

**PREDICTION OF INDIVIDUAL LOG
INTERNODE INDEX FROM ESTIMATED
STAND MEAN INTERNODE LENGTH**

J.A. TURNER

Report No. 42 May 1998

FOREST & FARM PLANTATION MANAGEMENT COOPERATIVE

EXECUTIVE SUMMARY

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The prediction of site mean internode index (IIX) from estimates of mean internode length (MIL) in Standpak presently uses a single \log_{10} MIL model for all sites and genetic material. The development of a MIL/ IIX relationship using a logistic sigmoidal model derived from nationally aggregated data increased the accuracy of stand mean IIX prediction, particularly at high and low levels of MIL. Prediction of individual log IIX from estimates of site mean IIX are presently made in Standpak using a three-way distribution which calculates percentage of logs with $\text{IIX}=0$, $0 < \text{IIX} \leq 0.2182$, and $\text{IIX} > 0.2182$, and the mean IIX of logs with $\text{IIX} > 0.2182$. Using the extended branch database the three-way distribution was refitted, and additional predictive equations developed to allow users to define a *threshold IIX* for grading. Simple regression equations were also developed to enable prediction of percentage of logs, and mean IIX of those logs, greater than a user-defined *threshold IIX*. The models developed appear to be reasonable predictors of site mean IIX, and mean IIX for aggregations of logs in the three-way distribution. Models were validated using second log internode length data collected from nine Genetics and Tree Improvement progeny trials across New Zealand (Turner *et al.* 1997). Validation showed that there is no bias in estimates of the percentage of logs with $0 < \text{IIX} \leq \text{threshold}$. All the models for estimating mean IIX, and percentages and means of logs with $\text{IIX} > \text{threshold}$ were not biased by stocking or genetic improvement. The models developed are to be incorporated into Standpak to enable users to predict log IIX from their own estimates of stand MIL.

Objective: To improve the prediction of individual log internode index (IIX) from estimates of mean internode length (MIL).

PREDICTION OF INDIVIDUAL LOG INTERNODE INDEX FROM ESTIMATED STAND MEAN INTERNODE LENGTH

INTRODUCTION

Silvicultural practices involving radiata pine in New Zealand have placed an emphasis on the production of clearwood (knot-free wood) by pruning the butt log and carrying out early thinnings to increase diameter growth on pruned trees (Sutton 1984). These practices have been warranted because of the relatively large size and persistence of branches in unpruned radiata pine, and the financial premiums that are placed on clear wood. These premiums also apply to clear cuttings, which when combined with improvements in timber utilisation technology, have allowed the present processing of short clear lengths. With this technological ability it has become apparent that the unpruned second log and even third log may yield substantial volumes of clear cuttings from internodes, therefore, there has been an increasing interest in accurate prediction of mean internode length (MIL), internode index (IIX) and hence, clear cuttings from internode lengths in radiata pine.

Mean internode length (MIL) and internode index (IIX) are measures of the level of clear cuttings within a log. IIX specifically relates to the proportion of a log length which is made up of clear cuttings of 0.6 m or greater. MIL (Figure 1) and IIX (Figure 2) are calculated by the equations given below:

$$\text{MIL} = \frac{\sum \text{length (m) of internodes in branched section of log}}{\text{number of internode lengths in branched section of log}}$$

$$\text{IIX} = \frac{\sum (\text{internode lengths} > 0.6\text{m})}{\text{total log length}}$$

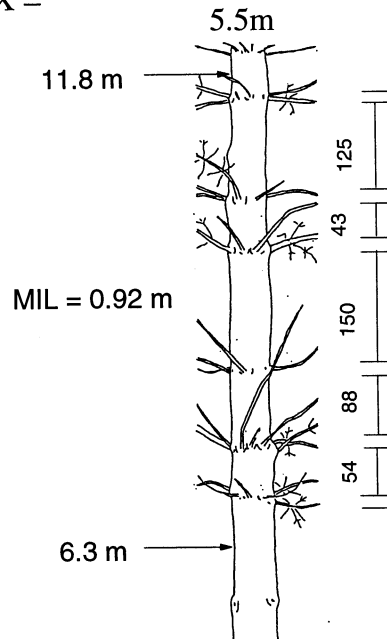


Figure 1: Mean internode length (MIL) calculation.

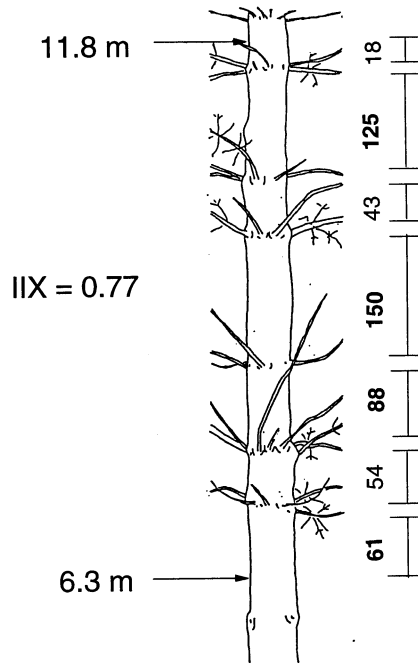


Figure 2: Internode index (IIX) calculation. Note that only those internode length measurements shown in bold (≥ 0.60 m) were used in the calculation of IIX.

While IIX provides a more useful measure of the potential to cut clears from a branched log, it is expensive to make the internode length measurements necessary to calculate IIX. Estimates of MIL are, however, more readily estimable, using whorl counts and estimates of average whorl depth (Woods & Carson 1988). From these parameters MIL may be calculated using the following formulae (Woods & Carson 1988):

$$MIL = \frac{l - (n \times d)}{n + (I - 1)}$$

where *MIL* is mean internode length for the log length measured;

l is the length of stem or log being measured;

n is the number of branch and/ or stem cone whorls per length of stem or log being measured;

d whorl depth (estimated);

I is the number of times for each stem or log that the end of the indicated "log" does not coincide with a branch or stem cone whorl, ie., 0, 1, or 2.

The use of functions to allow prediction of IIX from whorl count based MIL estimates allows relatively cheap prediction of potential clear cuttings from a stand.

Prediction of IIX for logs from MIL estimates within Standpak (Figure 3) is a two step process. First, the stand level IIX is estimated from MIL (Log Making Module). Then IIX for each log within the stand is calculated based on the expected distribution of individual log IIX within the stand (Log Grading Module) (Figure 4).

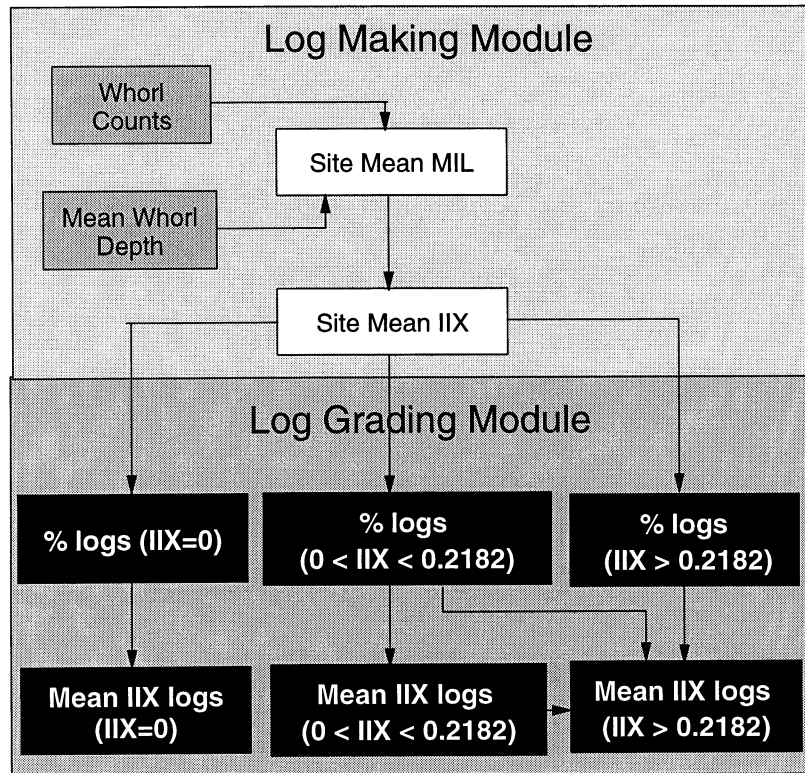


Figure 3: Flow diagram showing steps taken by Standpak in the calculation of individual log IIX for log grading. Boxes shaded grey are user inputs. Boxes shaded black are Standpak outputs used to grade logs.

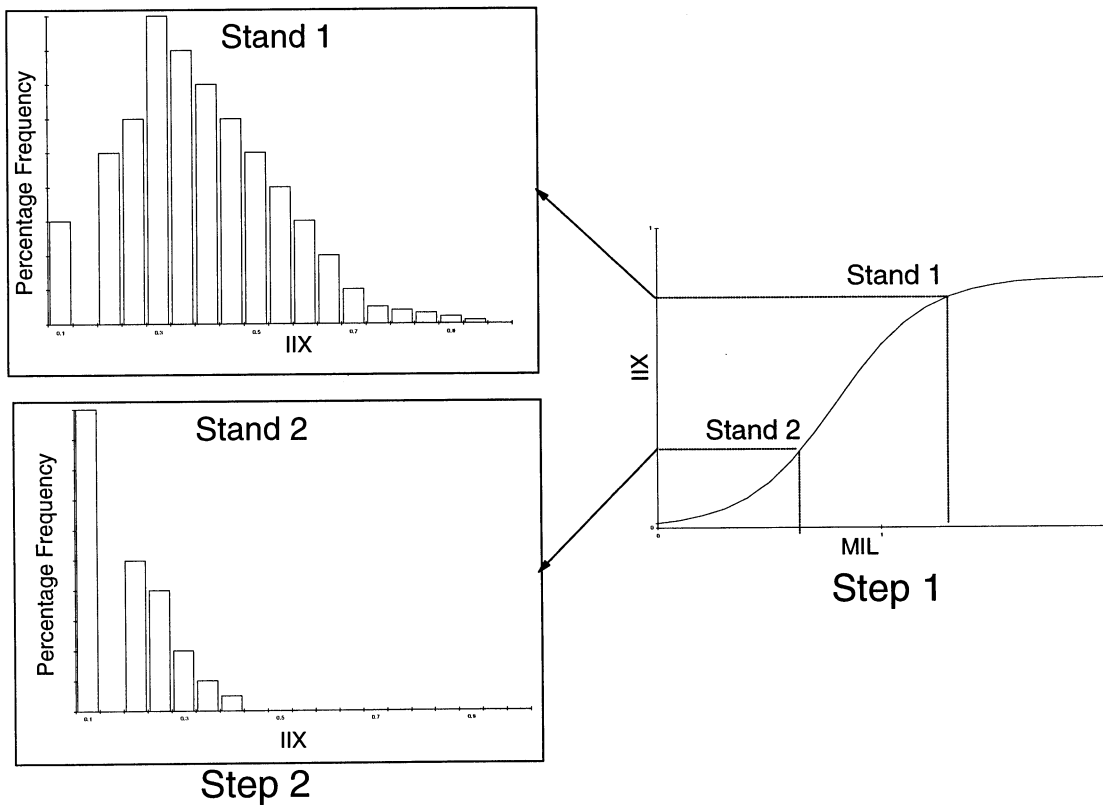


Figure 4: The individual log internode index (IIX) estimation modelling process, illustrated using two stands as examples.

