FRI Project Record

No. 5534

MODELLING INDIVIDUAL TREE SURVIVAL OF RADIATA PINE IN NEW ZEALAND PROGRESS TO JULY 1996

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EXECUTIVE SUMMARY

Data from the PSP system (Nelder trials and unthinned Central North Island data) were used to develop a model for individual tree survival. A logistic model using the natural logarithm of stocking, the natural logarithm of stand mean diameter and tree diameter in relation to stand mean diameter was produced. The model provided logical predictions and the residuals were small. The model was also tested on a validation data set with good results. Tests of the models performance when applied to thinned data and through time in conjunction with a growth model remains to be done.

TABLE OF CONTENTS

1. INTRODUCTION

This report describes the development of a model to predict individual tree survival. The final objective of the work is to produce a model for trees past all silvicultural treatments ie from mid rotation and onwards. The model will be part of a set of functions comprising a distance-independent, individual tree growth model.

1.1 Background

The probability of survival is (1-probability of mortality). As most models developed have used the concept of mortality rather than survival the term mortality is used here when reviewing the literature.

The probability of mortality for individual trees can either be estimated directly, or a two-step process that first determines stand level mortality and then allocates that total mortality to individual trees, can be used. The former approach has been used here because it makes it possible to utilise tree level information and to use the model on its own without information about stand level mortality. Also stand level mortality models are already available and duplication of that work did not seem meaningful.

For distance-independent individual tree mortality models, the most common approach has been a logistic model (Avila and Burkhart, 1992, Buchman et al 1983, Hamilton 1986). Lowell and Mitchell (1987) used success criteria to develop a probabilistic, logistic model for simultaneous estimation of diameter increment and mortality. Hann and Wang (1990) combined their logistic mortality model with a maximum stand density line to adjust mortality. Guan and Gertner (1991) suggested that a parallel distributed processing system (neural network) would provide advantages over, for instance, the logistic model when modelling mortality. They also found that the distribution generated by the parallel distributed processing system approached the logistic model.

Various variables have been included in the different models. They can be divided into four groups depending on the property they describe (Hamilton, 1986):

- Tree size
- Stand density
- A trees competitive position within the stand
- Growth rate (or vigour)

Measures of tree competition that have been used are the relation between stand dbh and tree dbh (e g by Manley,1981), height/mean height of dominant and co dominant trees (Avila and Burkhart, 1992), and sum of the basal area of the trees larger than the subject tree (Hann and Wang 1990). Other variables have been: Crown ratio, stocking, basal area, site index, age, crown closure factor at the top of the tree, and various other crown competition factors.

A problem that frequently occurs when analysing mortality data is different time periods between measurements. The actual probability of death divided by length of the growing period was used by Amateis and Burkhardt (1989). Monserud (1976) used the length of the growing period in the exponent. Manley (1981) gave all the live trees a sampling factor based on the total number of live trees on the plots multiplied by the length of their growing periods, i e the total number of live tree years divided by the total number of live trees sampled. Dead trees were given the weight one as they can only die once.

It was decided to model survival rather than mortality as survival is not an absorbing state and annual probabilities can be multiplied to obtain the probability over a number of years (Vanclay, 1994). Thus the formulation $P_{survival} = \left(\frac{1}{1+e^{f()}} \right)^i$ was used, where i is the time between measurements to accommodate for different re-measurement intervals. This assumes that the probability of survival is constant with time which is not true but as measurements with intervals longer than four years was excluded from the data this assumption was regarded as acceptable.

Many models (e g Buchman et al 1983 and Hamilton 1986) have been based on observed or predicted diameter growth. These models have to be used in conjunction with a diameter growth model or the actual diameter increments must be known. Buchman et al (1983) used dbh and diameter growth rate non linearly in their logistic function. Manley (1981) found observed diameter increment to be a good indicator of imminent death but also highlighted the fact that a tree with no diameter increment may be regarded as dead already. It was decided not to use diameter increments in this model, because when used for prediction there is no advantage to using variables indirectly via the diameter increment prediction.

2. DATA

Data for the study was retrieved from the Permanent Sample Plot data base. As the information had not been collected expressly for the purpose of studying mortality, variables like crown ratios and descriptions of a trees vigour were not available. For the initial model development only unthinned material was used. Two data sets were extracted; one with all the data from the nelder trials and one with all unthinned data available for the central North Island except the nelders. The two data sets contained the same variables. Different combinations and transcriptions of the basic tree and stand variables were computed. Table 1 shows the variables included. Trees that were only measured once were deleted from the data, as were observations where the time between measurements exceeded 4 years.

Table 1. Variables.

Notation	Description
Dbh	Diameter breast height (cm)
Height	Height (m)
Ba	Basal area of the tree (m^2)
Sph	Stems per hectare
Bapl	Basal area of plot (m^2/ha)
Mth	Mean top height (m)
Mtd	Mean top diameter(cm)
Mndbh	Mean diameter of plot (cm)
Si	Site index
Age	Age of the stand in years
Reldbh	The ratio of tree dbh and mean plot dbh $\frac{Dbh}{Mndbh}$
Relsp	Relative spacing $\frac{1000}{Mth\sqrt{Sph}}$
Hdbh	$\frac{Height}{Dbh}$
Bal	Accumulated basal area of all trees with larger dbh than the subject tree expressed per hectare
*Gs1**	$\frac{10000}{Sph}\frac{Dbh}{MnDbh}$
*Gs2**	$\frac{10000}{Sph}\frac{Dbh^2}{MnDbh^2}$
*Gs3**	$\frac{10000}{Sph}\frac{Dbh^3}{MnDbh^3}$
Sdbh	$\sqrt{Dbh}$
Idbh	$\frac{1}{Dbh}$
Logdbh	Natural logarithm of *Dbh*
Logsph	Natural logarithm of *Sph*
Lmndbh	Natural logarithm of *Mndbh*
Logbal	Natural logarithm of *Bal*
i	Time to the next measurement in years and fractions of years
Status	Status at the next measurement 1 if the tree is alive and 0 if it is dead. A tree is deemed dead if it does not have any green needles.

* Growing space indices developed and used by Grace (1996, unpublished) for modelling branch growth.

2.1 The Nelder Data

A nelder experiment consists of a set of concentric circles with the same number of trees planted in each circle so that stockings decrease with distance from the centre. No thinnings were supposed to have occurred in the nelder trials on the PSP-system. The nelder data set covered a range of ages from 0 to 27 years. As mortality at very low ages is more likely to be caused by factors other than competition everything younger than 3 years was excluded from the data. Observations where *height* or *dbh* was missing were also excluded. Appendix A lists the plots in the final data set. The ranges of some variables in the nelder data set are in Table 2.

Table 2. Tree Variable Ranges - Nelder data set

Variable	N	Min	Mean	Max	Std Dev.
Dbh (cm)	7411	0.5	7.9	64.4	6.0
Height (m)	7411	1.4	5.7	42.8	4.8
Sph	7411	280	3440	26154	4737
Age	7411	3.0	5.4	27.0	3.0

Of the total number of observations, 56 were recorded as dead.

2.2 Central North Island Data

Everything meeting the following criteria was retrieved from the permanent sample plot data base:

- Planted after 1960
- Older than 4 years
- Unthinned
- From the central North Island growth modelling region
- Not a nelder experiment

Trees without a measured height were kept in the data set even if that meant that *height* or *height/dbh*-ratio could not be used as a predicting variable. Only a third of the trees were measured for heights and the height-measured part of the data set had a higher survival than the part of the data set missing heights. The height trees are supposed to be sampled across the diameter range but heights are not measured on non-healthy looking trees. Appendix B lists all the plots in the data set.

The data set was split randomly into two parts; approximately one third (6543) of the observations were used in the data analyses and the remaining two thirds were used as a validation sample. Table 3 shows the ranges of some tree variables.

Table 3. Tree Variable Ranges for the Central North Island Data

Variable	N	Min	Mean	Max	Std Dev.
Dbh **(cm)**	6543	0.5	19.1	68.7	9.3
Height **(m)**	1881	1.1	14.5	46.9	8.9
Sph	6543	124	1497	3200	954
Age	6543	4.3	12.5	30.0	5.4

A total of 171 observations were recorded as dead.

3. ANALYSIS

3.1 Analysis of the Nelder Data

The first part of the analysis was done with the nelder data to utilise the extreme stockings. The plan was to produce a model including the stocking effect and later see if that model could be applied to the central North Island data set.

The survival pattern of the nelder data over some different variables are plotted in figures C1 - C5 (Appendix C).

The chosen logistic model $P_{survival} = \left(\frac{1}{1+e^{f()}}\right)^{i}$ was rearranged to a linear form:

$f() = \ln(Status^{\frac{-1}{i}} - 1)$

This linearisation was done to enable the calculations of correlations and the use of the selection option in proc reg (SAS) to screen variables. Surviving trees were given the status 0.99 and dead trees were given the status 0.01 to make the calculation of *f* possible. The selection option in proc reg (SAS) was used as a help to pick out useful variable combinations to predict *f*.

As an alternative approach to the selective regression, models were fitted including variables one by one according to "correlation ranking" until non significant parameters were obtained. The correlations between *f* and all variables included in the data set were calculated. Table 4 lists the variables with the highest correlation with *f*.

Table 4. Correlations with *f* - Nelder Data.

	Variable	Correlation	p
Individual Tree Level			
	Bal	0.15	0.0001
	Hdbh	0.11	0.0001
	Reldbh	-0.09	0.0001
Plot Level			
	Age	0.08	0.0001
	Bapl	0.07	0.0001
	Vol	0.06	0.0001
	Mtd	0.06	0.0001
	MnHt	0.05	0.0001

After the initial variable screening the original logistic model formulation and the original survival values (0 and 1) were used in proc nlin (SAS) to fit the models to be tested. Twenty models with significant coefficients and low mean residual square were tested. Models that were apparently illogical ie where survival increased with smaller growing space or greater basal area of larger trees, were abandoned. Table 5 lists the models regarded as being the most interesting. The residual mean squares were compared and the predictions were plotted over *dbh* and other variables to ensure realistic behaviour. The mean residuals per variable class were calculated and plotted against the various class variables.

Table 5. Models from the Nelder Data.

Model	Variables in Model	Mean Residual Square
1	Intercept, *Logsph, Lmndbh, Reldbh*	0.00661
2	Intercept, *Bapl, Reldbh,*	0.00686
3	Intercept, *Dbh, Mtd, Gs3*	0.00683

The residuals from models 1 and 2 showed a slight correlation with age and age was incorporated into the models but with little improvement. Incidentally model 2 is the same formulation that was favoured by Manley (1981).

3.2 Analysis of the Central North Island Data

The central North Island data were analysed in the same way as the nelders. Figures C6 - C11 (Appendix C) show the proportion of survivals per class of *Dbh, Sph, Bal, Reldbh, Age* and *Si* for the central North Island data.

Table 6 shows the variables with the highest correlations with *f* for the central North Island data set.

Table 6. Correlations with *f* - Central North Island Data Set.

	Variable	Correlation	p
Individual Tree Level			
	Reldbh	-0.22	0.0001
	Bal	0.21	0.0001
	Dbh	-0.17	0.0001
Plot Level			
	LogSph	0.11	0.0001
	Sph	0.11	0.0001
	Si	-0.09	0.0001
	MnDbh	-0.07	0.0001
	Relsp	-0.07	0.0001

The three most promising models from the analysis of the nelder data (Table 5) were applied to the central North Island sample. It was clear from the error patterns that the coefficients were unsuitable and that the models had to be refitted to be of any use. The models were fitted to the new data set. Model 1 and 2 were fitted successfully but model 3 did not seem to be appropriate for the data.

