of genetic selection, projected total cubic foot volume at age 100 decreased. When the multipliers were increased further to simulate the highest level of selection, projected volume then increased. Projected stand basal area on the observed stands did not approach levels that would lead to reductions in growth because of excessive density in any of the simulations. This indicated that the behavior might be the

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result of the stochastic elements of the height, crown ratio, or basal area increment components of the Stand Prognosis Model.

To examine this hypothesis, 10 seeds for the random number generator were selected. For a set of stands that had displayed this anomalous behavior, model runs were made with and without multipliers for each random seed using both versions 5.2 and 6.0 of the Inland Empire variant of the Stand Prognosis Model. The results of these runs are displayed in tables la and lb. Estimates of the increase in total cubic foot volume attributable to genetically improved stock range from.3.46 to 18.15 percent when version 5.2 is used and from 1.92 to 8.64 percent when version 6.0 is used. The Monte Carlo ratio of means estimates of genetic gain, based on these 10 simulations, were 9.29 percent for version 5.2 and 6.65 percent for version 6.0. The corresponding Monte Carlo mean of ratios estimates of genetic gain are 9.37 percent for version 5.2 and 6.65 percent for version 6.0. Although the estimates of gain for version 6.0 are lower than for version 5.2, for each version the range of estimates is substantial. In each case several estimates of genetic gain appear to be at the extremes of the distribution of possible estimates. Clearly, the use of different random seeds can result in different estimates of genetic gain. The results of analyses discussed in the remainder of this paper are similar for versions 5.2 and 6.0. Thus, results will be presented only for version 6.0. Recommendations are valid for users of either version and may also apply to users of other Prognosis variants.

A review of the stochastic components of the Stand Prognosis Model explains this variation in model output. The only difference between versions 5.2 and 6.0 that affects the stochastic components is the addition to version 6.0 of a procedure for representing the serial correlation between successive increment predictions (Stage and Wykoff in preparation) to improve the estimation of the random component of diameter increment. The effect of this change should be a small increase in the variability of output produced by model runs made with different random number seeds. The remaining stochastic components are the same in each version.

For trees greater than 3 inches diameter at breast height (d.b.h.), if record tripling is completed (if the projection has completed two cycles or 1,350 tree records have been created), the basal area increment model includes a stochastic component. When a tree record reaches 3 inches d.b.h., a crown ratio is estimated for the record. This procedure has a stochastic component. For trees less than 3 inches d.b.h., the height growth model includes a stochastic component (even if record tripling is still occurring). Further, the predicted height growth for trees in a species-defined diameter range is a weighted average of a value from the small tree height increment model (with a stochastic component) and a value from the large tree height increment model (with no stochastic component). For most species this diameter range is either 1 or 2 inches

Table 1a—Monte Carlo replications of estimates of genetic gain in total cubic foot volume at age 100 using version 5.2 of the Stand Prognosis Model

Replication	Volume without genetic gain	Volume with genetic gain	Genetic gain
	- - - - - Ft^3/acre - - - - -		*Percent*
1	9,853	10,672	8.31
2	10,199	10,954	7.40
3	9,555	10,611	11.05
4	9,909	10,862	9.62
5	9,367	11,067	18.15
6	10,154	11,026	8.59
7	10,268	10,623	3.46
8	9,563	10,373	8.47
9	9,510	10,336	8.69
10	9,989	10,983	9.95
Monte Carlo estimate	9,837	10,751	9.29
No stochastic component	9,211	10,032	8.91

Table 2a—Monte Carlo replications of estimates of genetic gain in total cubic foot volume at age 100 using version 6.0 of the Stand Prognosis Model

Replication	Volume without genetic gain	Volume with genetic gain	Genetic gain
	- - - - - Ft^3/acre - - - - -		*Percent*
1	10,107	10,711	5.98
2	9,747	10,479	7.51
3	10,027	10,619	5.90
4	9,729	10,454	7.45
5	10,091	10,769	6.72
6	10,363	11,246	8.52
7	10,291	10,900	5.92
8	9,875	10,065	1.92
9	10,224	11,033	7.91
10	9,689	10,562	8.64
Monte Carlo estimate	10,014	10,680	6.65
No stochastic component	9,487	9,964	5.03

through 10 inches. Thus, any use of multipliers that affects when individual trees cross the 3- and 10-inch diameter boundaries also Sects how the stochastic components of the models are realized. Similar effects can be expected from any management alternative such as thinning strategy) that affects the timing of the growth of individual trees across these boundaries. Clearly, under these circumstances, selection of the same random seed does not assure the model user that the same sequence of random numbers will be used in the same way in repeated runs of the program.

Several characteristics of the sample stand may have an impact on the magnitude of this effect. An increase in the number of individual tree records leads to an increased number of calls to the random number generator. This has the effect of damping the influence of any single random number and thus should decrease the amount of variation between runs made with different random seeds. The effect of turning off the record tripling feature of the model is the opposite of that just described. All runs discussed in this note were made with the record tripling component of the program in effect. A decrease in variation in stand composition results in an increase in the amount of replication of conditions within the stand. Again, the effect of any single random number is damped, and the variation between runs made with different random seeds should be decreased.