Step 1: Prediction of Stand Average IIX from MIL

Two equations are presently available for the prediction of stand average internode index (IIX) from mean internode length (MIL). The equation currently used in STANDPAK and developed by Whiteside (unpubl.) is (Figure 5):

$$IIX = (1.343(\log_{10}(MIL))) + 0.7697 \quad [\text{Equation 1}]$$

with the constraint:

$$\text{if } (IIX) < 0.0 \text{ then } IIX = 0.0$$

Another equation, derived by Woods and Carson (1988) for improved breeds, is (Figure 5):

$$IIX = -0.0731 + 0.8904(MIL) \quad [\text{Equation 2}]$$

Woods and Carson (1988) developed four separate equations for predicting IIX from MIL for:

- long internode breed at Woodhill;
- all other breeds at Woodhill;
- long internode breed on other sites;
- other breeds and other sites.

These four equations all have the same slope for the MIL/ IIX relationship, however, they differ in their intercept.

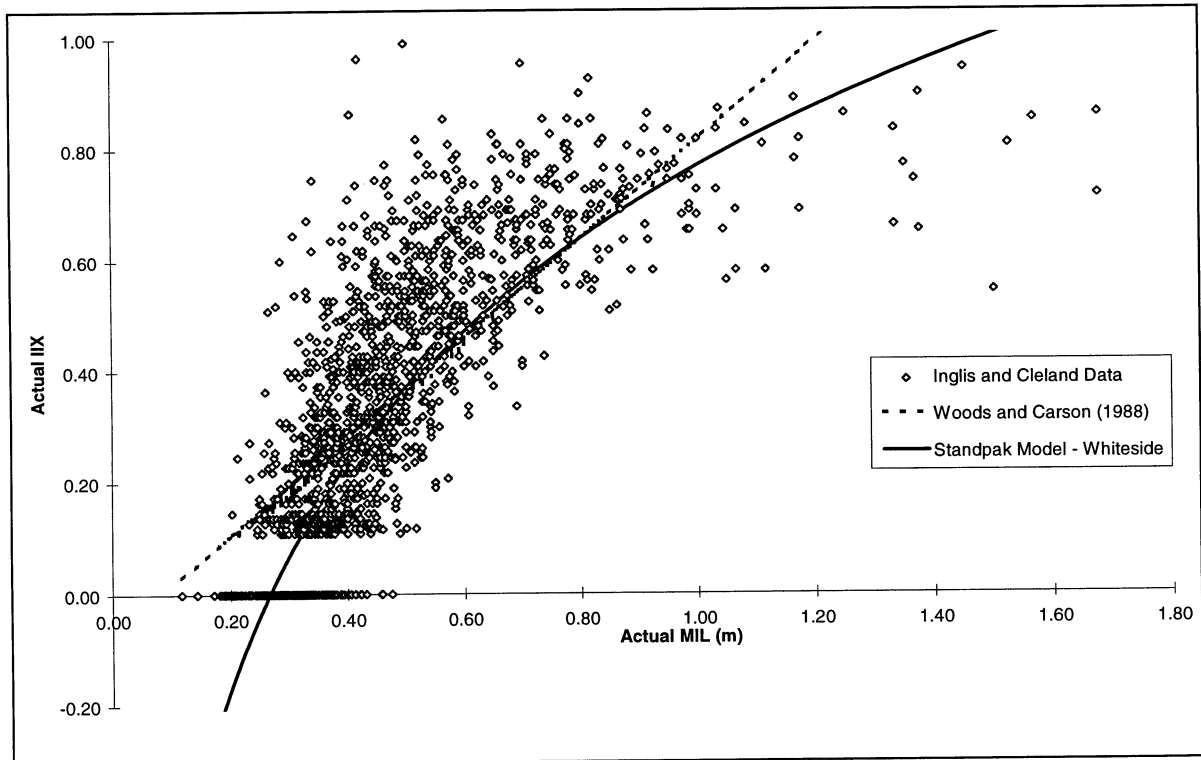


Figure 5: Woods and Carson (1988) linear model and the \log_{10} MIL model, developed by Whiteside (unpubl.), and used in Standpak, plotted against data collected by Inglis and Cleland (1982).

The fitting of linear regression and \log_{10} MIL equations to MIL/ IIX data appears to be inappropriate particularly for predicting IIX at high levels of MIL (Figure 5). Both the linear regression model (Woods & Carson 1988) and the \log_{10} model (Whiteside unpubl.) over-predict IIX for high levels of MIL, while the linear model also over-predicts IIX for low levels of MIL and the \log_{10} model under-predicts IIX for low levels of MIL. Data from an extended branch database enables validation of the present model implemented in Standpak, and the opportunity to develop a sigmoidal model for prediction of IIX from MIL.

Step 2: Individual Log IIX Prediction

At present STANDPAK estimates individual log IIX from stand average IIX using a three-way distribution (Whiteside unpubl.).

Percentages of Logs

The three-way distribution estimates percentages of logs with:

- IIX = 0;
- $0 < \text{IIX} \leq 0.2182$;
- $\text{IIX} > 0.2182$;

using the following respective equations:

$$(\% \text{IIX}=0) = -70.03 \log_{10}(\overline{\text{IIX}}) - 21.5 \quad [\text{Equation 3}]$$

$$(\% \text{IIX} > 0.2182) = 183.42 \left(\sqrt{\overline{\text{IIX}}} \right) \quad [\text{Equation 4}]$$

$$(0 < \% \text{IIX} \leq 0.2182) = 100 - (\% \text{IIX}=0) - (\% \text{IIX} > 0.2182) \quad [\text{Equation 5}]$$

Mean IIX for Logs

The mean IIX for logs with $\text{IIX} > 0.2182$ and $0 < \text{IIX} \leq 0.2182$ are given by the following equations:

$$\overline{\text{IIX}} > 0.2182 = \frac{100(\overline{\text{IIX}}) - 0.132(0 < \% \text{IIX} \leq 0.2182)}{(\% \text{IIX} > 0.2182)} \quad [\text{Equation 6}]$$

$$(0 < \% \text{IIX} \leq 0.2182) = 0.132 \quad [\text{Equation 7}]$$

The availability of new data allows the opportunity to further improve prediction of the three-way distribution of individual log IIX. To improve flexibility in specifying three-way distribution estimates of percentages of logs, the option of a user-defined *threshold* rather than a set IIX of 0.2182 will also be explored (Figure 6).

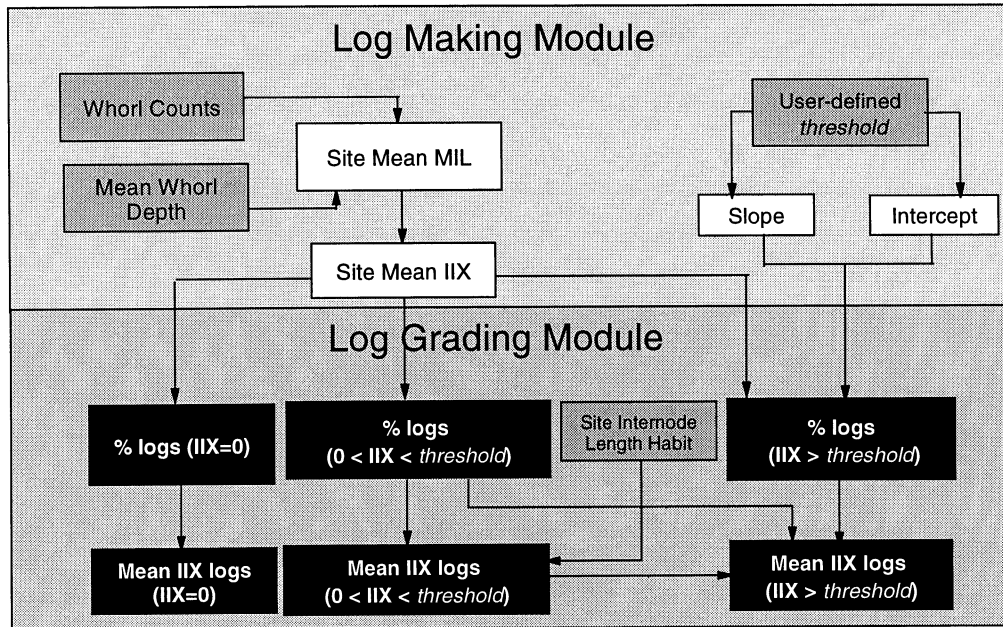


Figure 6: Flow diagram showing steps taken by Standpak in the calculation of individual log IIX for log grading including a user-defined *threshold* IIX. Grey boxes are user inputs. Black boxes are Standpak outputs used to grade logs.