Two additional models were obtained by analysing the central North Island data. All models that were regarded as interesting are listed in Table 7.

Table 7. Models for the Central North Island Data set

Model*	Variables in Model	Mean Residual Square
1	Intercept, *Logsph, Lmndbh, Reldbh*	0.0219
2	Intercept, *Bapl, Reldbh*	0.0271
4	Intercept, *Mtd, Gs2*	0.0224
5	Intercept, *Bal, Logsph, Reldbh*	0.0220

***Models with the same variables have the same number in both data sets.**

The residuals were analysed and model 1 appeared to be the most suitable model also for this data set. The residuals over predicted values, *Dbh, Sph, Mndbh* and *Reldbh* are shown in Figures C12 - C16 in Appendix C. The residuals were also analysed with age and si without any trends. Predictions from model 1 were plotted against extremes of all variables included in the model to ensure its logical behaviour. Figure 1 shows the predicted probabilities of survival over *Dbh* for three different levels of *Sph.* Figures C17 - C18 in Appendix C show the predictions over *Sph* and *Mndbh.* The figures in Appendix D show the predicted probabilities of survival over *Reldbh* for a range of *Mndbh* and *Sph.*

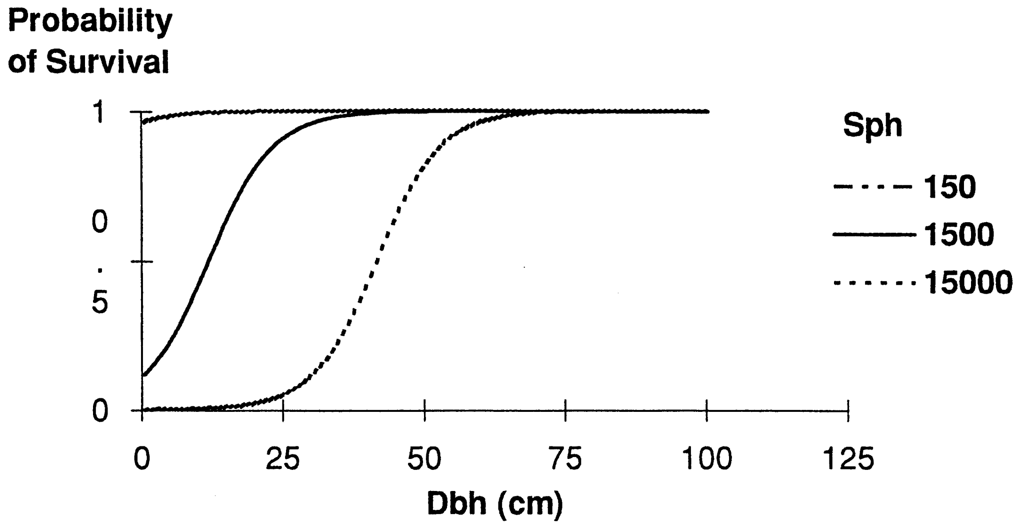

Figure 1. Predicted Probability of Survival over *Dbh* (*Mndbh* is set to 30 cm).

Modell and its coefficients when fitted to the central North Island data set are:

$$P_{survival} = \left(\frac{1}{1+e^{a0+a1\cdot Logsph+a2\cdot Lmndbh+a3\cdot Reldbh}} \right)^{i}$$

Where	a0=-25.275928	(s.e. 2.282234)
	a1=2.287932	(s.e. 0.196982)
	a2=3.127215	(s.e. 0.301646)
	a3=-5.293191	(s.e. 0.252741)

3.3 Incorporating Background Mortality

The work here has attempted to model non-catastrophic mortality due to competition. There is however a second type of mortality that is non-catastrophic; the random occasional death of trees because of factors like armillaria, thinning damage etcetera. This type of mortality can be regarded as a background mortality that will always occur regardless of stand density and tree size. A possibility to consider that mortality in a model would be to add a parameter *a* to the logistic function: $P_{survival} = \left(\frac{a}{1+e^{f()}} \right)^{i}$ rather than setting *a* to 1 as previously done. The function would hence be constrained between 0 and *a* rather than between 0 and 1. The practical implications of this would be that predicted probability of survival for any tree would always be less than 1. An attempt was made to fit model 1 with the addition of *a*. Despite a starting value of a of 0.9 the value of *a* was estimated to 1.001. This implies that the maximum value of predicted survival would be more than 1. However a being so close to one indicates that it is not possible to model background mortality with this data set. An attempt to add another parameter c to the model:

$$P_{survival} = \left(c + \frac{a}{1+e^{f()}} \right)^{i}$$ so that the model would be constrained between c and $a+c$ also failed.

3.3 Validation

The model was applied to the central North Island test data and the error patterns over some variables and over the predictions can be seen in Figures C19 - C20 (Appendix C). Figure 2 shows the predicted proportion of survivals by dbh-class compared to the actual proportion of survivals.

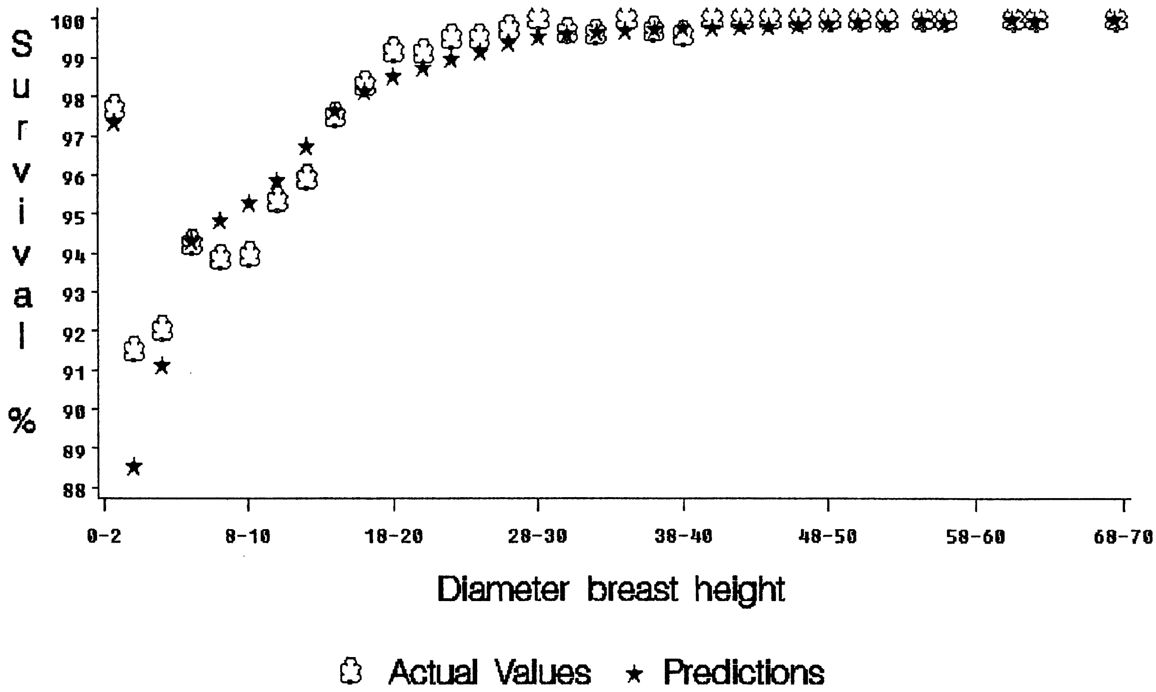

Figure 2. Comparison Between Predicted and Actual Percentages of Survivals when Model 1 was applied to the Central North Island Test Data (by Class of *Dbh*).

4. DISCUSSION

The model derived her does not display any major flaws. It is encouraging that the general form of the model is suitable for both data sets. Predicted values are logical over extreme ranges of predicting variables as shown in Figure 1 and in Figures C17 and C18 (Appendix C). The mean errors are small when the model is applied to the test sample (Figures C19 and C20, Appendix C). However the model derived here should be seen as a step on the way to produce a model for trees from midrotation and onwards rather than a finished product. As only unthinned material was used when deriving and testing the model the next step should be to test whether this formulation is applicable also to thinned stands. Testing the model through time in conjunction with a growth model also remains to be done.

Another area of future exploration is testing the model and perhaps refitting or reformulating it for other growth modelling regions.

5. REFERENCES

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APPENDIX A. PLOTS USED IN THE NELDER DATA SET

RO 1858 0 3 1
RO 1858 0 3 10
RO 1858 0 3 11
RO 1858 0 3 12
RO 1858 0 3 13
RO 1858 0 3 14
RO 1858 0 3 15
RO 1858 0 3 16
RO 1858 0 3 17
RO 1858 0 3 18
RO 1858 0 3 19
RO 1858 0 3 2
RO 1858 0 3 20
RO 1858 0 3 3
RO 1858 0 3 4
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RO 1858 0 3 6
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RO 1858 0 3 9
RO 2046 0 1 1
RO 2046 0 1 10
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WN 366 0 1 3
WN 366 0 1 4
WN 366 0 1 5
WN 366 0 1 6
WN 366 0 1 7
WN 366 0 1 8
WN 366 0 1 9

APPENDIX B. PLOTS USED IN THE CENTRAL NORTH ISLAND DATA SET

RO 1083 1 1 0
RO 1083 1 5 0
RO 1083 1 6 0
RO 1083 1 7 0
RO 1083 2 11 0
RO 1083 2 12 0
RO 1083 2 19 0
RO 1083 2 6 0
RO 1085 2 1 0
RO 1085 2 2 0
RO 1085 2 3 0
RO 1814 0 14 0
RO 1814 0 17 0
RO 1814 0 23 0
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RO 1850 33 38 0
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RO 2098 0 18 34
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RO 2103 2 5 21
RO 2103 2 6 41
RO 2103 2 7 31
RO 2103 2 8 51
RO 2103 2 9 41
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RO 789 0 2 0
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APPENDIX C. FIGURES.

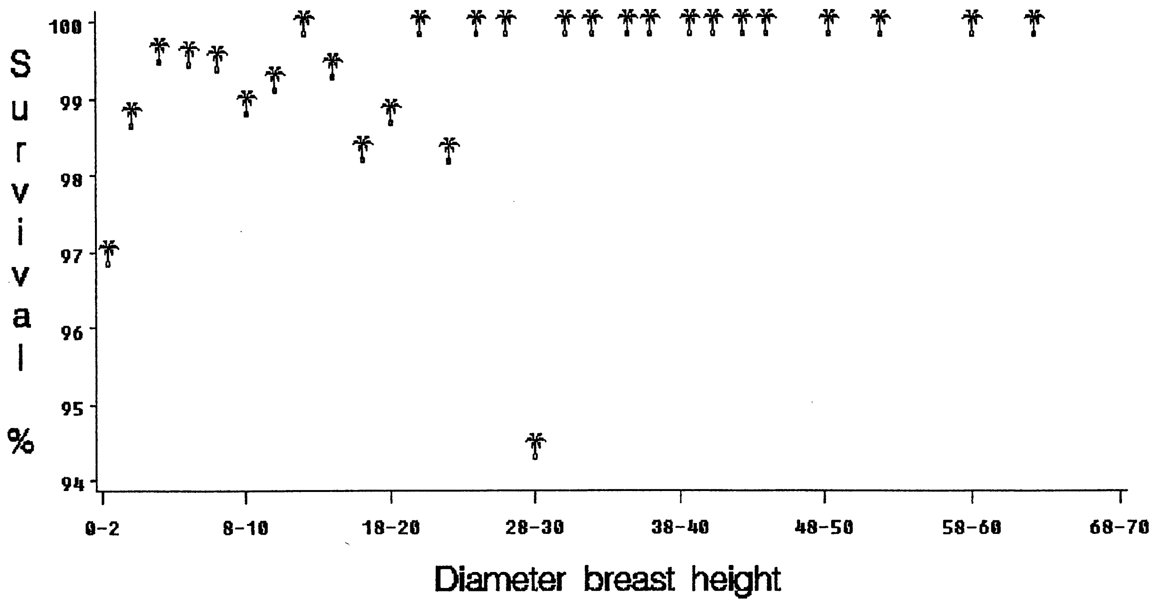


Figure C1 . Percentage of Survivals by Class of *Dbh* - Nelder Data.