Intended uses of the results of a projection also may have a major impact on the seriousness of problems caused by the stochastic nature of Prognosis model output. For example, when aggregate yield tables are being constructed, stands may provide the necessary replication to minimize the effect discussed in this paper. The impact is potentially most severe in cases such as the previously discussed estimation of increase in volume at age 100 attributable to genetically improved stock. In such cases different growth rates are applied to the two stands being compared from the time of stand establishment. This maximizes the potential number of differences in the sequence of random numbers between the two stands. An example of a case in which the impact may be of intermediate seriousness is provided by an evaluation of the difference in volume removed from a stand up to age 100 that can be attributed to a commercial thinning. In this case the sequence of random numbers is unaltered until the time of thinning. The only stochastic component of the model that would be affected by a commercial thinning is the timing of growth of some of the trees past the 10-inch diameter bound. Thus, it would be expected that the variation in estimates of the effect of a commercial thinning might be much smaller than the variation observed in estimates of genetic gain.

POSSIBLE SOLUTIONS

Three potential methods will be considered as means for minimizing or eliminating stochastic variation from comparisons of alternative model runs. The methods are (1) to suppress the stochastic aspects of the Stand Prognosis Model, (2) to use Monte Carlo simulation to estimate differences in treatment alternatives, and (3) to increase the number of tree records in the sample stand either by increased sampling or by splitting each existing tree record into multiple records (with appropriately reduced weight). The remainder of this paper evaluates these alternatives and makes recommendations based on the evaluation.

The simplest of these methods is to suppress the stochastic components of the models by the use of the DGSTDEV keyword Wykoff and others 1982). This keyword controls the limits of the normal distribution from which random errors are drawn. When it is set to 0, the stochastic components of the Stand Prognosis Model are suppressed.

The use of Monte Carlo simulation to estimate the gain in stand volume expected from genetically improved stock requires knowledge about the magnitude of variation resulting from repeated runs of the Stand Prognosis Model using different random seeds. For this portion of the study, 100 random number seeds were selected. For each seed, two runs of the model were made to simulate stand development with and without genetically improved stock. Results of this analysis are summarized in a series of tables and graphs. The mean and standard deviation of total cubic volume with multipliers, total cubic volume without multipliers, and genetic gain at age 100 are reported for 10, 20, 40, 50, 60, 80, and 100 replications. The estimate of genetic gain is the mean of ratios estimate. The number of replications to be used to compare alternative treatments (such as genetically improved stock vs. standard stock) must be determined by evaluating the tradeoff between added stability in the Monte Carlo estimates of these values resulting from further replication and the added costs associated with obtaining further replication. In this note estimates will be considered to have stabilized when Monte Carlo estimates based on additional replications vary by less than 4 percent.

These analyses are based on a sample stand containing 50 tree records. The third alternative for reducing the impact of stochastic variation on model results is to increase the number of tree records in the sample stand. To examine this effect, I increased the number of tree records in the sample stand to 150, maintaining the same distribution of diameters and heights. After two rounds of record tripling, this stand contains 1,350 records rather than 450. This should result in a reduction in the variation between model runs starting from different random seeds.

The analyses discussed thus far have included variation due to differences in the time each tree record passed over each of the diameter bounds (3 and 10 inches d.b.h.). The next analysis examines the relative importance of these two diameter bounds. A second se of stands (created by projecting the two stands used in the previous analyses from age 14 to age 20) are used as starting points for these projections. A random seed that produced an "average" yield at age 100 was used to project the two original stands from age 14 to age 20. The majority of the trees in the resulting tree lists were greater than 3 inches d.b.h. All that were not 3 inches attained this size by the end of the next 10-year projection cycle. Thus, when these stands were used as starting values, variation in the time individual trees grew over the S-inch d.b.h. bound is eliminated from the analysis.

The final question to be considered in this note deals with evaluating the impact of stochastic variation on comparisons of the estimated effects of management alternatives on stand development. The example used in the analysis is a thinning strategy in which 40 percent of the trees represented by each record were removed. The impact is evaluated both for stands made up primarily of trees less than 3 inches d.b.h. at the time of thinning (case 1) and for stands containing trees primarily greater than 3 inches d.b.h. at the time of thinning (case 2). The stand used in each case for projection is the stand used in the previous analyses to simulate an "average" stand (as opposed to the stand with genetically improved stock). The stand is thinned at age 14 for case 1 and at age 40 for case 2.

All stands used as input for these analyses were ponderosa pine plantations planted at a density of 450 trees per acre. Although stand development would obviously be different for different species or different management alternatives, the relative magnitude of the variation attributable to the stochastic components of the model should be expected to be similar.

RESULTS

When one selects the alternative of suppressing the stochastic components of the model, estimates of total volume associated with each model run will be too low. Because of the differential impact of the stochastic components of the model on the growth of fast and slow growing trees (that is, the reduction in volume growth of the fastest growing trees is greater than the reduction in volume growth of less rapidly growing trees), the estimate of genetic gain obtained when this alternative is followed will also be an underestimate. However, the results reported in table 1 demonstrate that, for this example, the magnitude of underestimation is not large when compared to the gain estimated with 10 Monte Carlo replications.

When the simulations are begun at age 14 with a stand made up of 50 tree records, Monte Carlo estimates of the mean and standard deviation of genetic gain exhibit little variation after 40 to 50 replications are made (table 2 and fig. 1). For many applications of the Stand Prognosis Model, this might be considered an excessive number of replications. After 20 replications, Monte Carlo estimates of total cubic volume at age 100 for both genetically improved stock and standard stock are within 1 percent of the estimates resulting from 100 replications. The Monte Carlo estimate of genetic gain based on 20 replications is within 6 percent of the estimate of genetic gain based on 100 replications. Both estimates of total cubic volume based on 10 replications are also within 1 percent of the 100 replication values. The estimate of genetic gain based on 10 replications overestimates the value based on 100 replications by only 3.3 percent. The size of the standard error of the mean (standard deviation from table 2 divided by the square root of the number of replications) for each of these estimates suggests that, for most applications, none of the above differences are likely to be of practical importance.