DATABASE

The extended branch database (Inglis & Cleland 1982; Tombleson *et al.* 1990; Knowles & Kimberley 1992; Kimberley & Knowles 1993; McInnes 1997) from which internode length data was derived for this study, contained a total of 4001 logs, from 6 log classes (Table 1), with most of these being second or third logs. An ANOVA identified no significant ($p > 0.05$) difference in the MIL/ IIX relationship between log classes using the equation currently implemented in Standpak (Whiteside unpubl.). Analyses were, therefore, performed with all log classes amalgamated.

Table 1: Log height classes used in the study.

Log	Number of Logs	Height
First	36	0.3-5.8
Second	567	5.8-11.3
Third	581	11.3-16.8
Fourth	169	16.8-22.3
Fifth	152	22.3-27.8
Sixth	106	27.8-33.8

All first logs which had not been measured for internode length from 0.2-0.3 m were assumed to have been pruned and were therefore discarded from the dataset. 690 of the second logs (17% of all the logs in the database) contained in the database had been partly pruned. No information was available identifying exactly where logs were pruned to. It was, therefore, assumed that second logs which had over 1.2 m from the log end to the first whorl had been partly pruned. These logs were discarded from the

data set as IIX calculated for them would be incorrect. The removal of these logs adds a potential bias against long internode trees if the actual log end is greater than 1.2 m.

The final dataset of 3 473 logs contained internode length data for 35 sites. 94% of the log data came from forest sites, and the remaining 6% from farm sites. The sites cover a wide spread of average MIL and IIX (Table 2). Genetic material represented in the database ranged from GF7 to GF14, and includes long internode¹ (LI) material (Table 3).

Table 2: Number of logs measured, site mean internode length (MIL), and site mean internode index (IIX) for individual locations.

Region	Location	Site Type	No. of Logs	MIL	IIX
Auckland			307	0.37	0.18
	Aupouri	forest	56	0.36	0.21
	Whangapoua	forest	106	0.40	0.21
	Whatawhata	farm	20	0.26	0.08
	Woodhill	forest	125	0.37	0.16
Rotorua			1934	0.43	0.27
	Goudies	forest	23	0.40	0.24
	Kaingaroa	forest	691	0.41	0.21
	Matea	forest	28	0.37	0.24
	Ngatira (LI) ²	farm	46	0.67	0.49
	Ngatira (GF14)	farm	59	0.42	0.22
	Northern Boundary	forest	220	0.43	0.30
	Omataroa	forest	108	0.46	0.37
	Rotoehu	forest	182	0.44	0.27
	Tarawera	forest	408	0.47	0.34
	Tikitere	farm	59	0.34	0.15
	Waimihia	forest	58	0.34	0.21
	Waratah	forest	27	0.35	0.15
	Whakarewarewa	forest	25	0.43	0.33
Hawkes Bay			136	0.40	0.24
	Gwavas	forest	64	0.39	0.23
	Mohaka	forest	72	0.41	0.25
Wellington			112	0.33	0.16
	Ngaumu	forest	45	0.38	0.23
	Waitarere	forest	67	0.30	0.11
Nelson			48	0.44	0.30
	Golden Downs	forest	48	0.44	0.30
Westland			369	0.54	0.45
	Mawheranui	forest	26	0.56	0.49
	Nemona	forest	47	0.50	0.39
	Tawhai	forest	199	0.58	0.52
	Waimia	forest	97	0.45	0.34

¹ The LI material in the database is not from the “870” series selection, but is from a climbing select (open pollinated) collection by Tony Shelbourne made of the parents in the “870” selection series which emphasised long internodes (Knowles pers. comm.).

² Branch habit measurements made at Ngatira are from a trial containing a long internode¹ seedlot.

Canterbury			121	0.44	0.30
	Ashley	forest	38	0.42	0.24
	Geraldine	forest	33	0.47	0.36
	Hanmer	forest	50	0.43	0.30
Southland			446	0.46	0.34
	Beaumont	forest	42	0.43	0.31
	Berwick	forest	157	0.44	0.31
	Dusky	forest	42	0.48	0.40
	Hokonui	forest	29	0.46	0.33
	Longwood	forest	34	0.41	0.30
	Otago Coast	farm	16	0.45	0.32
	Otago Coast	forest	74	0.50	0.38
	Slopedown	forest	52	0.53	0.41

Table 3: Number of logs in the branch database by genetic origin.

Genetic Material	Number of Logs
unknown	401
GF7	2742
GF12	25
GF14	259
LI ¹	46

A 'validation' data set was formed from second log (6.3 to 11.8 m) internode length data collected from ten Genetics and Tree Improvement progeny trials across New Zealand (Turner *et al.* 1997).

Table 4: Summary details of the 'validation' data set, including site average mean internode length, and internode index.

Region	Forest	Cpt	Genetic Material	No. of Logs	MIL	IIX
Auckland sands	Woodhill		GF14	398	0.34	0.11
Rotorua	Kaingaroa	1350	GF16	96	0.54	0.32
	Kaingaroa	905	GF14	111	0.48	0.26
	Kaingaroa	905	LI	103	0.64	0.45
	Kaingaroa	327	GF14	351	0.54	0.35
	Awahohonu		GF14	107	0.46	0.26
Nelson	Golden Downs		GF14	336	0.59	0.38
Canterbury	Eyrewell		GF14	320	0.40	0.23
Westland	Mawheranui		GF14	107	0.47	0.34
Southland	Taringatura		GF14	109	0.53	0.31

ANALYSIS

Prediction of Stand Average IIX From MIL

Five models were compared, by location, for their fit to the MIL/ IIX data:

1. the present LOG_{10} model used in STANDPAK (Equation 1) (Whiteside unpubl.);
2. the four linear models (Equation 2) developed by Woods and Carson (1988);
3. a logistic sigmoidal model (Equation 8);
4. a logistic sigmoidal model calculated from the data set as a whole (Equation 8).
5. a Morgan, Mercer, Flodin sigmoidal model (Equation 9) (Ratkowsky 1989);

$$\text{IIX} = \lambda \left[\frac{e^{\alpha + \beta \text{MIL}}}{1 + e^{\alpha + \beta \text{MIL}}} \right] + \gamma \quad [\text{Equation 8}]$$

$$\text{IIX} = \left[\frac{\beta e^{\gamma} + \alpha \text{MIL}^{\delta}}{e^{\gamma} + \alpha \text{MIL}^{\delta}} \right] + \lambda \quad [\text{Equation 9}]$$

where *IIX* is internode index;

MIL is mean internode length (m)

$\alpha, \beta, \delta, \gamma, \lambda$ are coefficients estimated from the data

The linear and log_{10} models were fitted using PROC REG, and the sigmoidal models were fitted using PROC NLIN in the SAS system (SAS Institute 1986). The five models were compared for their fit to the data in terms of their root mean square error (RMSE). The fit of the best model was then checked for biases in IIX estimates across regions by plotting residuals against MIL.

Individual Log IIX Prediction

Prediction of individual log IIX from stand average IIX is based on a three-way distribution of IIX. This three-way distribution requires the prediction of mean IIX and percentage of logs for the three aggregations. At present this three-way distribution is set as:

- $\text{IIX} = 0$;
- $0 < \text{IIX} \leq 0.2182$;
- $\text{IIX} > 0.2182$;

To improve the flexibility of log grading by IIX the option of allowing users to define a *threshold* IIX, rather than being restricted to an IIX of 0.2182 as set by Whiteside (unpubl.), was explored. Analyses were therefore performed to enable the prediction of mean IIX and percentage of logs for the following three aggregations:

- $\text{IIX} = 0$;
- $0 < \text{IIX} \leq \text{threshold}$;
- $\text{IIX} > \text{threshold}$;

where *threshold* is a user-defined IIX.

Percentages of Logs

Prediction of the percentage of logs with $IIX = 0$ is derived from stand mean IIX using a simple regression equation fitted with PROC GLM in the SAS system (SAS Institute 1986). Prediction of the percentage of logs with $IIX > threshold$, is clearly dependent on the user-defined *threshold*. For a particular *threshold*, the relationship between stand mean IIX and percentage IIX is derived from a regression equation with the slope (β) and intercept (α) being different depending on the *threshold* level set. Prediction of percentage IIX for different user-defined *thresholds* required prediction using simple regressions of α and β from the *threshold* fitted with PROC GLM in the SAS system (SAS Institute 1986).

Mean IIX of Logs

The mean IIX for each aggregation was derived from simple linear regression equations and basic arithmetic equations. Mean IIX for logs with $0 < IIX \leq threshold$ was determined from regression equations based on the user-defined *threshold* developed using simple regression techniques fitted with PROC GLM in the SAS system (SAS Institute 1986).

Validation of the models developed was performed by residual analysis on a 'validation' data set which was comprised of internode length measurements from a separate study of internode length habit in "850" families planted in progeny trials across New Zealand (Turner *et al.* 1997).

RESULTS AND DISCUSSION

Prediction of Stand Average IIX From MIL

The three basic model types; linear, \log_{10} , and sigmoidal differ in how they fit the data (Figure 7). The linear model (Woods & Carson 1988) over-predicts IIX for high and low MIL. The \log_{10} model (Whiteside unpubl.) reduces the level of over-prediction of IIX at high and low MIL, however, it still over-predicts, particularly at high MIL. Both models may also give nonsensical answers for IIX , ie., IIX greater than 1 are possible. The logistic sigmoidal model overcomes the problems of over-prediction, as well as giving logical estimates of IIX such that IIX can not be greater than 1.