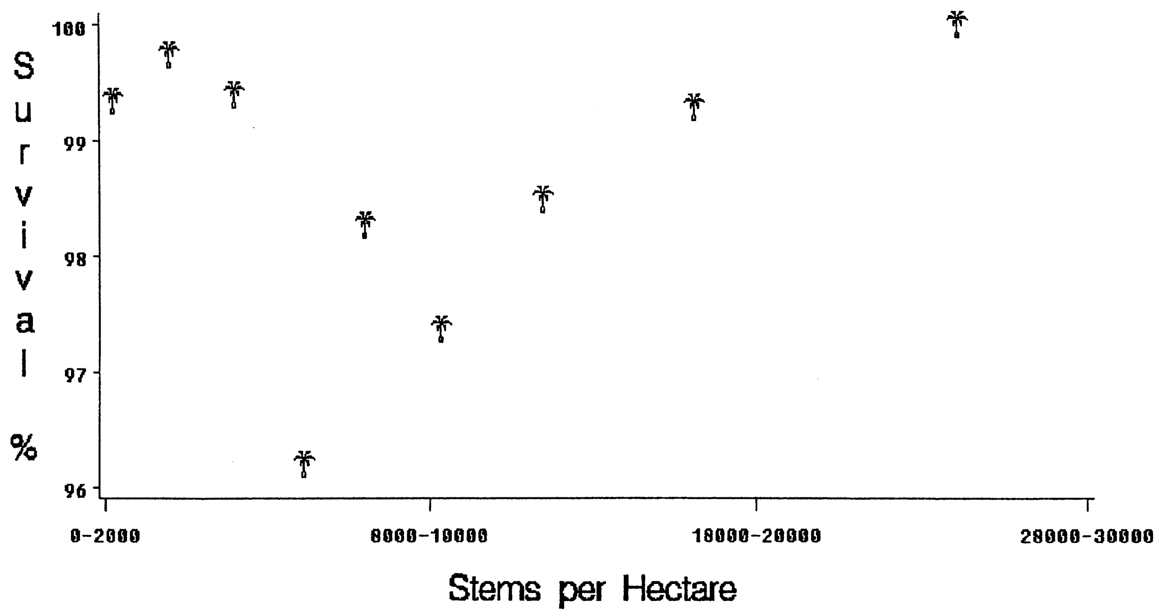


Figure C2 . Percentage of Survivals by Class of *Sph* - Nelder Data.

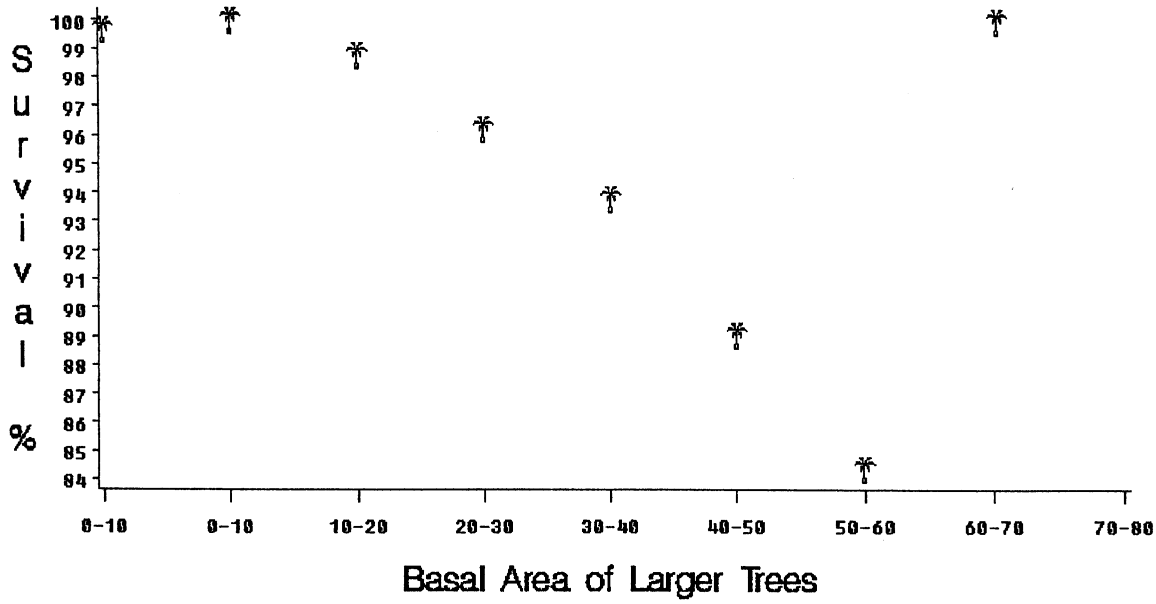


Figure C3. Percentage of Survivals by Class of *Bal* - Nelder Data.

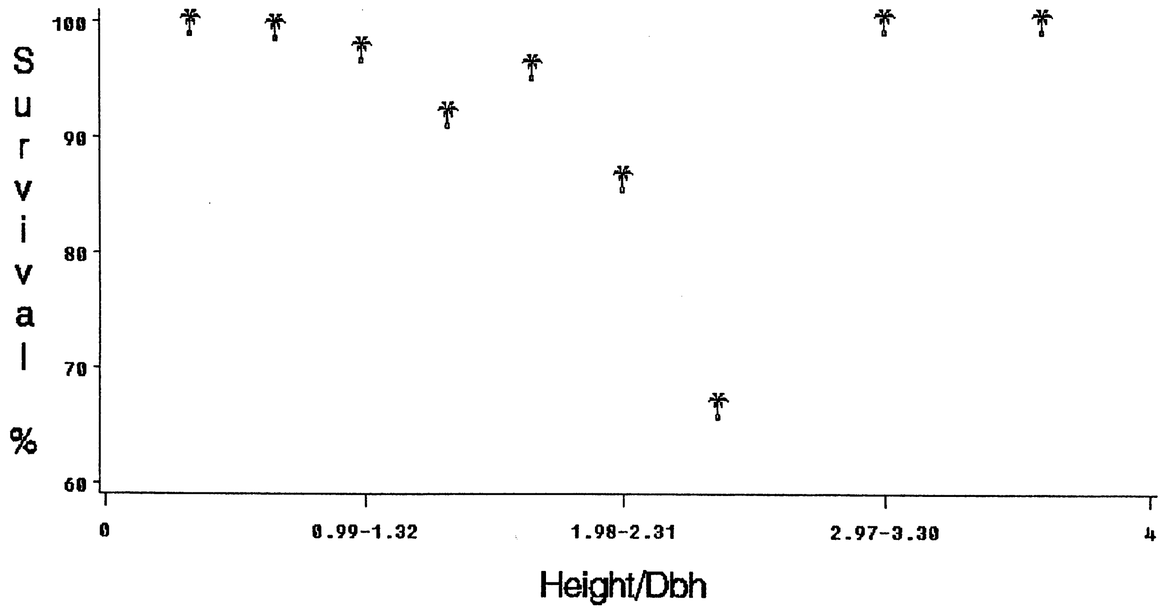


Figure C4 . Percentage of Survivals by Class of *Hdbh* - Nelder Data.

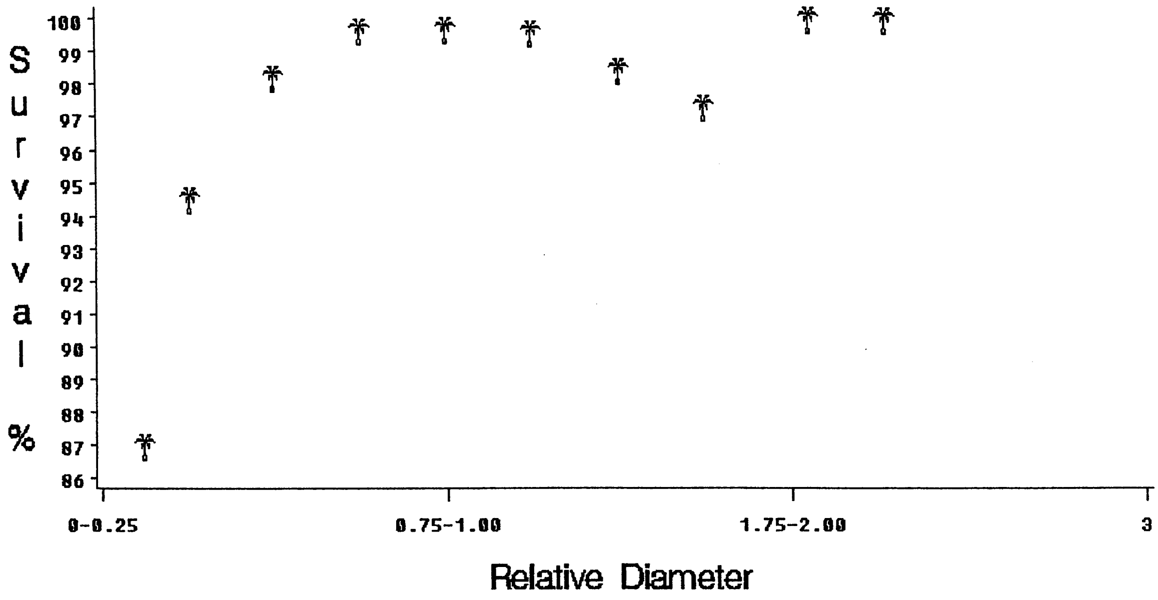


Figure C5 .Percentage of Survivals by Class of *Reldbh* - Nelder Data.

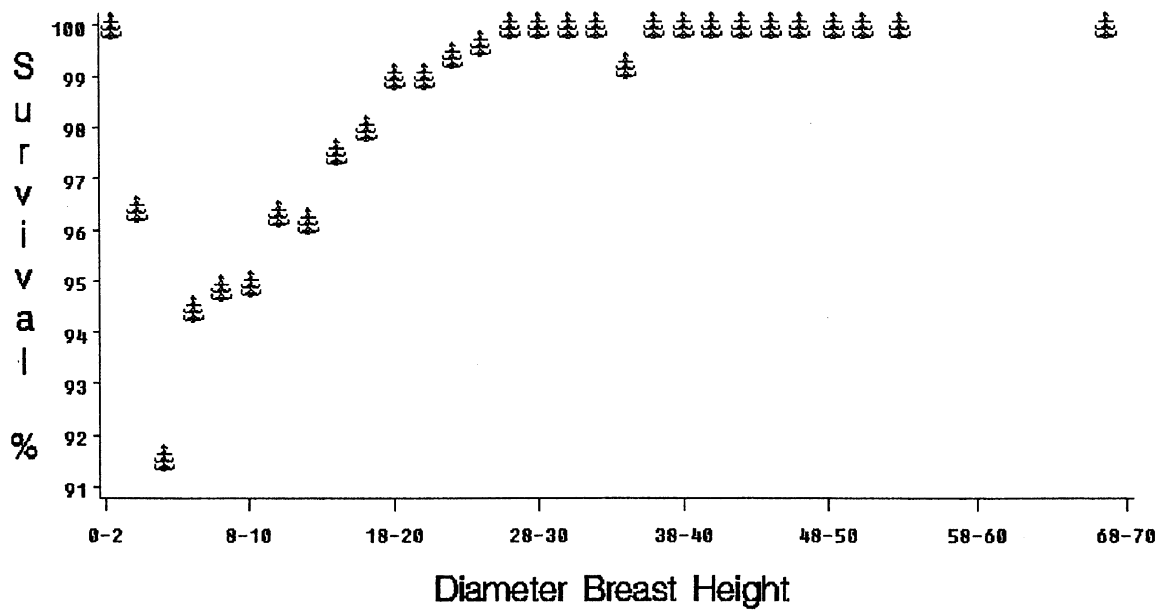


Figure C6. Percentage of Survivals by Class of *Dbh* - Central North Island Data.