The results of repeating the Monte Carlo analysis with the stand containing 150 tree records are presented in table 3 and figure 2. As expected, the variation for all statistics is reduced. The estimate of genetic gain has almost completely stabilized at 20 replications. Estimates of total volume show almost no variation after 40 replications.

The results of the Monte Carlo analysis based on simulations begun at age 20 with a stand containing 50 tree records, shown in table 4 and figure 3, are similar to the results obtained when stands with 150 tree records were projected from age 14 (most trees below the 3-inch d.b.h. bound). The almost complete lack of variation in Monte Carlo estimates of genetic gain and the reduction in the Monte Carlo estimate of standard deviation of genetic gain from that shown in table 3 support the hypothesis that much of the variation in estimates is introduced by variation in the timing of growth of individual trees past the 3-inch d.b.h. bound. Increasing the number of tree records in the sample stand reduces this effect but does not eliminate it.

Variation in the estimate of gain due to thinning in case 1 (table 5 and fig. 4) was only slightly greater than the variation in case 2 (table 6 and fig. 5). Most of the trees in the stand used for case 1 and case 2 either were already 3 inches d.b.h. prior to the scheduled thinning or grew over

Table 2—Monte Carlo estimates of genetic gain measured by differences in total cubic foot volume at age 100 using version 6.0 of the Stand Prognosis Model

Number of replications	Volume without genetic gain		Volume with genetic gain		Genetic gain	
	Ft^3/acre	*Std. dev.*	*Ft^3/acre*	*Std. dev.*	*Percent*	*Std. dev.*
10	10,014	243.8	10,680	333.2	6.65	1.953
20	10,070	223.8	10,680	321.7	6.07	2.874
40	10,069	217.6	10,699	326.5	6.29	3.336
50	10,073	217.8	10,693	319.2	6.18	3.164
60	10,074	206.1	10,702	311.2	6.26	3.087
80	10,061	210.6	10,696	303.9	6.33	3.123
100	10,058	204.8	10,704	297.8	6.44	3.111

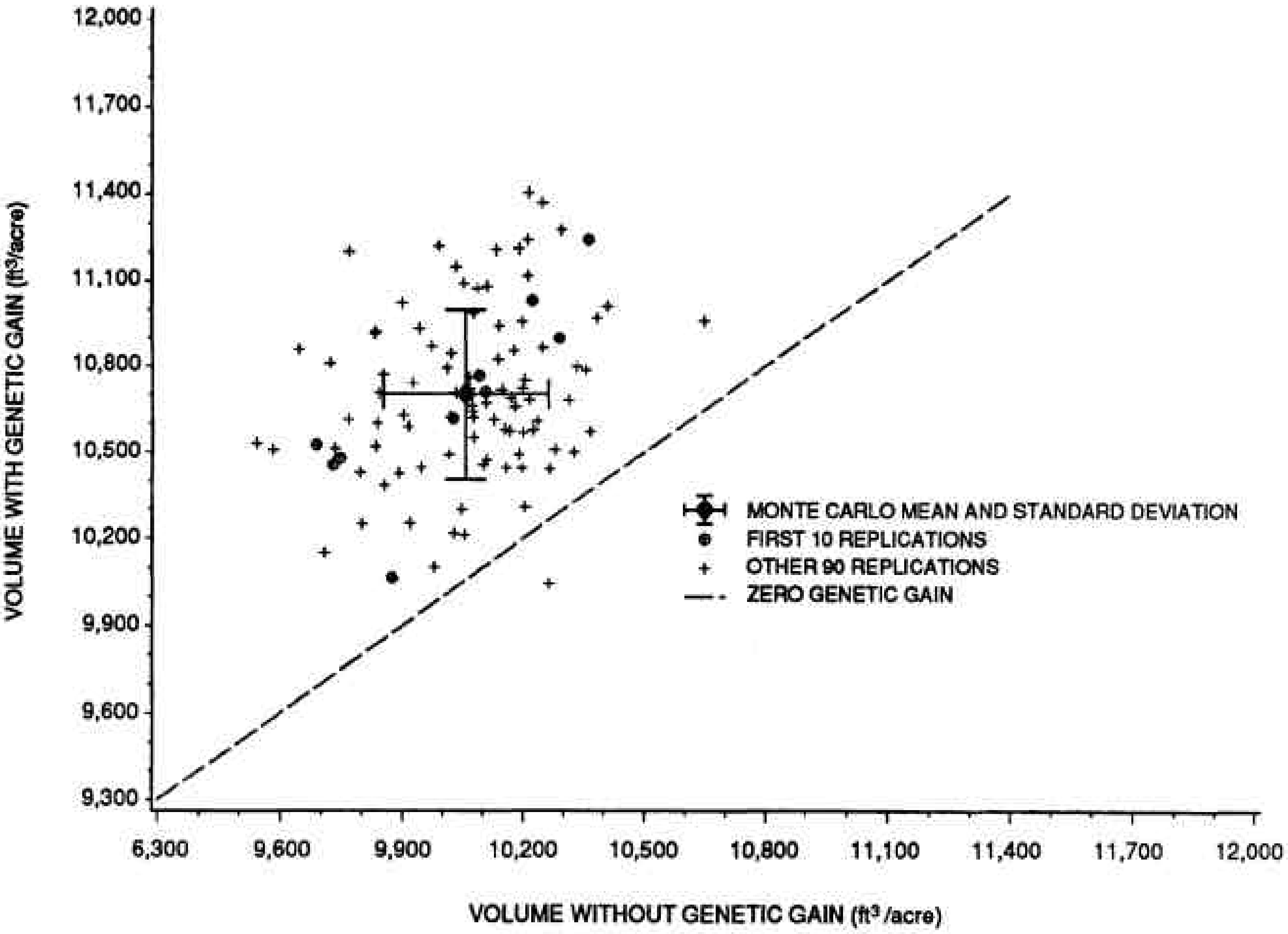

Figure 1—Distribution of individual estimates of volume at age 100 included in the Monte Carlo estimate of genetic gain using version 6.0 of the Stand Prognosis Model.