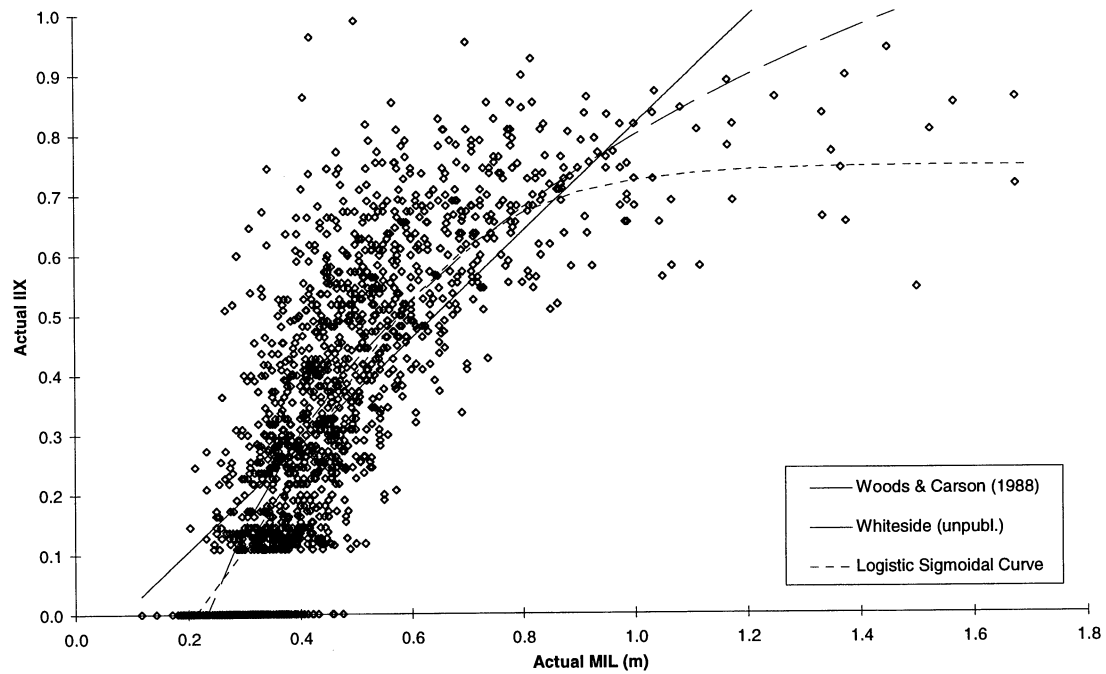


Figure 7: A subset of the internode length data (Inglis & Cleland 1982) with linear, \log_{10} and logistic sigmoidal models plotted. The Morgan, Mercer, Flodin sigmoidal has not been plotted because of its similarity to the logisitc sigmoidal curve.

The fit of the 5 equations to the data set was compared by comparing the root mean square error (RMSE) of regressions for each of the regions, locations and site types (Table 4). The sigmoidal model was found to be better than the linear equation on all but seven sites:- Woodhill, Geraldine, Matea, Waimihia, Waratah, Whakarewarewa, and the Otago Coast farm site. The sigmoidal model was also found to be better than the \log_{10} model on all but 9 sites. Geraldine, Hanmer, Waratah, Whakarewarewa, Hokonui, Longwood, the Otago Coast farm site, Ngaumu, and Mawheranui. The sigmoidal was better than the Morgan, Mercer, Flodin sigmoidal on all but three sites:- Golden Downs, Waratah, and Berwick. The overall national model derived using data from all sites, was found to be only marginally less precise at predicting IIX for the different locations than the individual location sigmoidal models, and is expected to be more robust in use.

Table 5: Comparison of root mean square error (RMSE) for individual locations from linear, logarithmic, Morgan, Mercer, Flodin sigmoidal, logistic sigmoidal and from a national model based on a sigmoidal function.

Region	Location	Site Type	Linear	Logarithmic	Morgan <i>et al</i> Sigmoidal	Sigmoidal	National Sigmoidal
Auckland						0.094	0.104
	Aupouri	forest	0.110	0.118	0.114	0.109	0.112
	Whangapoua	forest	0.091	0.105	0.094	0.089	0.108
	Whatawhata	farm	0.078	0.088	0.085	0.055	0.080
	Woodhill	forest	0.086	0.088	0.087	0.087	0.105
Rotorua						0.112	0.113
	Goudies	forest	0.071	0.072	0.073	0.061	0.072
	Kaingaroa	forest	0.115	0.106	0.109	0.100	0.110
	Matea	forest	0.089	0.097	0.094	0.090	0.102
	Ngatira (LI) ²	farm	0.160	0.137	- ³	0.133	0.140
	Ngatira (GF14)	farm	0.116	0.103	- ³	0.101	0.111
	Northern Boundary	forest	0.125	0.119	0.122	0.116	0.117
	Omataroa	forest	0.114	0.112	0.113	0.111	0.130
	Rotoehu	forest	0.123	0.109	0.101	0.101	0.105
	Tarawera	forest	0.133	0.124	0.127	0.116	0.119
	Tikitere	farm	0.095	0.098	0.096	0.093	0.095
	Waimihia	forest	0.128	0.131	0.130	0.129	0.135
	Waratah	forest	0.097	0.101	0.102	0.102	0.107
	Whakarewarewa	forest	0.109	0.109	- ³	0.114	0.124
Hawkes Bay						0.098	0.099
	Gwavas	forest	0.110	0.095	0.104	0.088	0.090
	Mohaka	forest	0.116	0.116	0.114	0.107	0.109
Wellington						0.092	0.096
	Ngaumu	forest	0.110	0.106	0.111	0.108	0.113
	Waitare	forest	0.089	0.092	0.089	0.079	0.086
Nelson						0.116	0.120
	Golden Downs	forest	0.137	0.123	0.115	0.116	0.120
Westland						0.111	0.122
	Mawheranui	forest	0.108	0.103	0.110	0.106	0.126
	Nemona	forest	0.137	0.121	0.118	0.117	0.123
	Tawhai	forest	0.134	0.112	0.125	0.106	0.128
	Waimia	forest	0.119	0.115	0.118	0.114	0.117
Canterbury						0.105	0.108
	Ashley	forest	0.123	0.094	0.112	0.088	0.090
	Geraldine	forest	0.107	0.105	0.109	0.107	0.109
	Hanmer	forest	0.123	0.118	0.124	0.120	0.126
Southland						0.118	0.123
	Beaumont	forest	0.133	0.109	0.126	0.105	0.116
	Berwick	forest	0.130	0.119	0.116	0.116	0.118
	Dusky	forest	0.170	0.152	0.168	0.145	0.173
	Hokonui	forest	0.092	0.084	0.092	0.084	0.102
	Longwood	forest	0.153	0.148	0.155	0.150	0.162
	Otago Coast	farm	0.105	0.106	0.113	0.108	0.112
	Otago Coast	forest	0.152	0.119	0.139	0.111	0.120
	Slopedown	forest	0.129	0.116	0.124	0.111	0.120

³ A root mean square error (RMSE) could not be calculated for this model as PROC NLIN failed to converge.

These results indicate that to predict IIX from stand mean MIL, the logistic sigmoidal model is better than the linear, \log_{10} , and Morgan, Mercer, Flodin sigmoidal model types. The logistic sigmoidal model can be used on a national basis without a high level of error, therefore there is little advantage in deriving equations for individual forests. The differences between actual and predicted IIX (residuals calculated as actual-predicted) were plotted against MIL for each region (Figures 6 to 13) to examine for any levels of MIL for which bias occurred. These figures suggest that the error in predicting IIX using the national logistic sigmoidal model can be expected to fall within ± 0.4 .

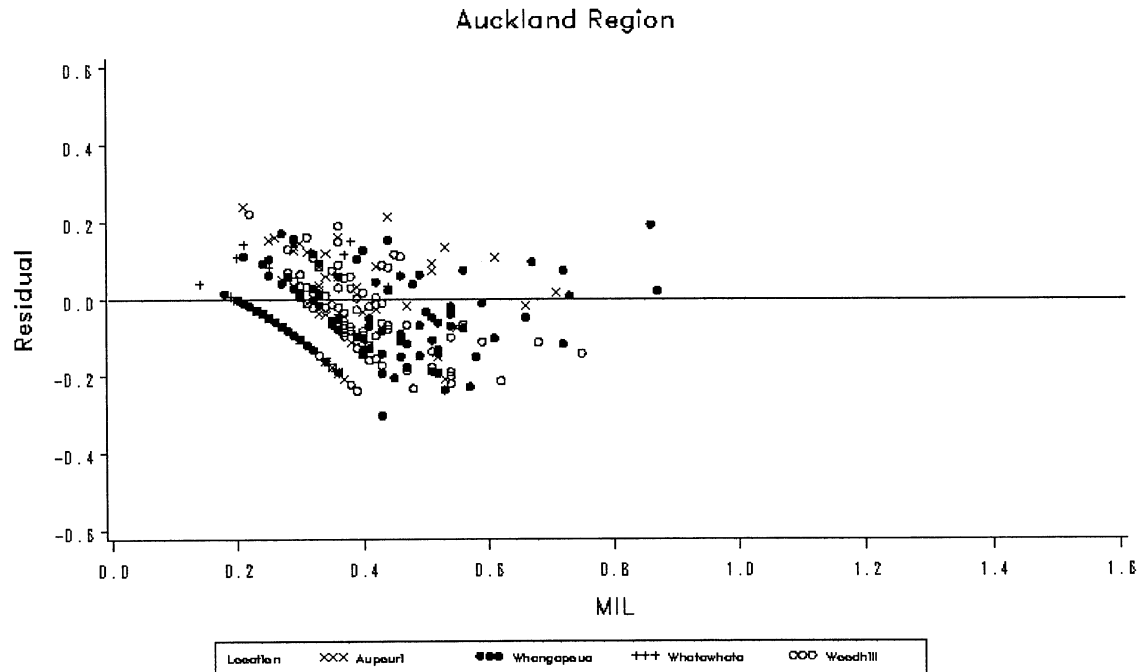


Figure 8: Errors in predicted IIX for Auckland region using the logistic sigmoidal model.