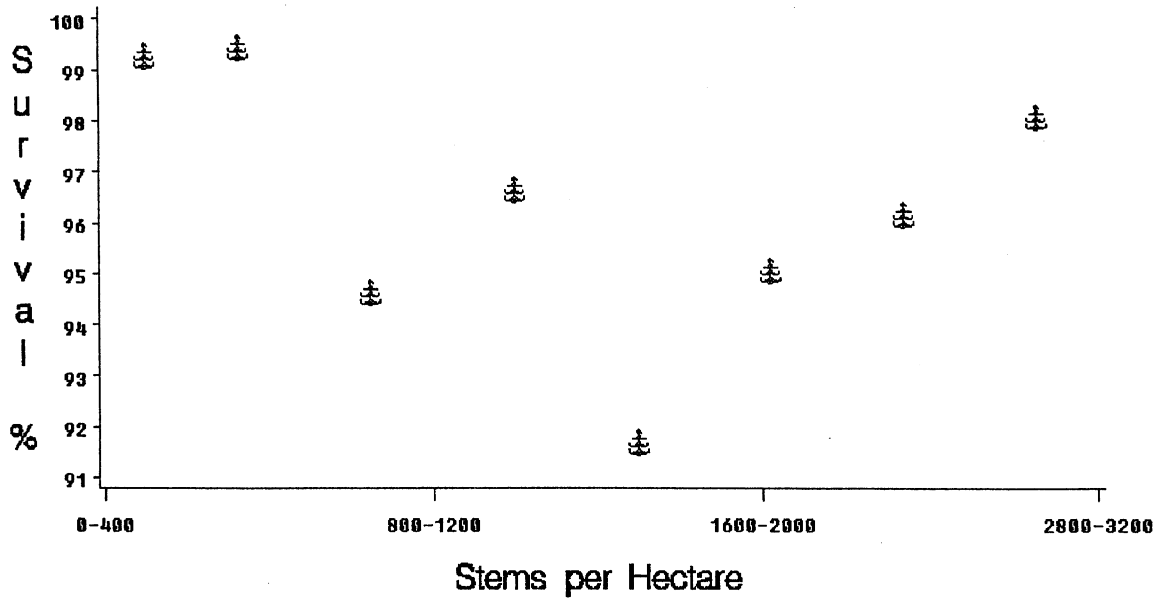


Figure C7. Percentage of Survivals by Class of *Sph* - Central North Island Data

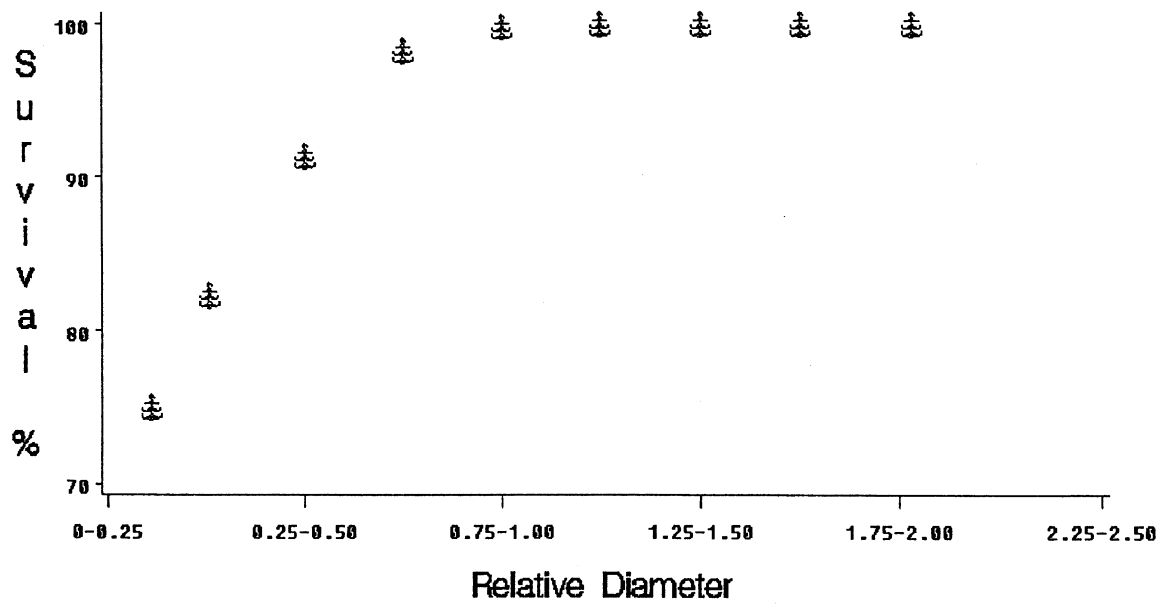


Figure C8. Percentage of Survivals by Class of *Reldbh* - Central North Island Data.

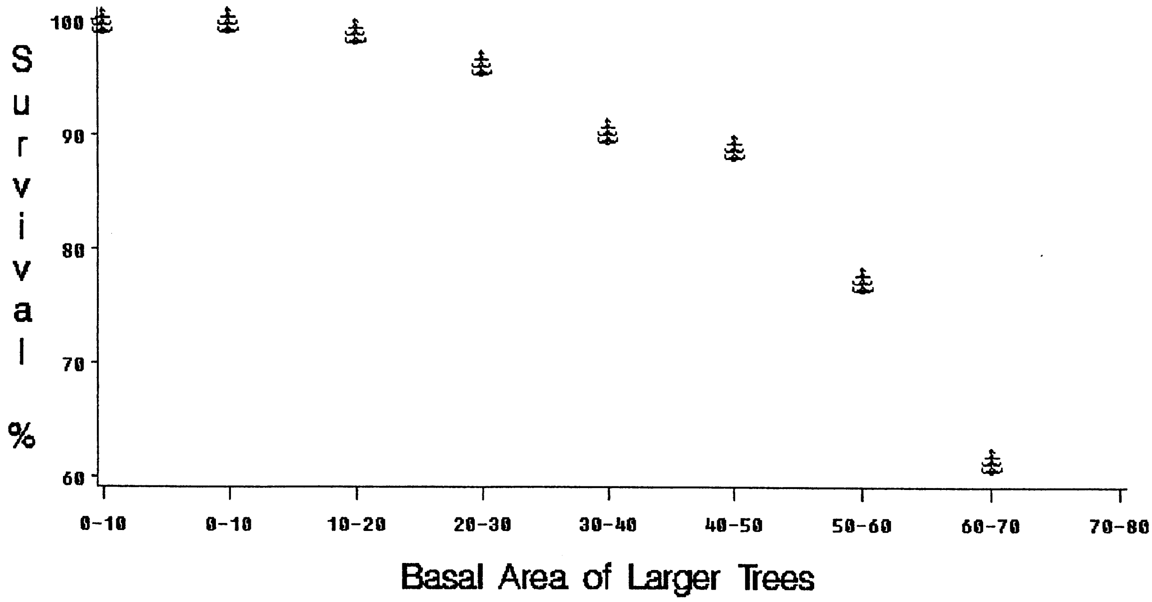


Figure C9. Percentage of Survivals by Class of *Bal* - Central North Island Data.

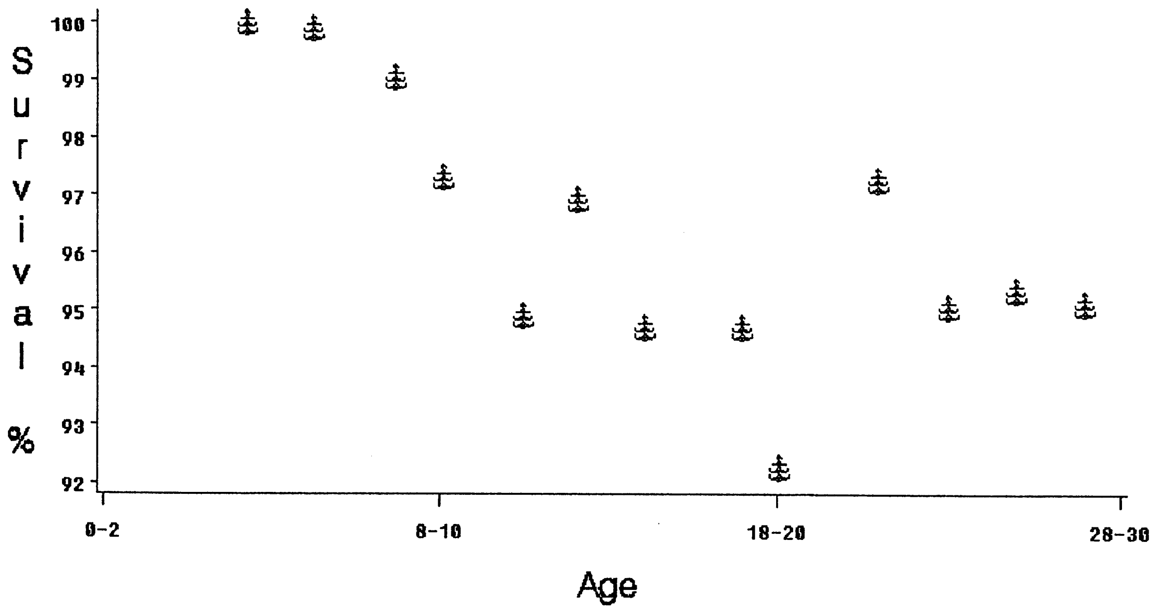


Figure C10. Percentage of Survivals by Class of *Age* - Central North Island Data.

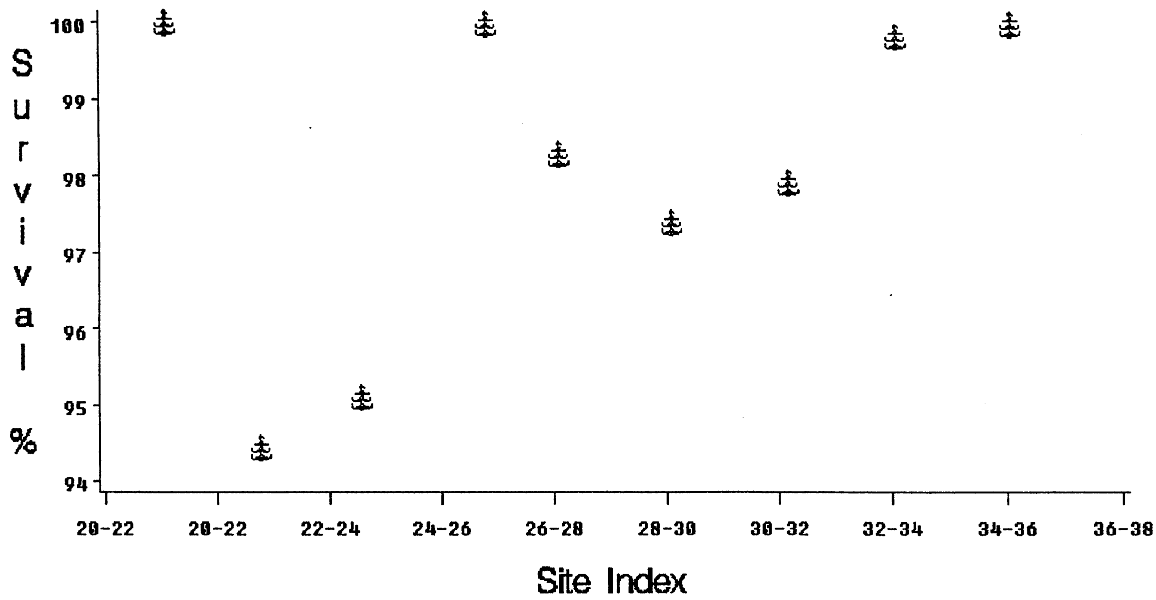


Figure 11. Percentage of Survivals by Class of *Si* - Central North Island Data.