Table 3—Monte Carlo estimates of genetic gain measured by differences in total cubic foot volume at age 100 when sample stand contains 150 tree records.

Number of replications	**Volume without genetic gain**		**Volume with genetic gain**		**Genetic gain**	
	Ft^3/acre	*Std. dev.*	*Ft^3/acre*	*Std. dev.*	*Percent*	*Std. dev.*
10	10,196	197.8	10,892	148.9	6.85	2.075
20	10,198	164.0	10,876	136.2	6.68	1.828
40	10,231	159.5	10,907	179.3	6.62	1.812
50	10,225	149.2	10,902	177.2	6.63	1.812
60	10,226	149.0	10,906	174.3	6.65	1.747
80	10,238	141.2	10,908	165.6	6.56	1.804
100	10,232	133.3	10,901	167.5	6.55	1.756

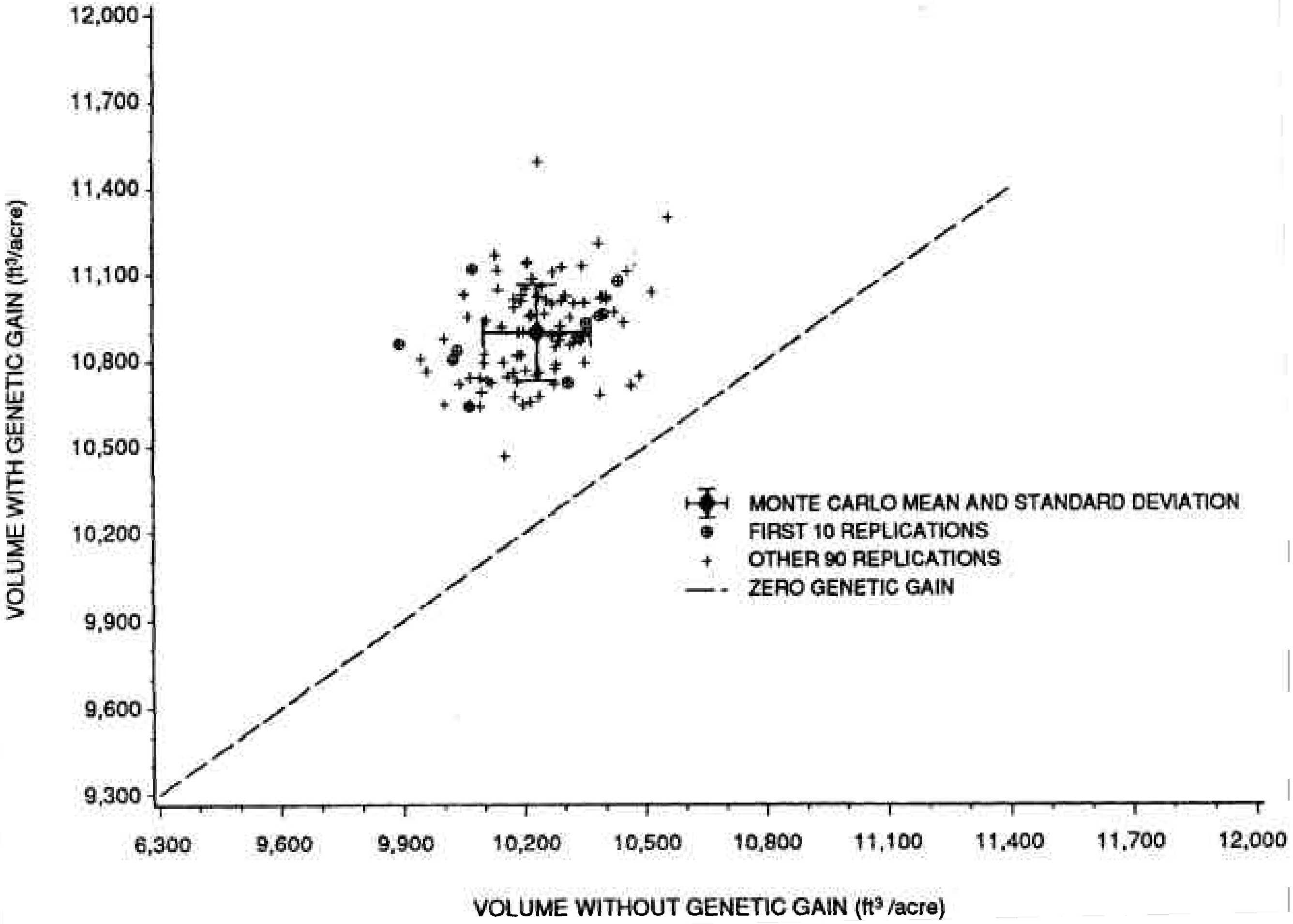

Figure 3—Distribution of individual estimates of volume at age 100 included in the Monte Carlo estimate of genetic gain when the majority of the trees in the sample stand are greater than 3 inches d.b.h.