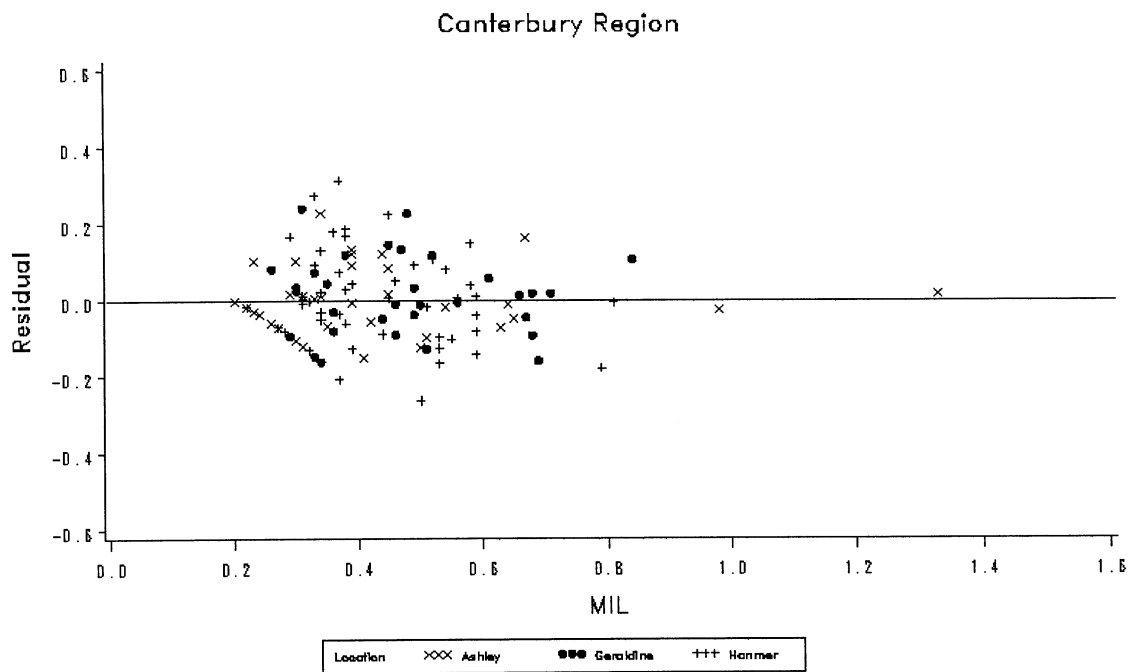


Figure 9: Errors in predicted IIX for Canterbury region using the logistic sigmoidal model.

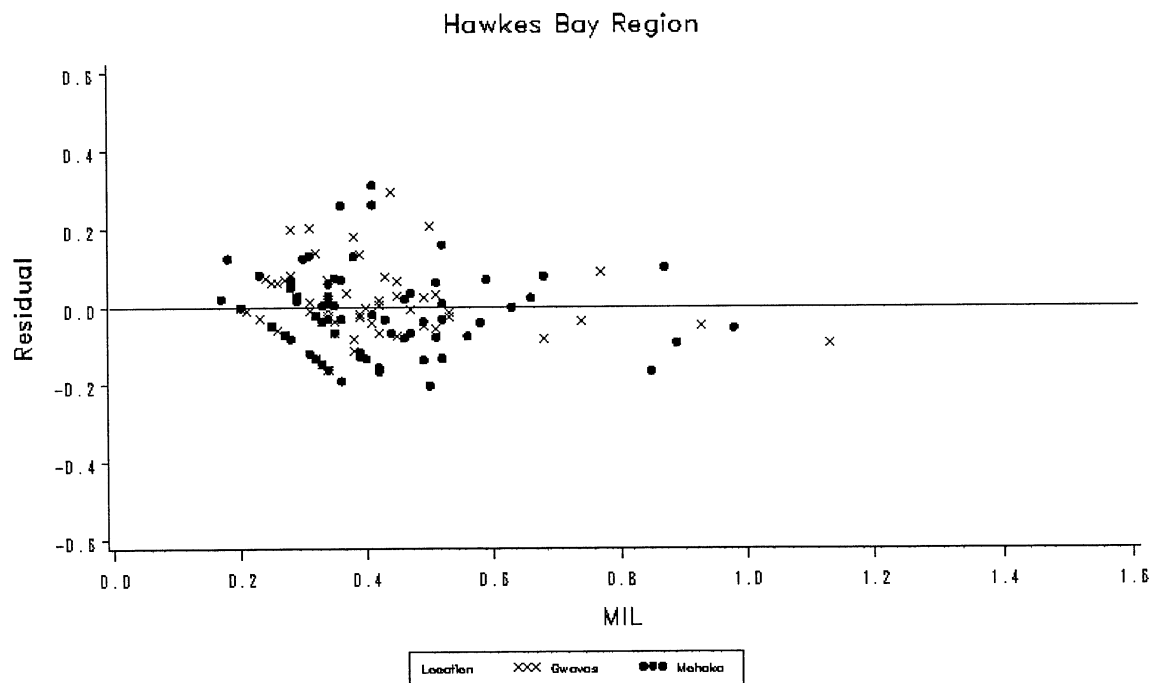


Figure 10: Errors in predicted IIX for Hawkes Bay region using the logistic sigmoidal model.

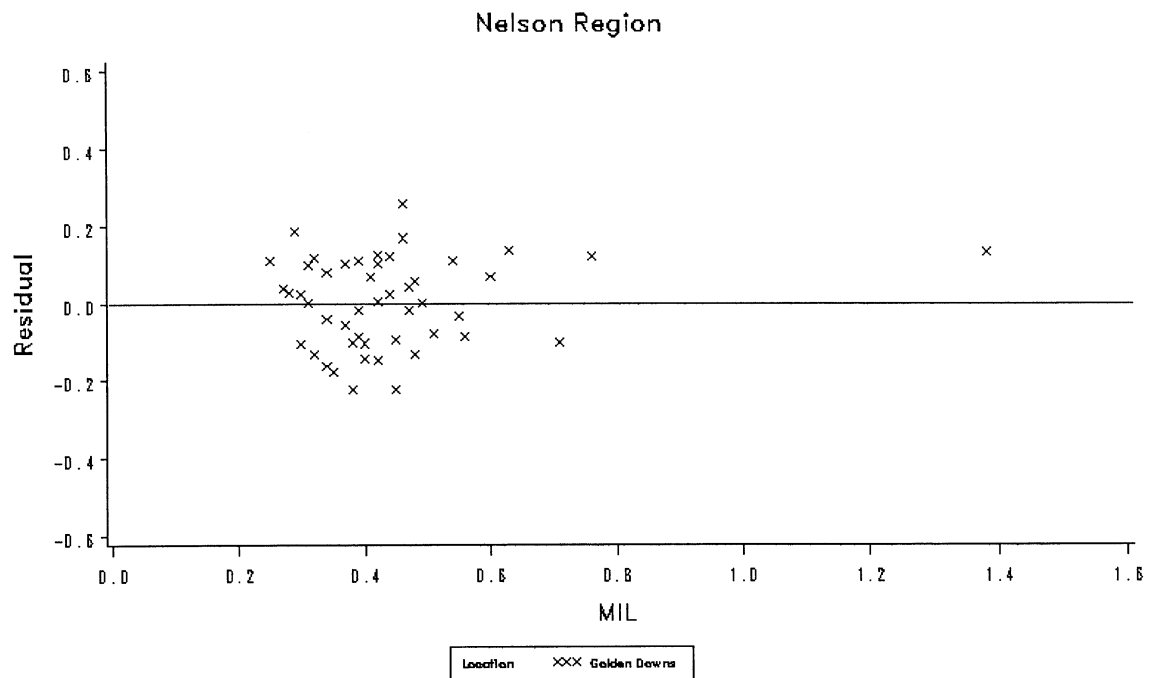


Figure 11: Errors in predicted IIX for Nelson region using the logistic sigmoidal model.

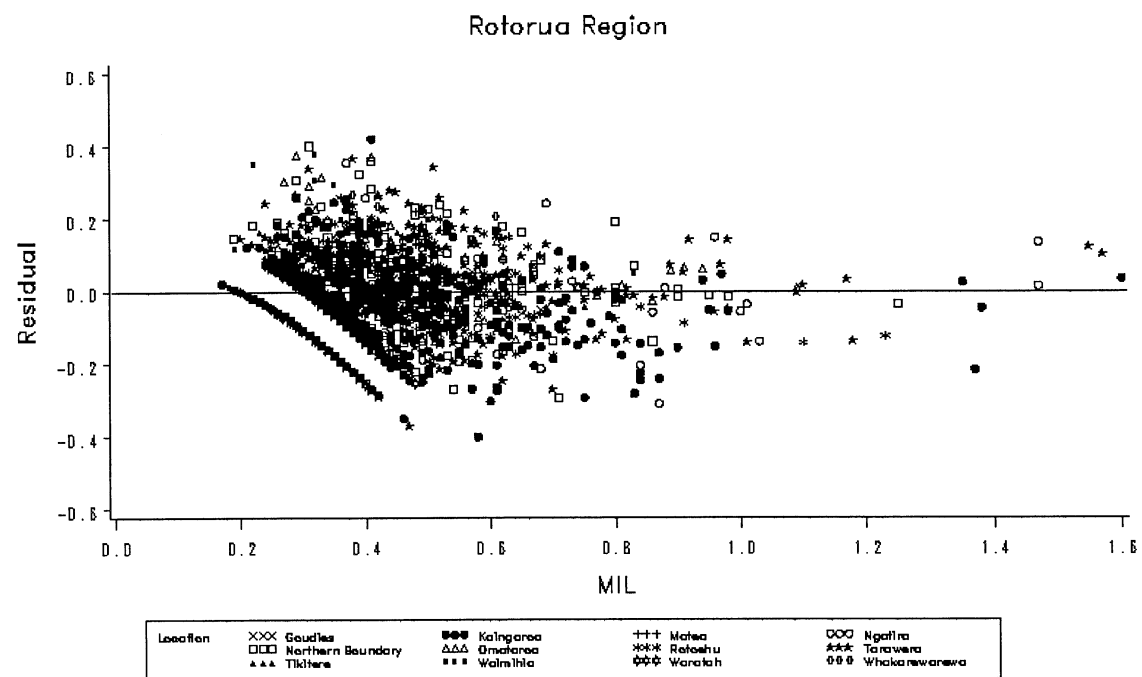


Figure 12: Errors in predicted IIX for Rotorua region using the logistic sigmoidal model.