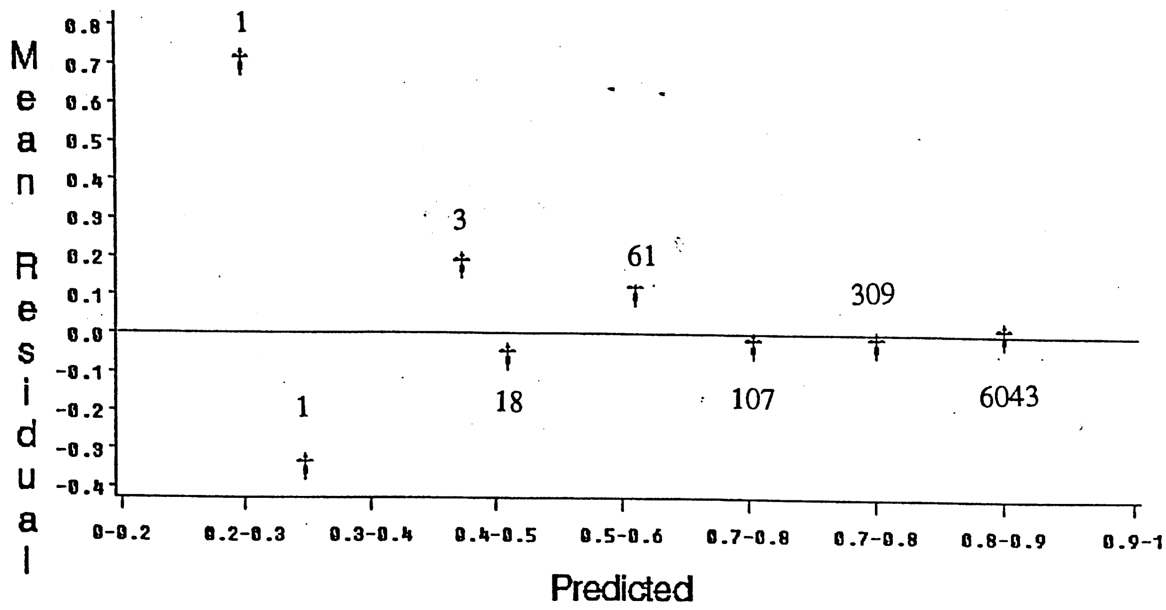


Figure C12. Mean Residuals from Model 1 by Class of Predictions - Central North Island Data. The Numbers of Observations are Shown.

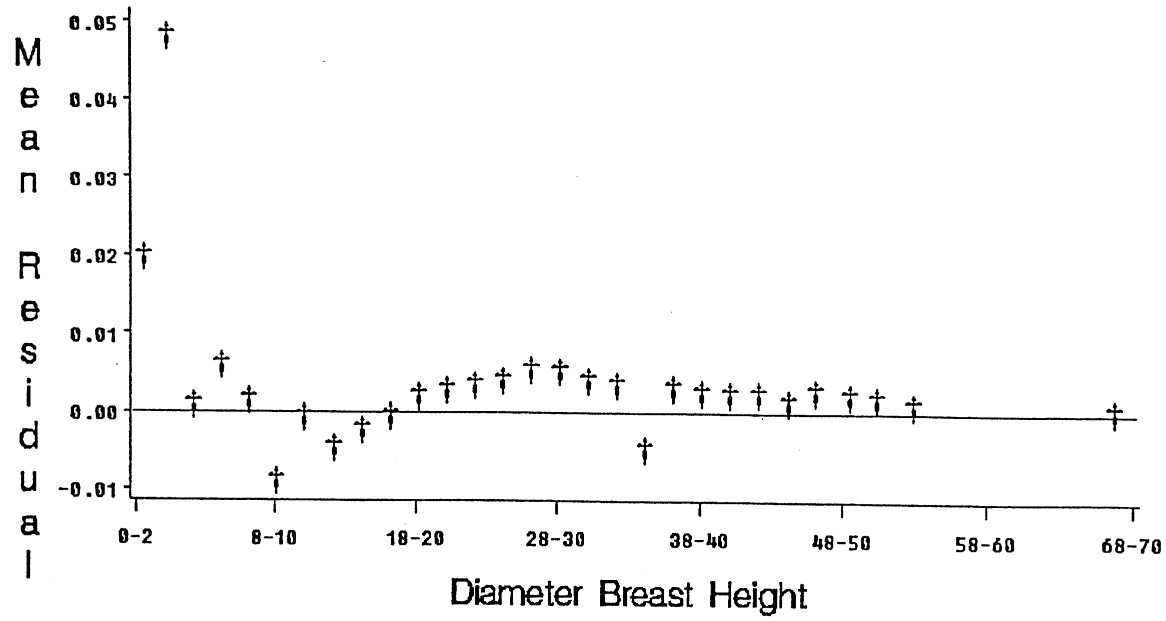


Figure C13. Mean Residuals from Model 1 by Class of *Dbh* - Central North Island Data.

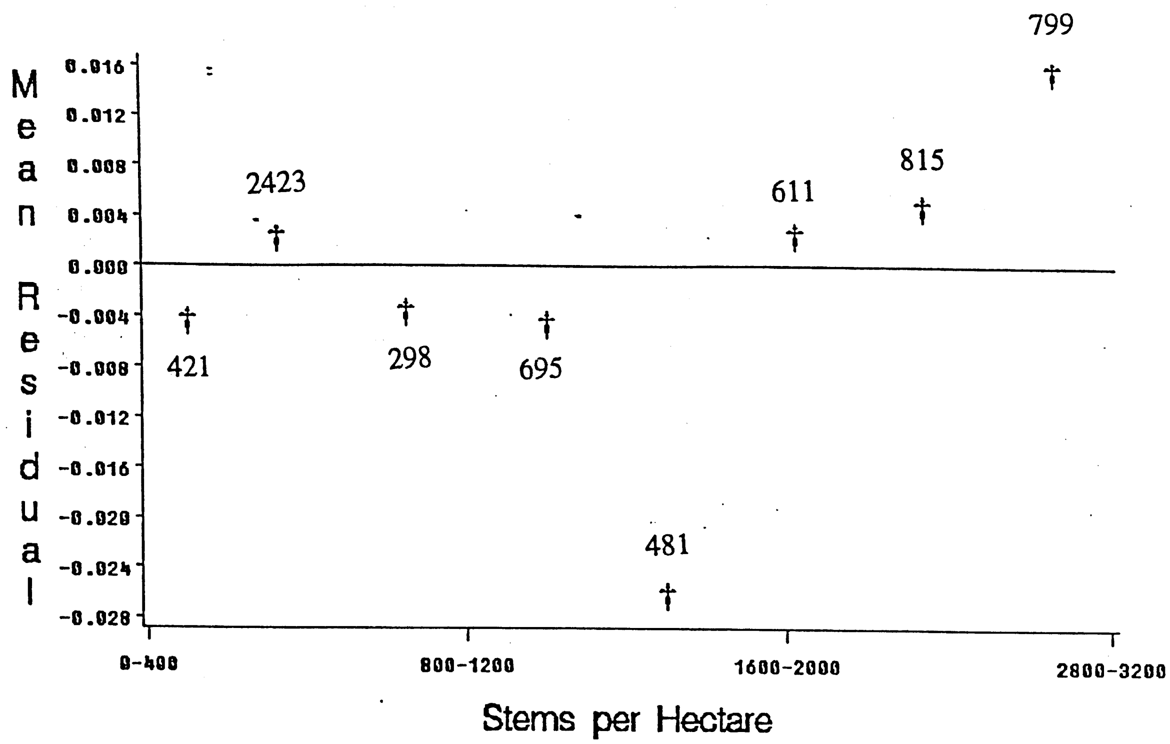


Figure 14. Mean Residuals from Model 1 by Class of *Sph* - Central North Island Data. The Numbers of Observations are Shown

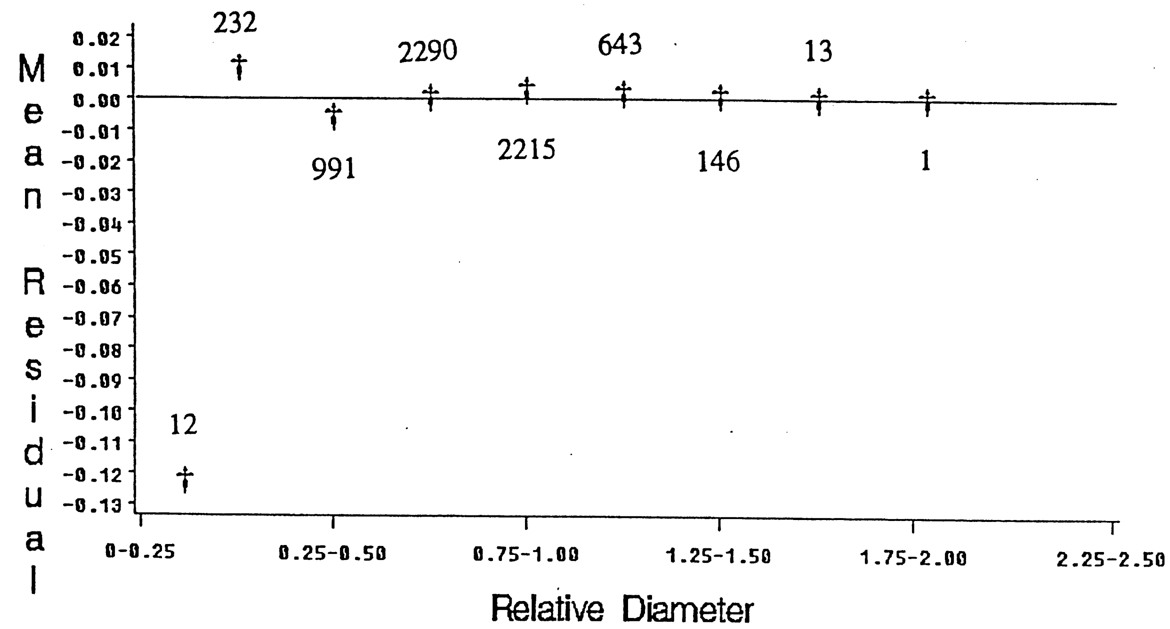


Figure C15. Mean Residuals from Model 1 by Class of *Reldbh* - Central North Island Data. The Numbers of Observations are Shown.