Table 4—Monte Carlo estimates of genetic gain measured by differences in total cubic foot volume at age 100 when the majority of the trees in the sample stand are greater than 3 inches d.b.h.

Number of replications	**Volume without genetic gain**		**Volume with genetic gain**		**Genetic gain**	
	Ft^3/acre	*Std. dev.*	*Ft^3/acre*	*Std. dev.*	*Percent*	*Std. dev.*
10	9,694	95.8	10,443	66.5	7.74	1.002
20	9,643	147.7	10,387	122.8	7.72	1.320
40	9,636	132.8	10,381	138.8	7.75	1.476
50	9,633	126.1	10,382	134.6	7.78	1.480
60	9,642	122.5	10,385	131.6	7.72	1.454
80	9,629	123.1	10,382	131.3	7.83	1.586
100	9,632	121.1	10,386	131.3	7.84	1.542

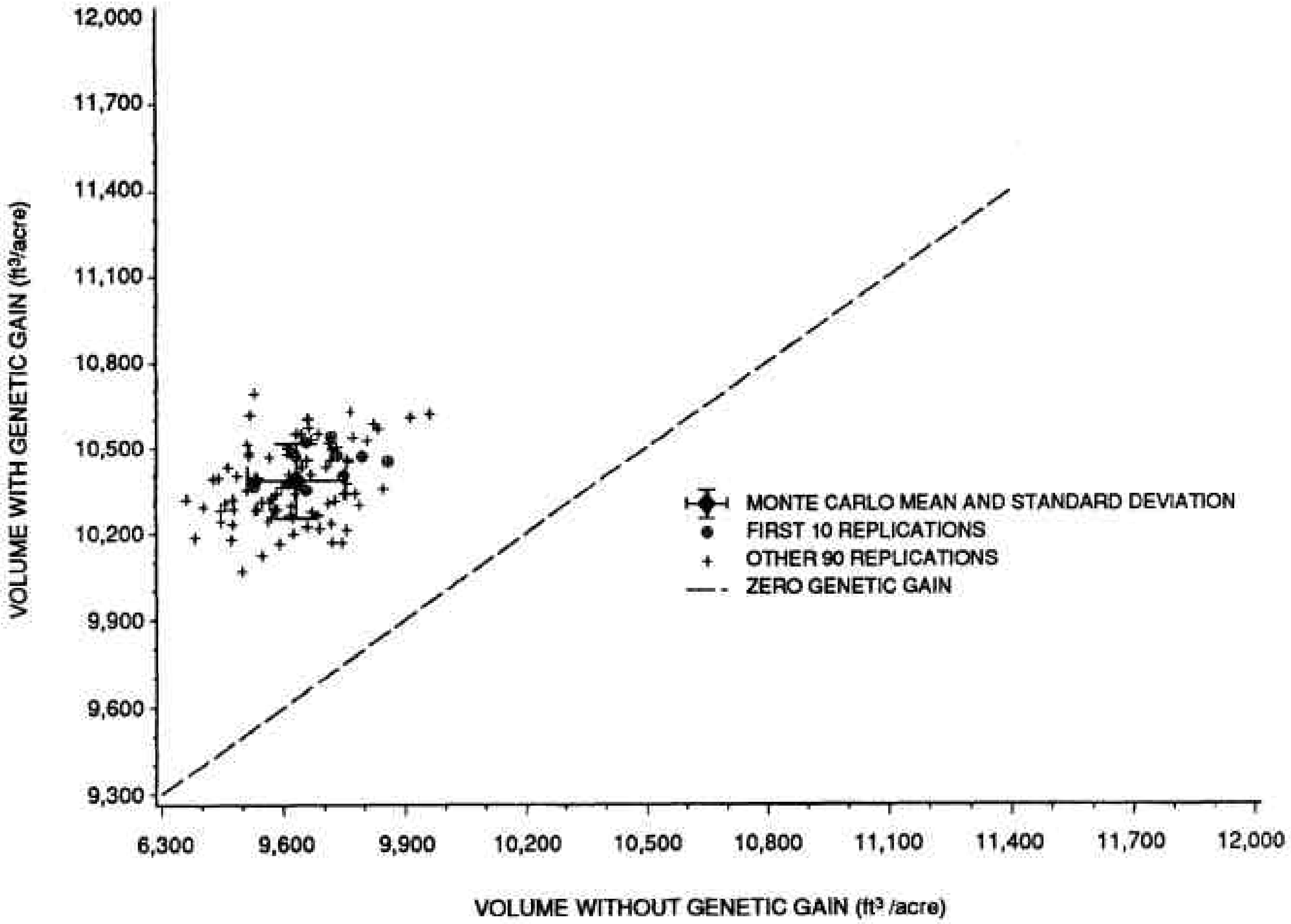

Figure 3—Distribution of individual estimates of volume at age 100 included in he Monte Carlo estimate of genetic gain when the majority of the trees in the sample stand are greater than 3 inches d.b.h.

Table 5—Monte Carlo estimates of gain from thinning measured by differences in total cubic foot volume removed from the stand by age 100 when the majority of the trees in the sample stand are less than 3 inches d.b.h.