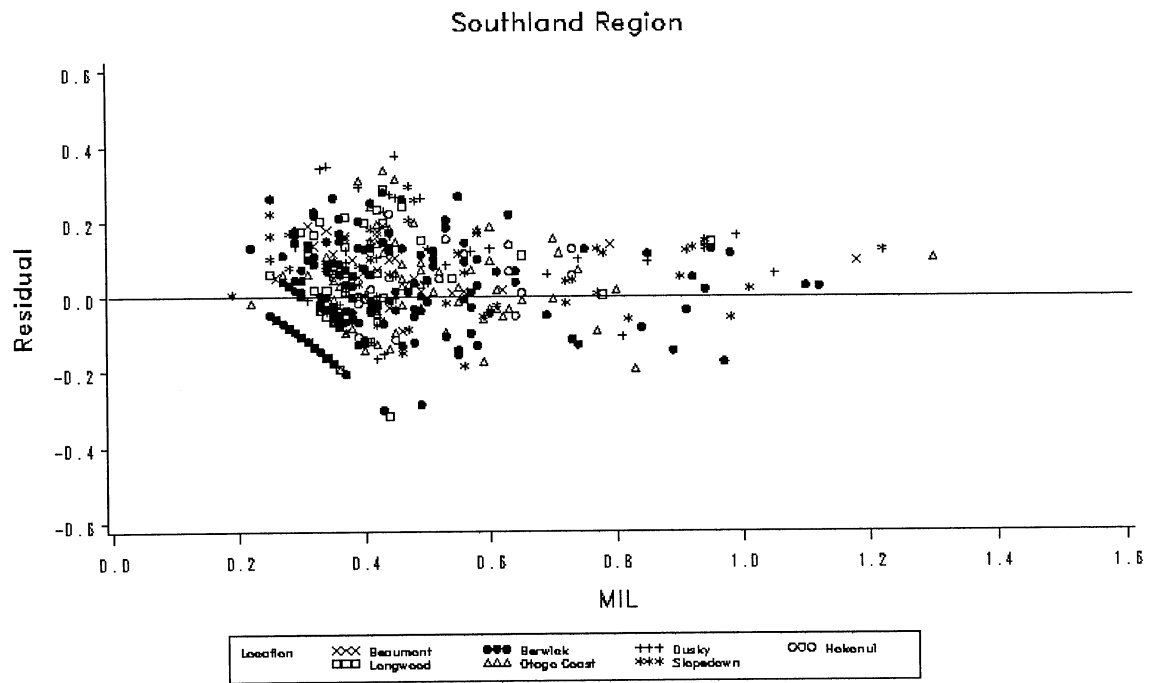


Figure 13: Errors in predicted IIX for Southland region using the logistic sigmoidal model.

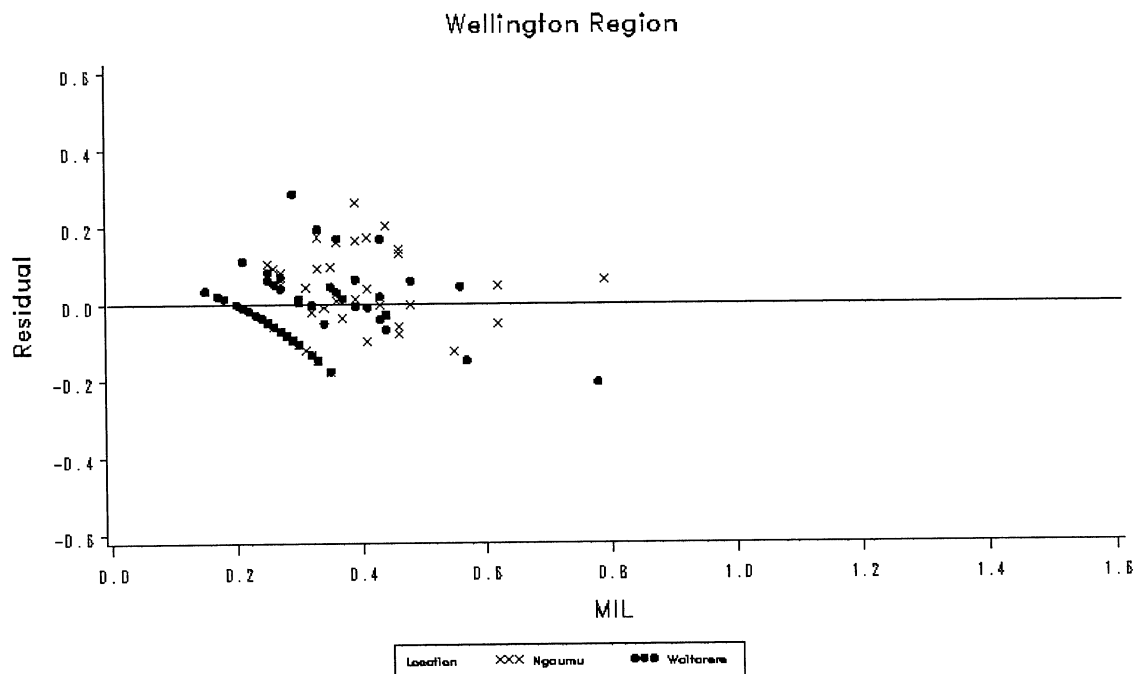


Figure 14: Errors in predicted IIX for Wellington region using the logistic sigmoidal model.

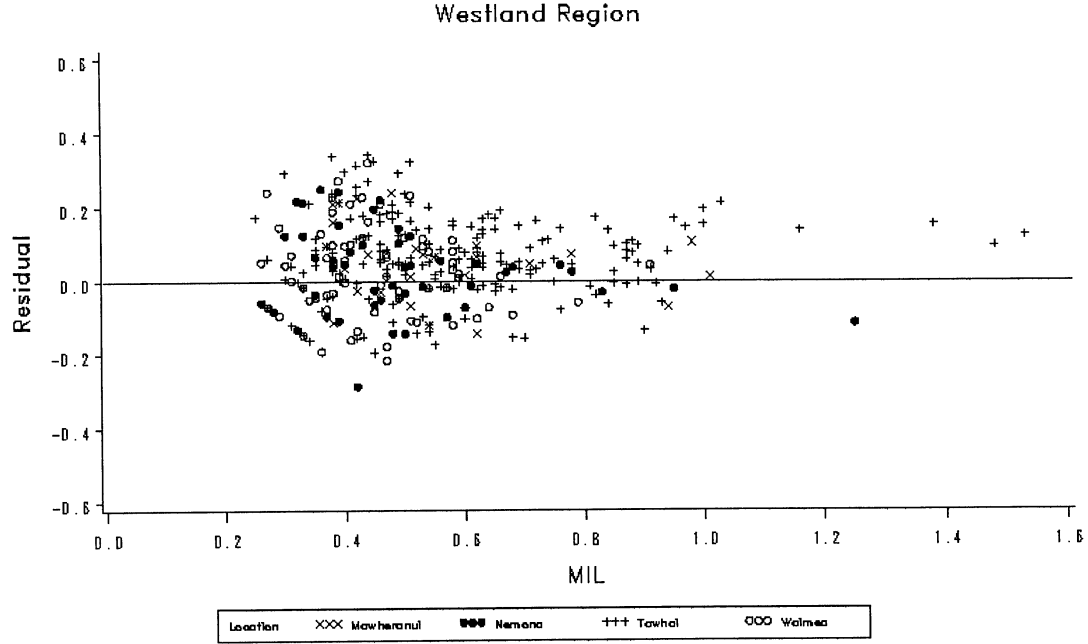


Figure 15: Errors in predicted IIX for Westland region using the logistic sigmoidal model.

Prediction of Log IIX from Stand Average IIX

The present method of prediction of individual log IIX uses a three-way distribution. Exploration of the distribution of individual log IIX (Figure 16) suggested that the fitting of an appropriate density function to the IIX data may not be possible due the high variability in the IIX distribution (Figure 16). Prediction of individual log IIX was therefore made through the adjustment of the log IIX predictive models presently in Standpak using the extended branch database.

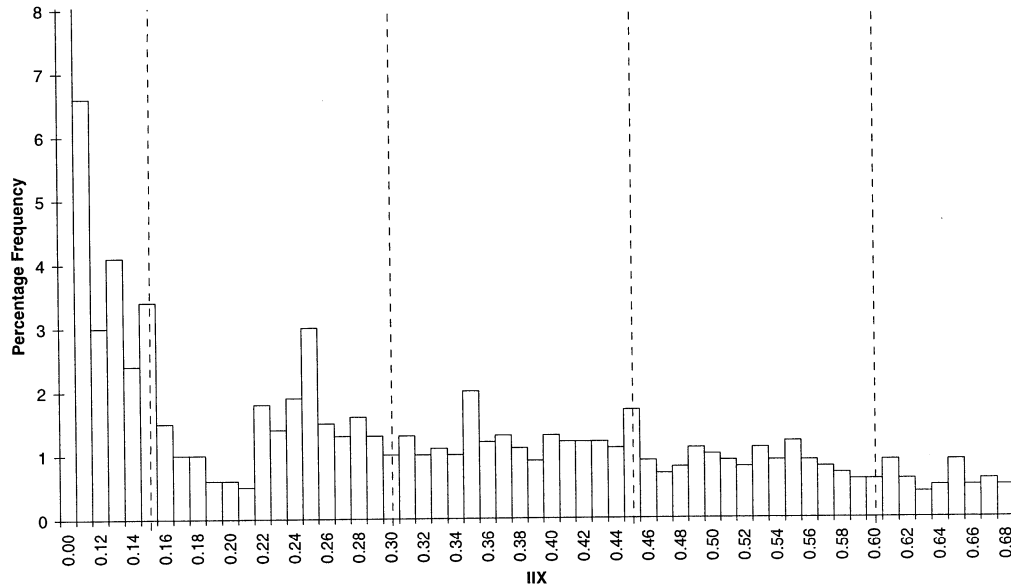


Figure 16: Percentage frequency distribution of individual log IIX for the study's dataset. Note that the percentage of logs with IIX=0 is not shown on the plot. Dashed lines indicate the user-defined *threshold* used in Table 6 below.