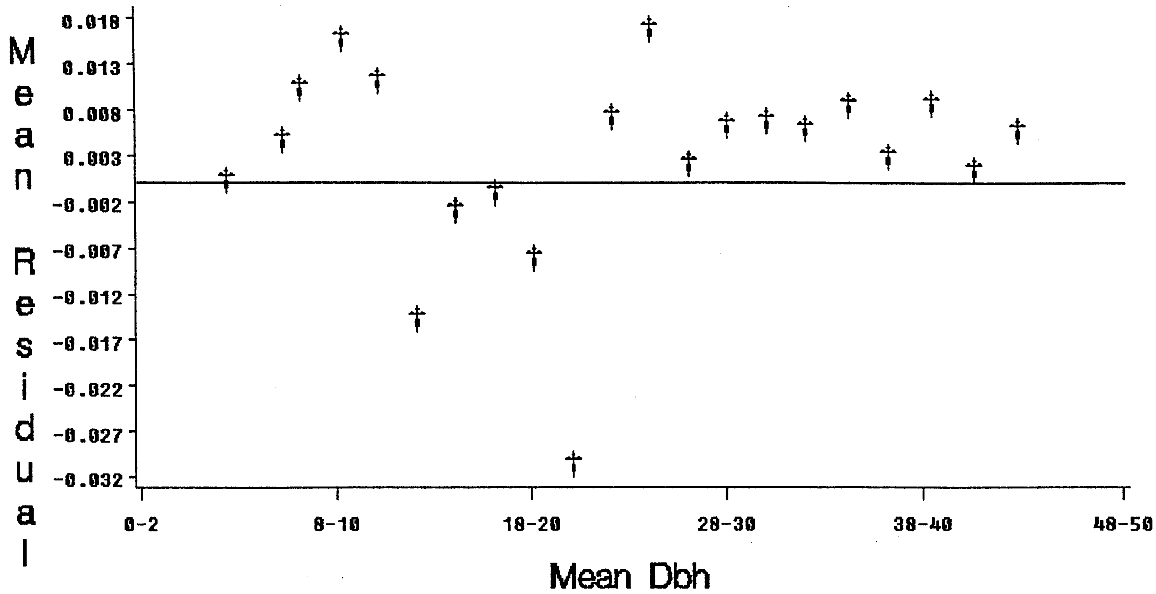


Figure C16. Mean Residuals from Model 1 by Class of *Mndbh* - Central North Island Data

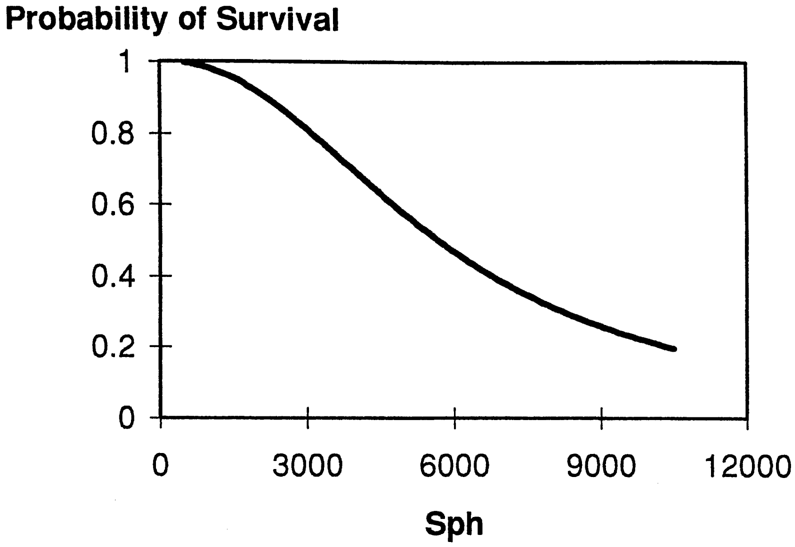


Figure C17. Predicted Probability of Survival over *Sph*. *Dbh* and *Mndbh* are Constant at 20 and 30 cm Respectively.

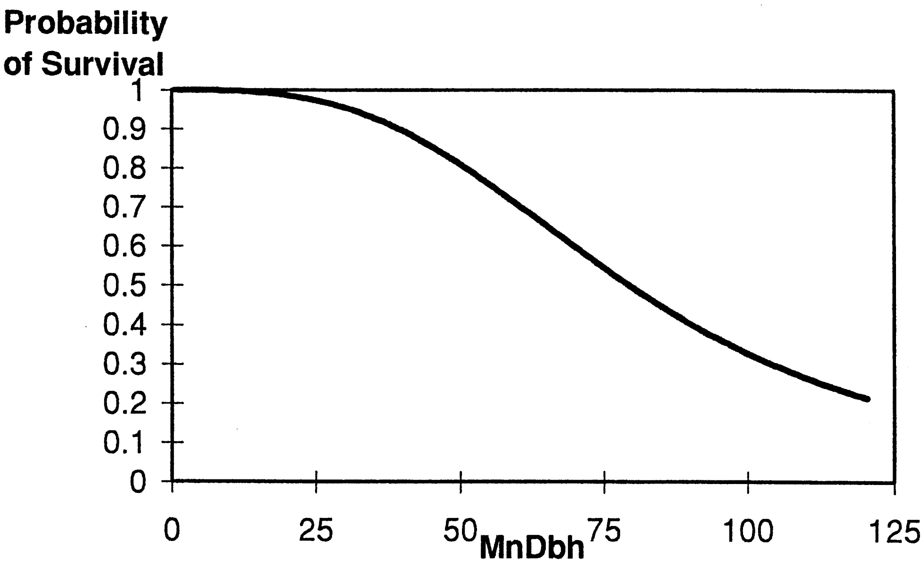


Figure C18. Predicted Probability of Survival over *Mndbh*. *Sph* and *Dbh* are Constant at 1500 and 20 Respectively.

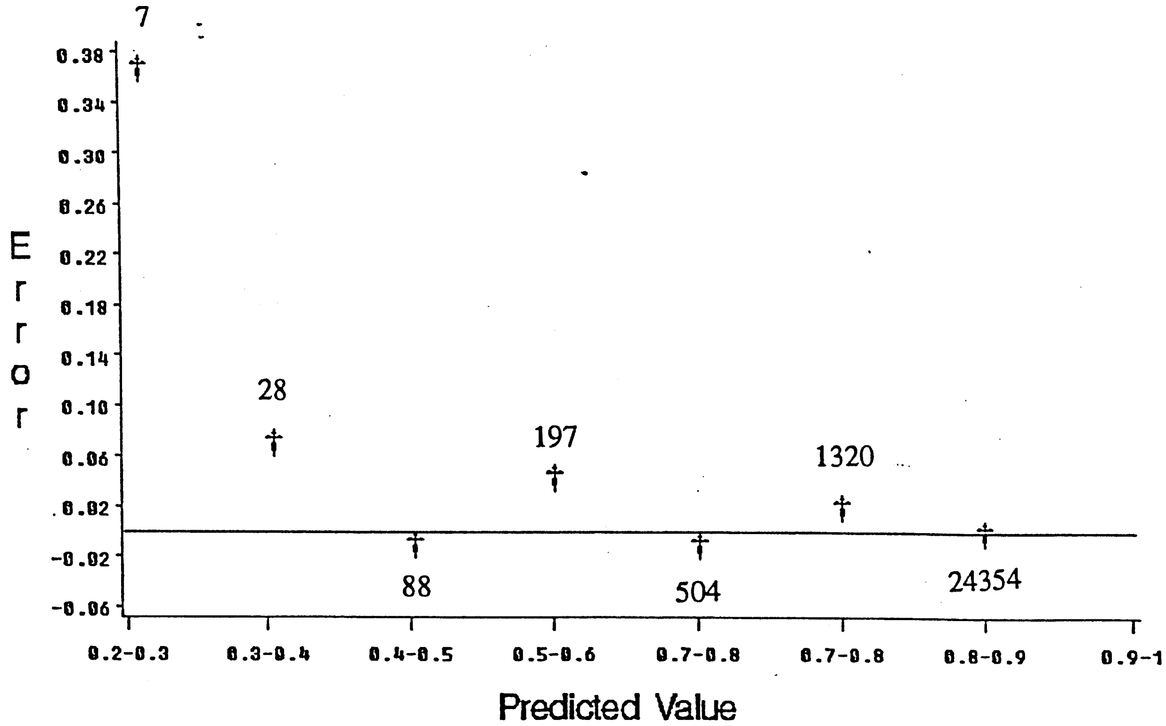


Figure C19. Mean Error by Class of Predicted Values - Model 1 Applied to the Central North Island Test Data. The Numbers of Observations are Shown.