Number of replications	Volume without thinning		Volume with thinning		Gain from thinning	
	Ft^3/acre	*Std. dev.*	*Ft^3/acre*	*Std. dev.*	*Percent*	*Std. dev.*
10	10,014	243.8	10,412	302.4	3.98	1.988
20	10,070	223.8	10,450	258.0	3.78	1.745
40	10,069	217.6	10,469	257.7	3.98	1.816
50	10,073	217.8	10,463	244.9	3.88	1.717
60	10,074	206.1	10,472	237.8	3.96	1.744
80	10,061	210.6	10,426	240.1	3.64	1.907
100	10,058	204.8	10,419	247.0	3.60	1.972

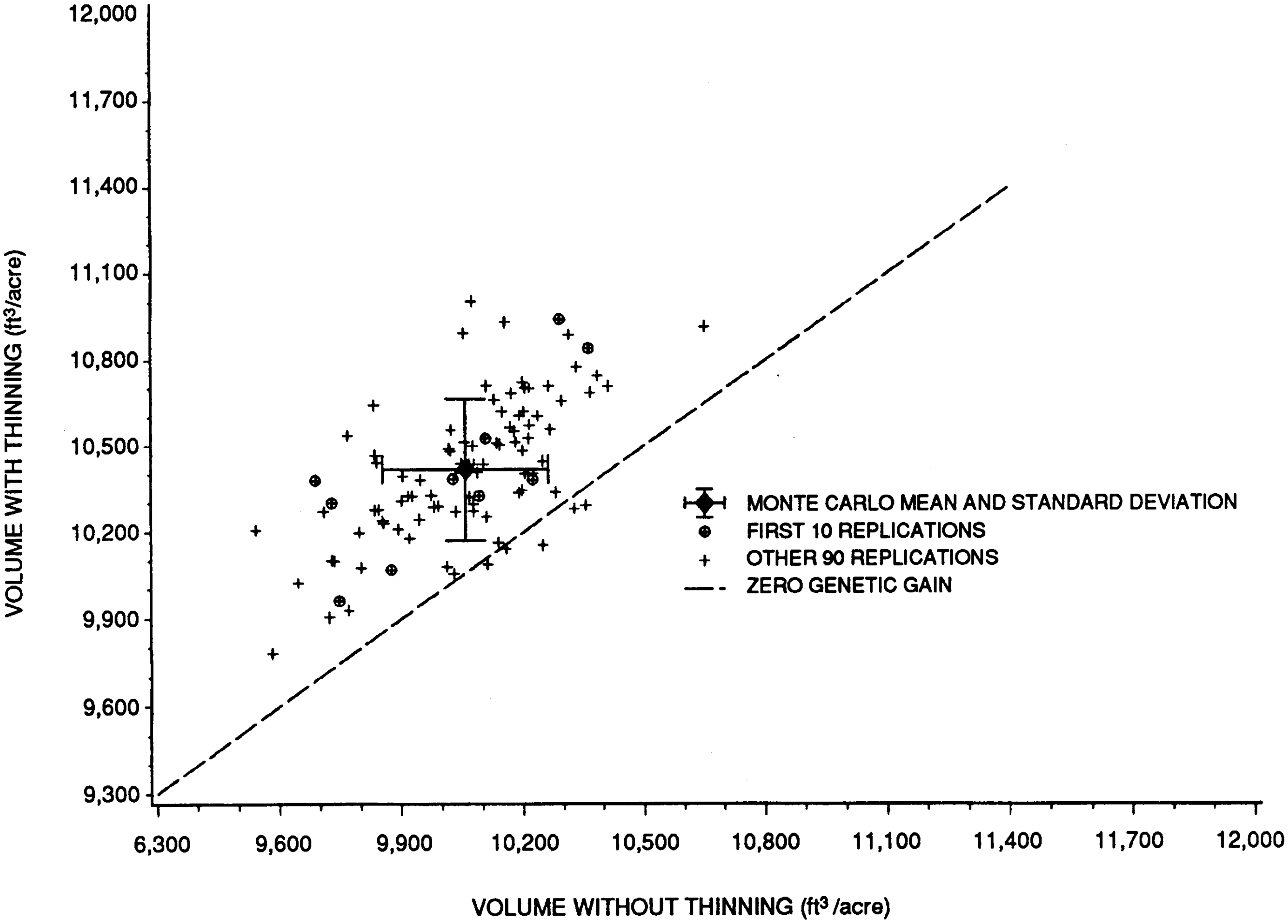

Figure 4—Distribution of individual estimates of volume at age 100 included in the Monte Carlo estimate of gain from thinning when the majority of the trees in the sample stand are less than 3 inches d.b.h. at the time of thinning.

Table 6—Monte Carlo estimates of gain from thinning measured by differences in total cubic foot volume removed from the stand by age 100 when the majority of the trees in the stand are greater than 3 inches d.b.h.

Number of replications	Volume without thinning		Volume with thinning		Gain from thinning	
	Ft³/acre	*Std. dev.*	*Ft³/acre*	*Std. dev.*	*Percent*	*Std. dev.*
10	10,014	243.8	10,998	307.9	9.82	1.143
20	10,070	223.8	10,964	268.3	8.87	1.463
40	10,069	217.6	10,982	261.8	9.07	1.254
50	10,073	217.8	10,987	253.6	9.08	1.244
60	10,074	206.1	10,985	244.3	9.05	1.227
80	10,061	210.6	10,959	238.1	8.92	1.301
100	10,058	204.8	10,950	236.9	8.87	1.453