Percentage of Logs

The relationship between site mean IIX and percentage frequency of logs for which IIX=0 was refitted using the extended branch habit database. Site average IIX was transformed using the natural log, as for the model presently in Standpak (Whiteside unpubl.), with the form of the refitted model being (Figure 17):

$$(\%IIX=0) = -70.03\log_{10}(\overline{IIX}) - 21.5 \quad [\text{Equation 10}]$$

with the constraint: if $(\%IIX=0) < 0.0\%$ then $(\%IIX=0) = 0.0\%$

This model has an R^2 of 0.89 and a root mean square error (RMSE) of 4.61.

The equation for prediction of the percentage frequency of logs for which $IIX > \text{threshold}$ from site mean IIX was refitted using the extended branch habit database. Site average IIX was transformed using the square root, as for the model presently used in Standpak (Whiteside unpubl.). The slope (β) and intercept (α) of the 'site mean IIX and percentage IIX $> \text{threshold}$ ' relationships differ depending on the *threshold* set (Table 6 and Figure 16).

Table 6: Intercept (α), slope (β), coefficient determination (R^2), and root mean square error (RMSE) for regression equations relating percentage frequency IIX $> \text{threshold}$ to the square root of site mean IIX.

Threshold IIX	α	β	R^2	RMSE
0.15	-34.91	184.62	0.95	3.99
0.30	-53.77	183.18	0.91	5.67
0.45	-58.88	156.65	0.90	4.59
0.60	-47.02	107.29	0.75	4.81

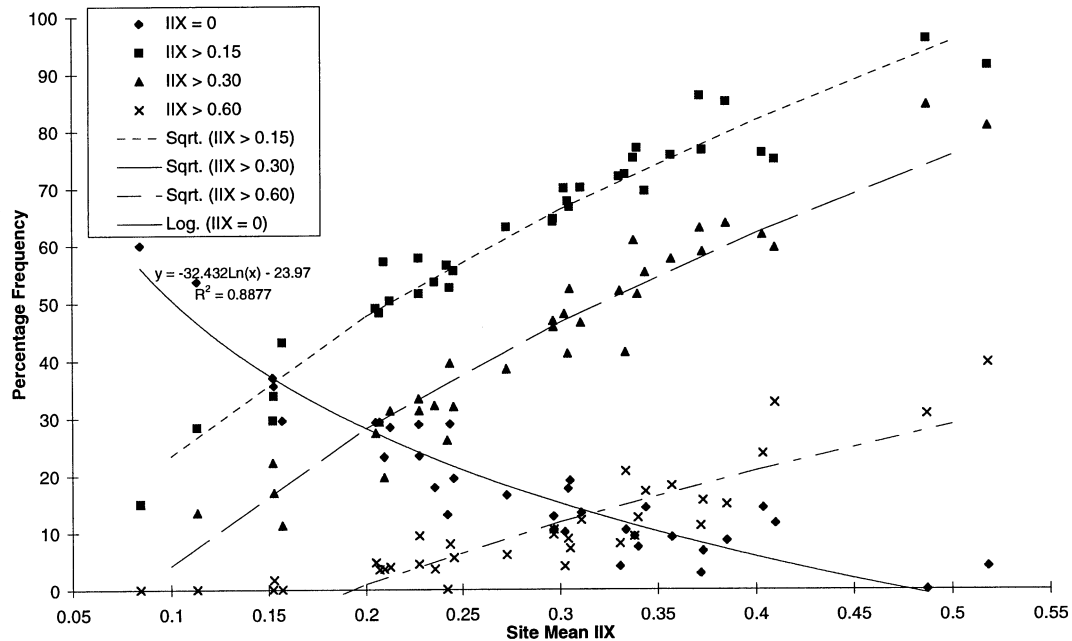


Figure 17: Relationship between site average IIX, and percentage frequency of logs with IIX=0, IIX > 0.15 IIX > 0.30 and IIX > 0.60 . Trend lines were fitted using regression analysis.

To allow users to define the *threshold* IIX, relationships between the user-defined *threshold*, and slope (β) and intercept (α) of the 'site mean IIX/ percentage frequency' relationships (Table 6 and Figure 17) were developed using regression analysis (Table 7, Figures 18 and 19).

Table 7: Intercept (α), slope for the IIX term (β_1), slope for the IIX² term (β_2) coefficient determination (R^2), and root mean square error (RMSE) for regression equations relating IIX *threshold* to the slope and intercept of the 'site mean IIX/ percentage frequency' relationship.

	α	β_1	β_2	R^2	RMSE
Slope	144.24	303.76	-597.23	0.98	9.10
Intercept	18.57	-369.03	428.99	0.94	4.86

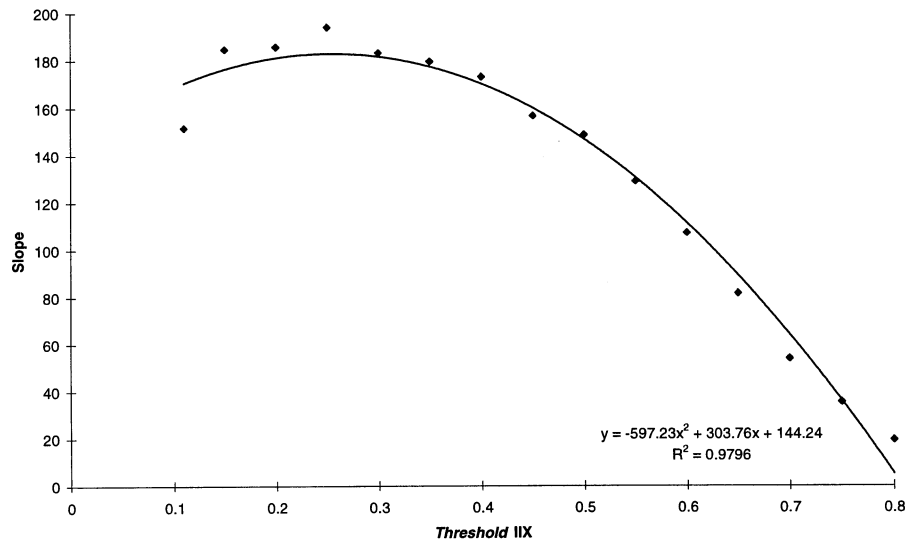


Figure 18: Relationship between *threshold* IIX and slope (β) of 'site average IIX/ percentage frequency' relationships with a regression trendline fitted.

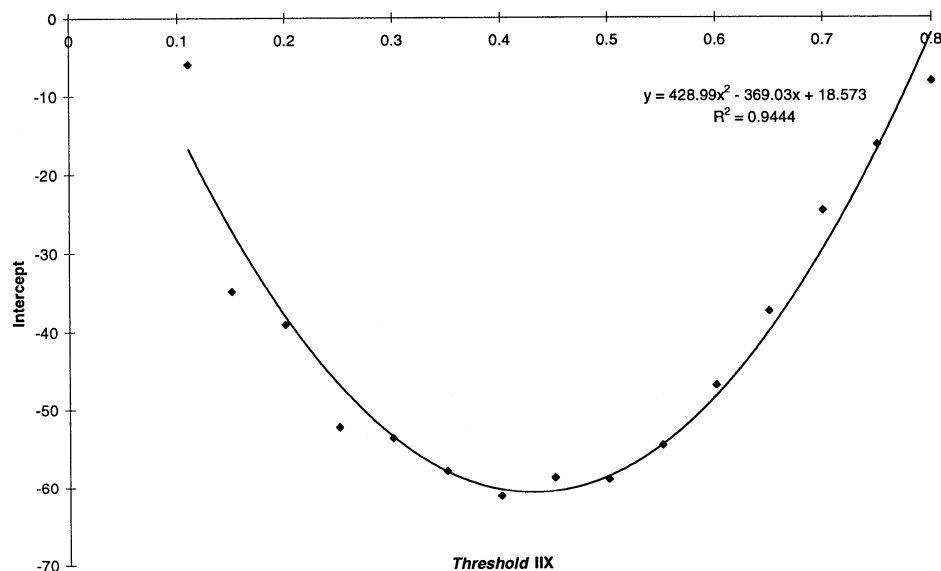


Figure 19: Relationship between *threshold* IIX and intercept (α) of 'site average IIX/ percentage frequency' relationships with a regression trendline fitted.

Mean IIX of Logs

The mean IIX for the $IIX=0$ class of the three-way distribution is 0. The mean IIX for $IIX > threshold$ was derived from the basic arithmetic equation:

$$\frac{\left[(100 \times \overline{IIX}) - \left((\% \log s(0 < IIX < threshold)) \times (\overline{IIX} \log s(0 < IIX < threshold)) \right) \right]}{[\% \log s(IIX > threshold)]}$$

Prediction of the mean IIX for the $0 < IIX < threshold$ class, was derived from three regression equations (Figure 20 and Table 8) relating mean IIX to the user-defined *threshold*, and differentiated on the basis of site internode length habit (short, medium, long). For long and medium internode length site types a linear equation was used. For short internode length sites a natural log transformation of *threshold* IIX was performed.