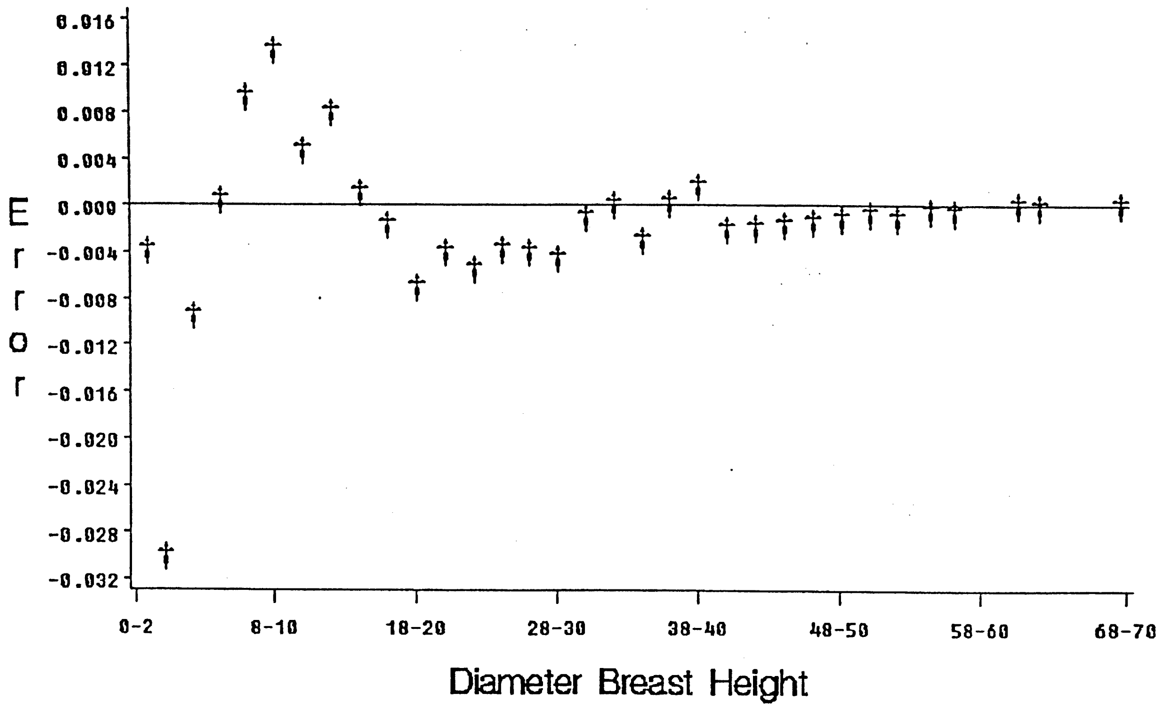
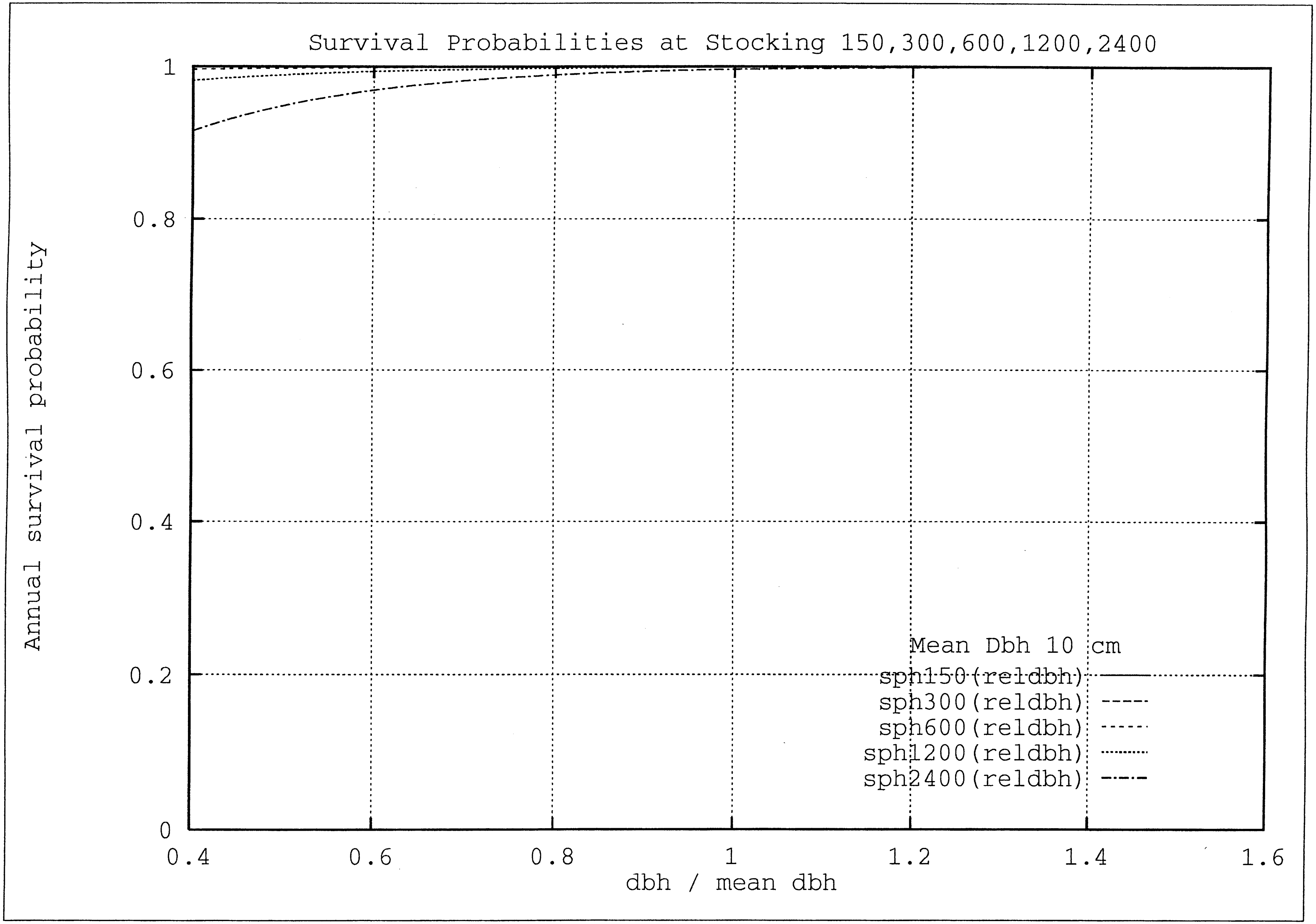
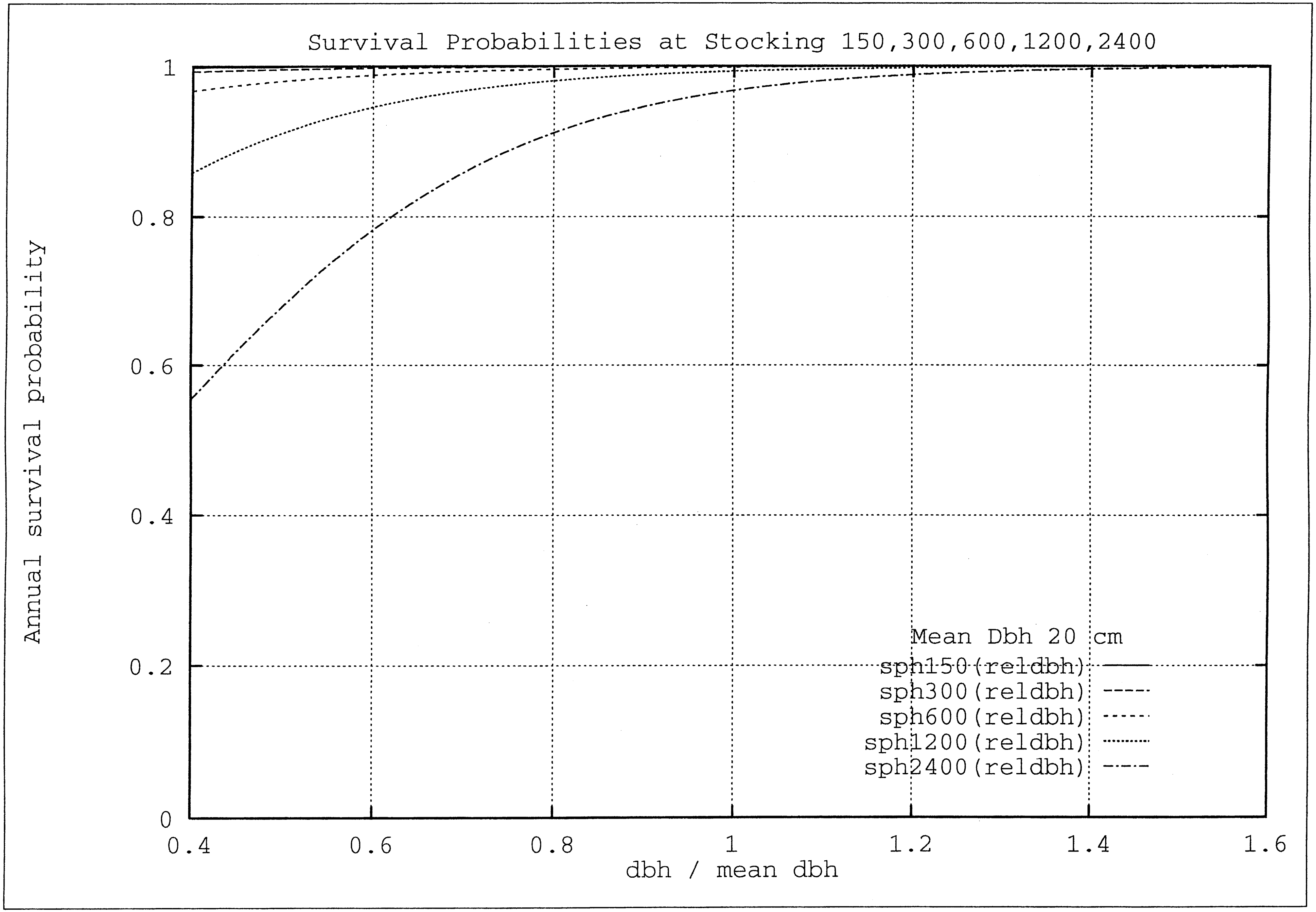


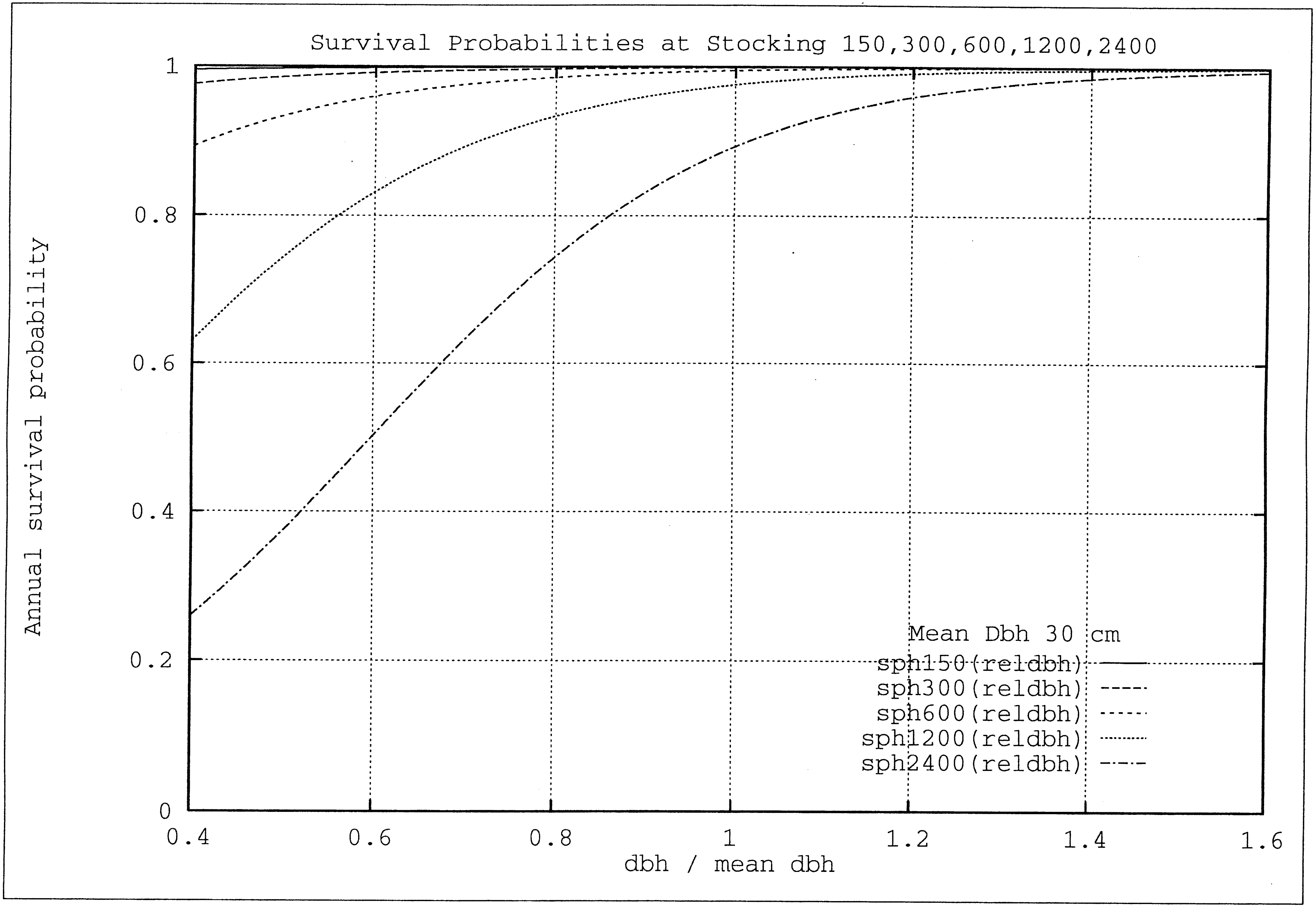
Figure C20. Mean Error by Class of *Dbh* - Model 1 Applied to the Central North Island Test Data.