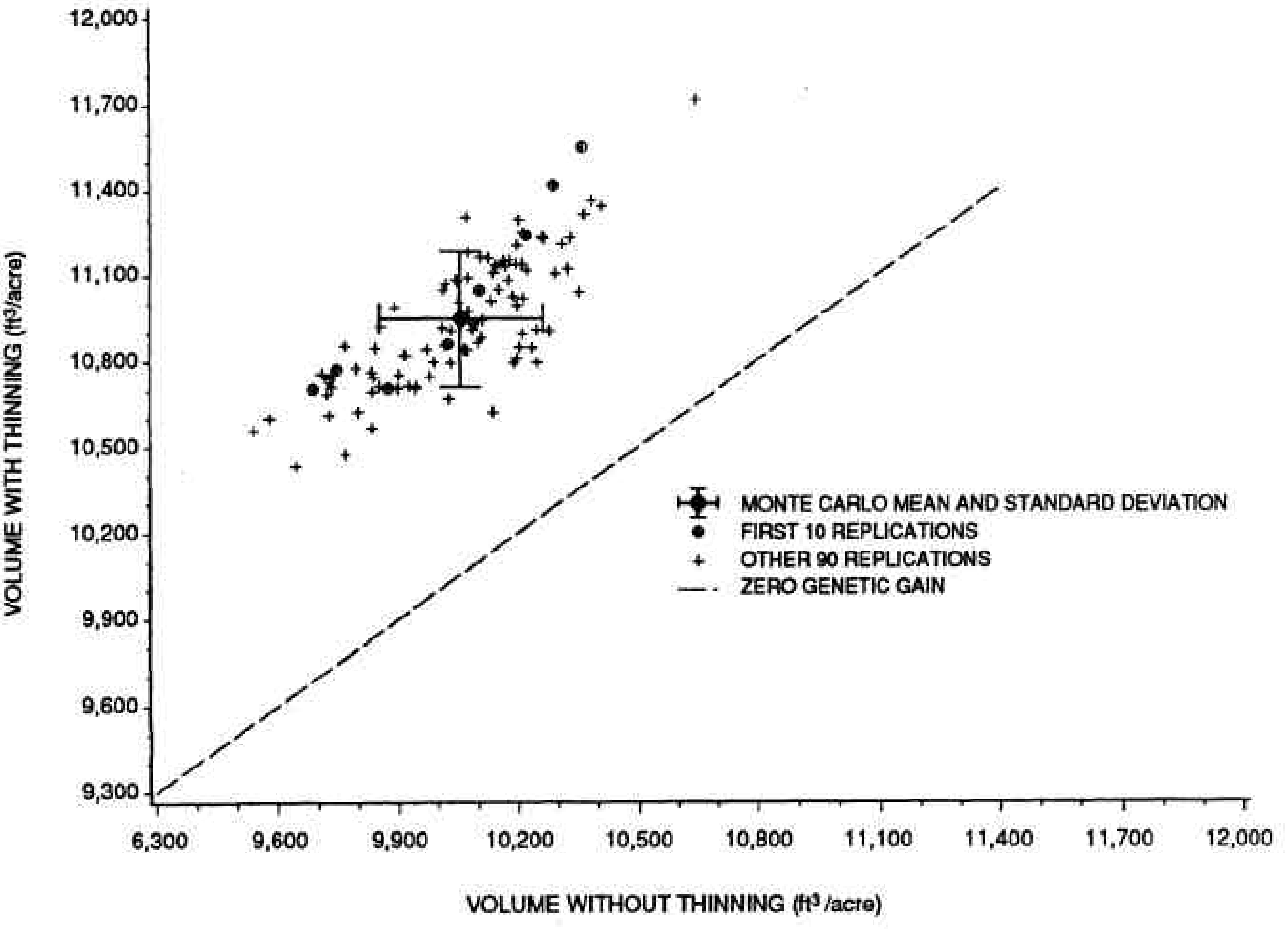

Figure 5—Distribution of individual estimates if volume at age 100 included in the Monte Carlo estimate of gain from thinning when the majority of the trees in the sample stand are greater than 3 inches d.b.h. at the time of thinning.

the 3-inch boundary in the next projection cycle regardless of whether the stand was thinned or not. Thus, this result was not unexpected. The variation in the estimate of gain due to thinning in these stands is essentially equal to the variation in the estimate of genetic gain when the projection was begun with a stand containing primarily trees greater than 3 inches. However, the variation is approximately half as great as the variation in the estimate of genetic gain when the stand with most trees less than 3 inches d.b.h. is used as input to the program. This result reinforces the suggestion that most of the impact of stochastic variation occurs due to differences in the timing of trees growing over the 3-inch d.b.h. boundary.

The Stand Prognosis Model is frequently used to simulate stand development under alternative management strategies. The analyses presented in this note have demonstrated that the stochastic components built into the Stand Prognosis Model can have an important impact on comparisons based on such simulations. These results were obtained using the Inland Empire variant of the Stand Prognosis Model. The impact when using other variants may be less because of differences in the way stochastic components are designed. Most other variants do not have a stochastic component in the crown ratio model and have a narrower diameter range within which large tree and small tree height increments are averaged. Although these differences may reduce the impact of stochastic variation on comparisons of treatment alternatives, they do not eliminate the impact. Thus, the problems discussed in this note should be of concern to users of all variants of the Stand Prognosis Model.

A review of the range of estimates resulting from the 100 replications made for each analysis emphasizes the potential problems that can arise when comparisons are made based on a single run of the model for each treatment alternative. Estimates of genetic gain based on projections begun at age 14 ranged from -2.124 to 14.667 (0.743 to 18.149 with version 5.2). Estimates of total cubic volume at age100 with no multipliers ranged from 9,543 to 10,650 ft^3. Estimates of total cubic volume at age100 when multipliers simulating genetic gain were included ranged from 10,046 to 11,408 ft^3. Although the range of estimates of total volume with and without the multipliers is similar, the correlation between the pairs of estimates resulting from the same random seed is only 0.296. Because it is assumed that the increased individual tree growth rates of genetically improved stock are in effect from the time of establishment, the set of individual tree records used to start the simulation of stand development for genetically improved stock is different from the set of tree records used to start the simulation for “average” stock. These differences accentuate the differences in the way the same sequence of random numbers is used by the Stand Prognosis Model, leading to this low correlation.

When the projections for estimating genetic gain were begun at age 20, the range in estimates of total volume at age 100 with no multipliers was 9,362 to 9,961 ft^3. Estimates of total volume at age 100 with multipliers ranged from 10,069 to 10,693 ft^3. This reduction in the range of estimates results primarily from removing timing of growth past the 3-inch d.b.h. boundary as a source of variation. Although the correlation between pairs of estimates resulting from the same random seed has increased to 0.358, the range of estimates of genetic gain is still substantial (4.362 to 12.215). Increasing the number of tree records from 50 to 150 but reverting to age 14 as a starting point for the projections leads to similar results. The range in estimates of genetic gain is from 2.389 to 12.280. In this case the variation due to differences in timing of growth past the 3-inch boundary is reduced by the increase in the number of tree records.

The impact of thinning on the way the stochastic components affect simulated stand development is somewhat different from that discussed in the two preceding paragraphs. Even when the stand is thinned at age 14, the immediate impact on d.b.h. growth rates has little influence on the rate at which trees grow past the 3-inch d.b.h. boundary (almost all trees grow past this boundary in the first projection cycle regardless of the thinning strategy applied). The range of estimates of total volume removed through age 100 was 9,543 to 10,650 ft^3 for the unthinned stand and 9,781 to 11,005 ft^3 for the thinned stand. The correlation between pairs of estimates resulting from the same random seed increased to 0.637. However, the range in estimates of gain due to thinning ranged from -0.917 to 9.252. Much of the increase in correlation is likely due to differences in the starting values used for the simulations. In this example, the same set of tree records is used as input to the Stand Prognosis Model for each alternative (thin vs. no thin). In the example dealing with estimating genetic gain, different growth rates were assumed from the time of stand establishment. Thus, for estimating genetic gain, the set of tree records used to start the two projections at age 14 included the effect of differing growth experienced by the stand up to that time. Delaying the thinning until age 40 had almost no impact on the range of estimates of total volume removed up to age 100. The correlation between pairs of estimates was increased to 0.798, and the range in estimates of gain due to thinning was reduced to 4.784 to 12.251.

RECOMMENDATIONS

If interest is centered on estimating gain attributable to a management alternative and there is not a need for high precision in the estimate of gain, the simple alternative of suppressing the stochastic components of the Stand Prognosis Model may provide an acceptable, but biased, approximation. However, if estimates of volume under each alternative are important, this solution will result in unacceptably low estimates for each alternative. In general, I do not recommend this alternative.

The results of the Monte Carlo analysis of the second alternative suggest that at least 10 replications (using a new random seed for each replication) are justified in many research applications. If high precision is required, 40 or 50 replications may be appropriate because the estimates of variance do not appear to stabilize until this many replications are included.

The analysis of the third alternative suggests that when the number of tree records in the sample stand is increased from 50 to 150, fewer replications are needed to attain the same level of precision. Thus, less than 10 replications are probably adequate for comparing alternative management strategies if the number of tree records can be increased to this level. For those situations requiring higher precision, 20, or at most 40, replications should suffice. When the sample stand consists only of trees greater than 3 inches d.b.h. or when the objective is to compare alternative management strategies that only affect stand development after a treatment (such as the thinning example discussed in this paper), a similar recommendation appears to be justified.

My overall recommendation to users of the Stand Prognosis Model is that in almost all applications of the model, it would be wise to make at least two or three projections (using different random seeds for the random number generator for each projection) rather than to rely on the results of a single simulation. For those cases where alternative management strategies that may affect the timing of the growth of individual trees past the 3- or 10-inch d.b.h. boundaries are to be compared and extremely high levels of precision are needed, 50 or more replications may be called for. The decision must be made by evaluating the tradeoff between the cost of making additional replications and the need for a higher level of precision in the values to be com pared. An additional factor that should be considered in making this decision is the level of precision that can be attached to projections of anything 100 years into the future. Regardless of the situation, users of the Stand Prognosis Model need to be aware of the magnitude of variation that may exist and make an informed decision based on the uses they intend to make of the model output.

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INTERMOUNTAIN RESEARCH STATION

The Intermountain Research Station provides scientific knowledge and technology to improve management, protection, and use of the forests and rangelands of the Intermountain West. Research is designed to meet the needs of National Forest managers, Federal and State agencies, industry, academic institutions, public and private organizations, and individuals. Results of research are made available through publications, symposia, workshops, training sessions, and personal contacts.

The Intermountain Research Station territory includes Montana, Idaho, Utah, Nevada, and western Wyoming. Eighty-five percent of the lands in the Station area, about 231 million acres, are classified as forest or rangeland. They include grasslands, deserts, shrublands, alpine areas, and forests. They provide fiber for forest industries, minerals and fossil fuels for energy and industrial development, water for domestic and industrial consumption, forage for livestock and wildlife, and recreation opportunities for millions of visitors.

Several Station units conduct research in additional western States, or have missions that are national or international in scope.

Station laboratories are located in:

Boise, Idaho

Bozeman, Montana (in cooperation with Montana State University)

Logan, Utah (in cooperation with Utah State University)

Missoula, Montana (in cooperation with the University of Montana)

Moscow, Idaho (in cooperation with the University of Idaho)

Ogden, Utah

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