APPENDIX D. PREDICTIONS FROM THE SURVIVAL MODEL

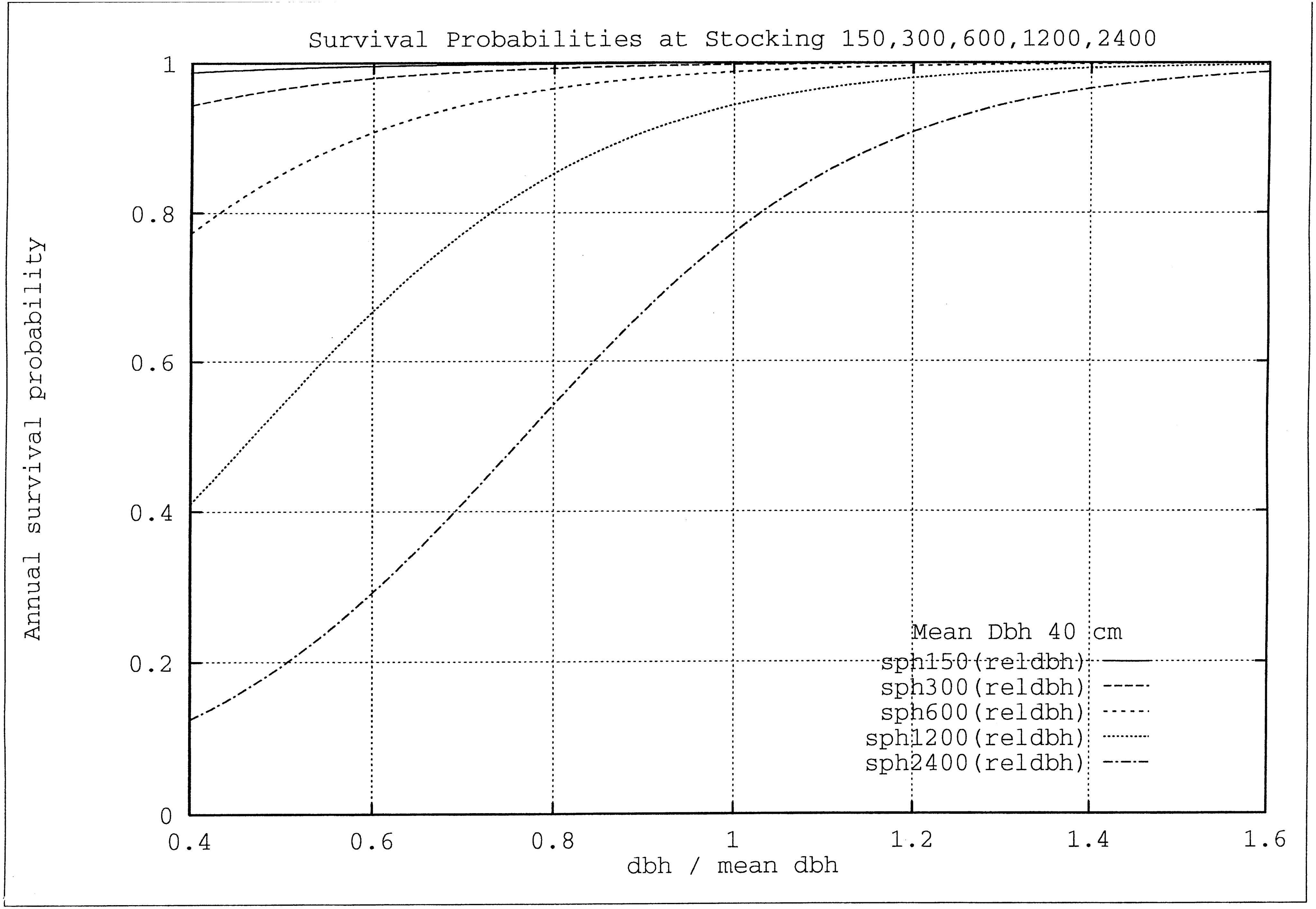

Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
dbh / mean dbh
Mean Dbh 10 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)
0
0.2
0.4
0.6
0.8
1
0.4
0.6
0.8
1
1.2
1.4
1.6

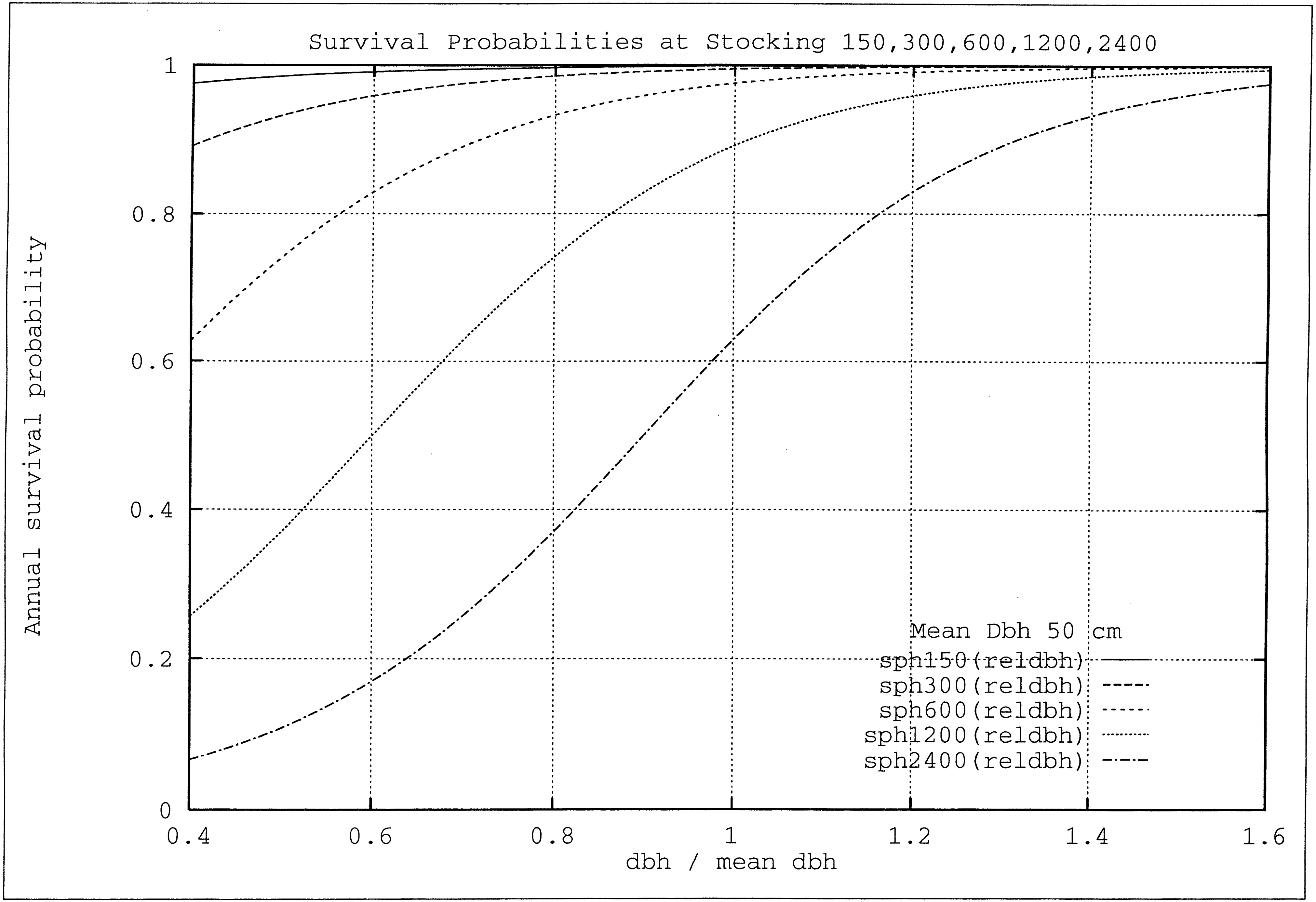


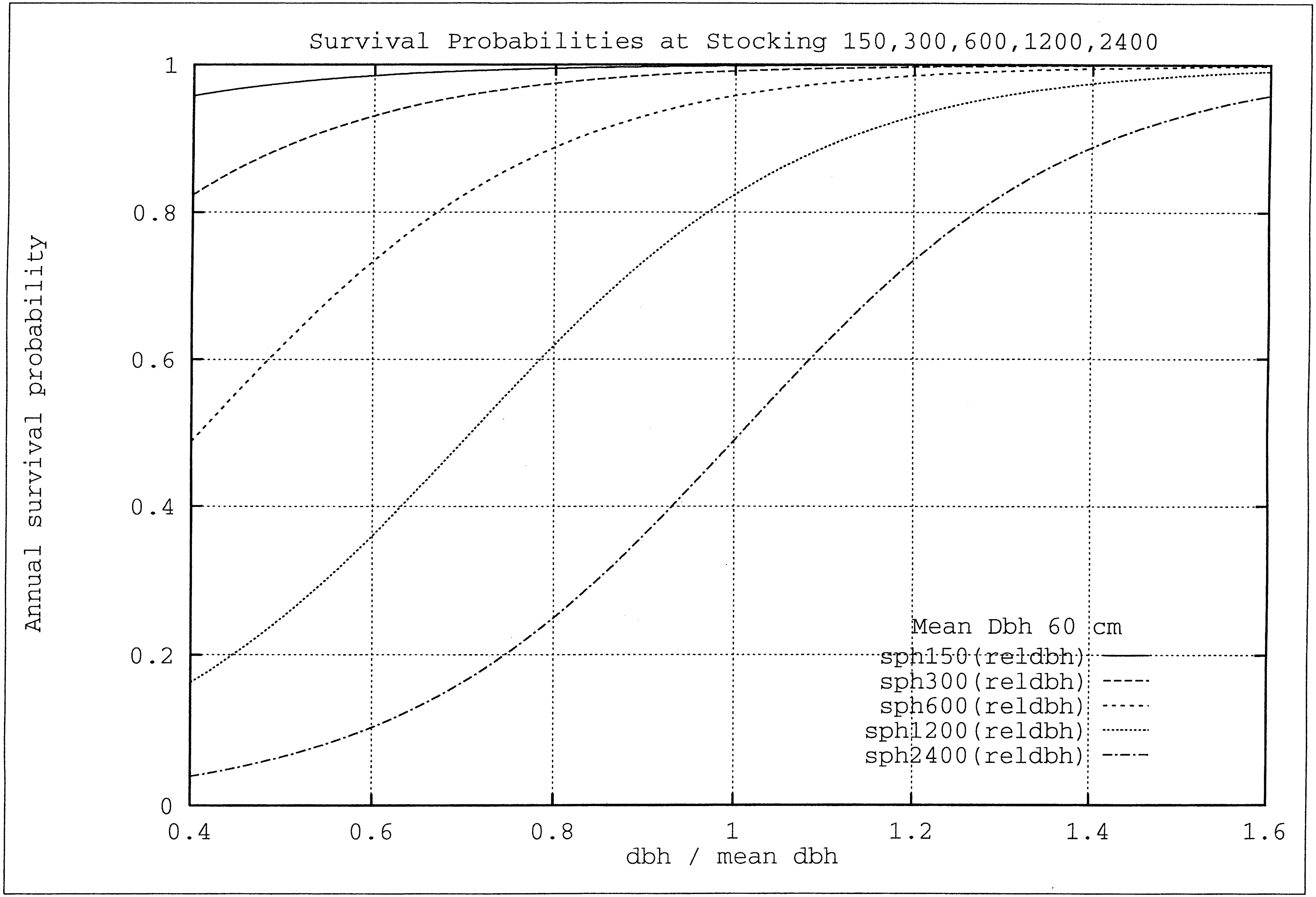
Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
1
0.8
0.6
0.4
0.2
0
0.4
0.6
0.8
1
1.2
1.4
1.6
dbh / mean dbh
Mean Dbh 20 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)



Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
dbh / mean dbh
0
0.2
0.4
0.6
0.8
1
0.4
0.6
0.8
1
1.2
1.4
1.6
Mean Dbh 30 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)


Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
1
0.8
0.6
0.4
0.2
0
0.4
0.6
0.8
1
1.2
1.4
1.6
dbh / mean dbh
Mean Dbh 40 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)


Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
dbh / mean dbh
0
0.2
0.4
0.6
0.8
1
0.4
0.6
0.8
1
1.2
1.4
1.6
Mean Dbh 50 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)



Survival Probabilities at Stocking 150,300,600,1200,2400
Annual survival probability
dbh / mean dbh
Mean Dbh 60 cm
sph150(reldbh)
sph300(reldbh)
sph600(reldbh)
sph1200(reldbh)
sph2400(reldbh)
0
0.2
0.4
0.6
0.8
1
0.4
0.6
0.8
1
1.2
1.4
1.6