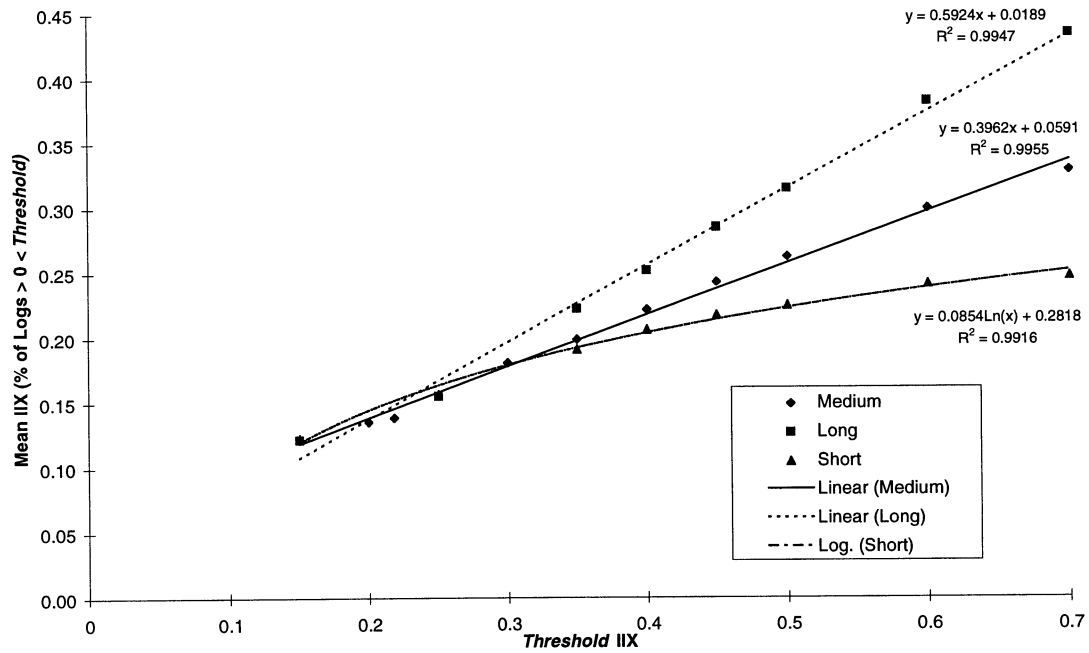


Figure 20: Relationships between mean IIX for the $0 < IIX < threshold$ class in the three-way distribution and the user-defined *threshold* IIX.

Table 8: Intercept (α), slope (β), and coefficient determination (R^2) for regression equations relating IIX *threshold* to the mean IIX (% logs ($0 < IIX < threshold$)).

	Threshold IIX	α	β	R^2
Long	linear	0.019	0.59	0.99
Medium	linear	0.059	0.39	1.00
Short	natural log	0.282	0.09	0.99

Validation

Internode length measurements from the ‘validation’ data set (Turner *et al.* 1997) were used to predict site mean IIX, percentage of logs with IIX=0, IIX > 0.15, IIX > 0.30, IIX > 0.60, and the mean IIX for the logs with $0 < \text{IIX} < \text{threshold}$ with the *thresholds* being set as 0.15, 0.30 and 0.60. The differences between actual and predicted values (residuals) were then plotted against the actual values to look for conditions under which error increased or bias was introduced. Figure 21 shows the errors in prediction of site mean IIX. Based on this plot, the error in predicting site mean IIX using Equation 8 can be expected to fall within ± 0.10 . Figure 22 shows the errors in prediction of the percentage of logs with IIX=0. Based on this plot, the model appears to predict the percentage of logs with IIX=0 to within $\pm 10\%$. Figures 27 to 29 show the errors in prediction of the percentage of logs with IIX > *threshold* with IIX > 0.15 being estimated to within $\pm 18\%$ and, IIX > 0.30 to within $\pm 15\%$. The estimate of percentage of logs with IIX > 0.60 appears to be slightly over-estimated by up to 14% indicating that estimates for high *threshold* may be slightly biased. Further validation of the models will therefore be necessary as additional internode length data is collected.

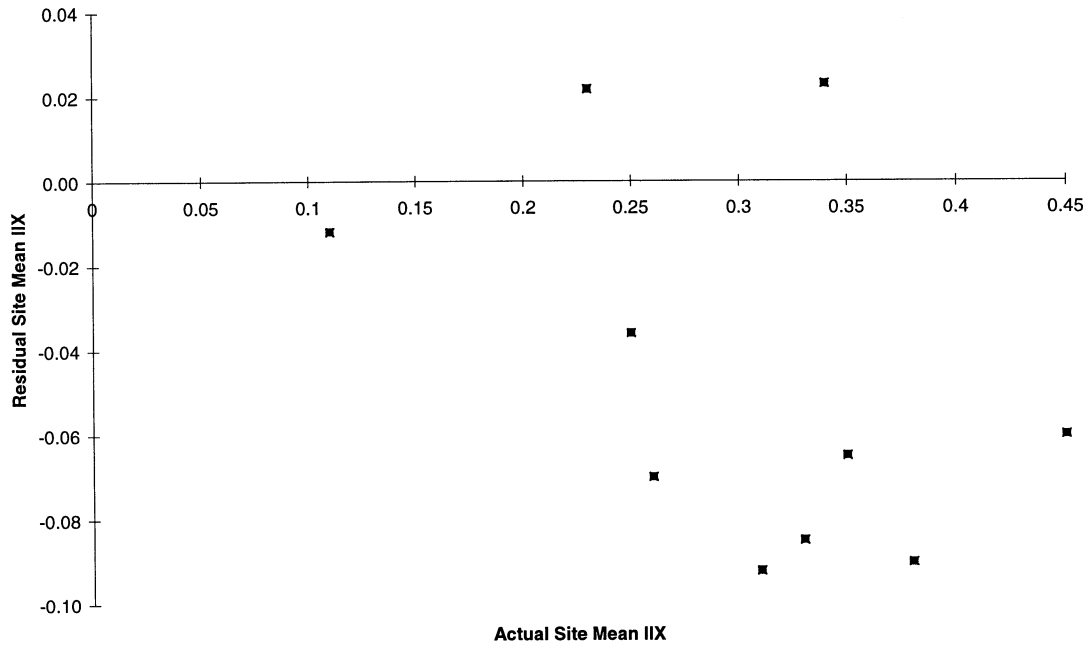


Figure 21: Errors in predicted site mean IIX using the logistic sigmoidal equation (Equation 8).

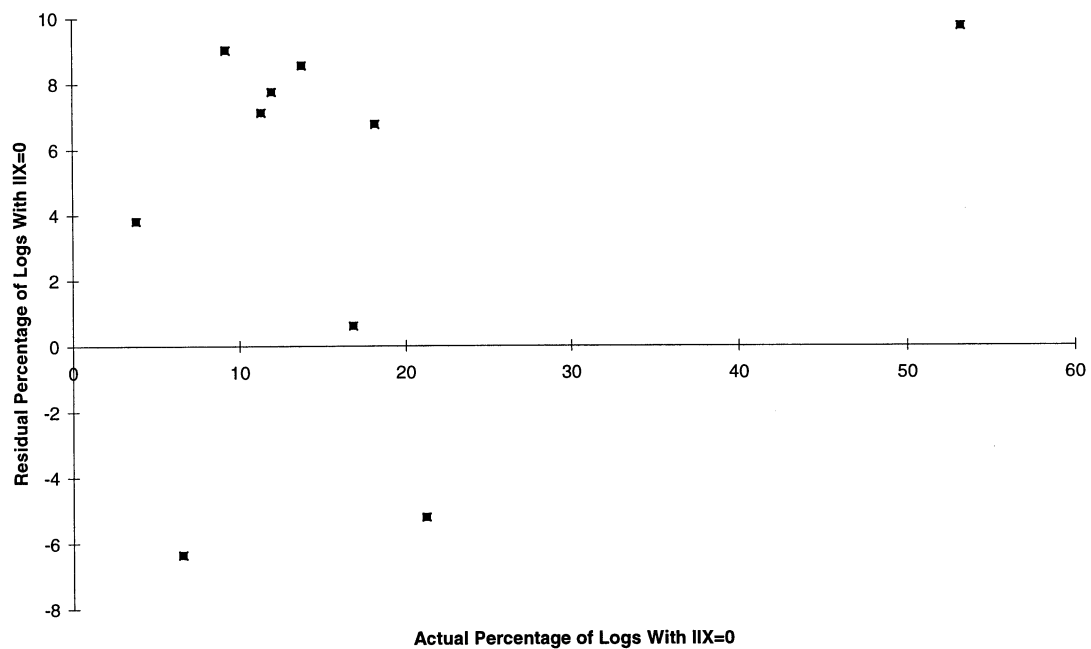


Figure 22: Errors in predicted percentage of logs with IIX=0.

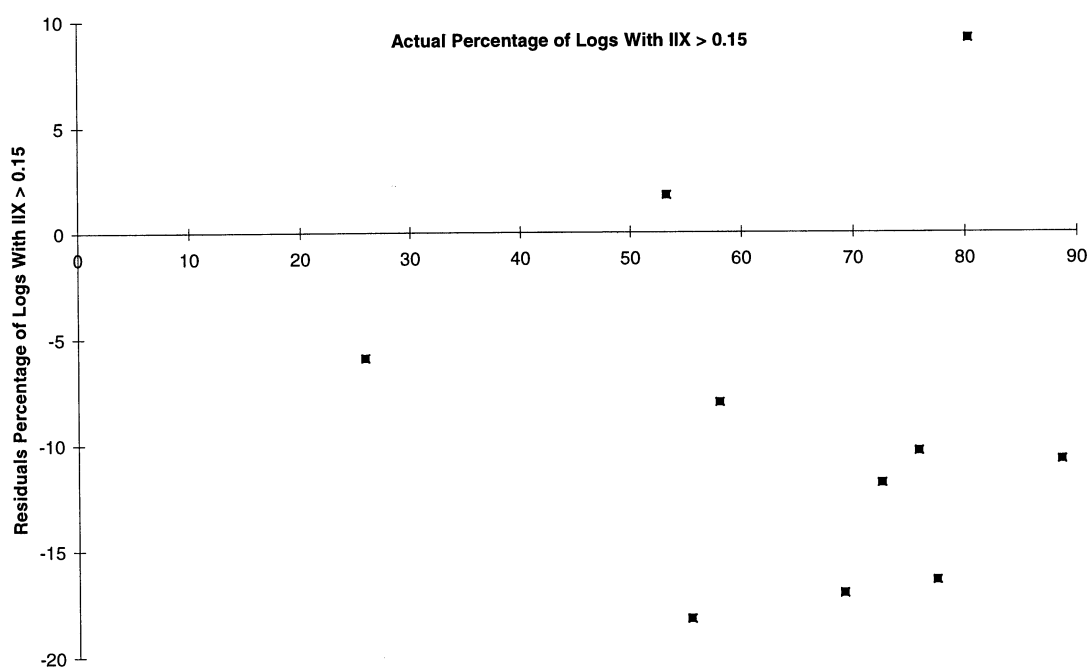


Figure 23: Errors in predicted percentage of logs with IIX > 0.15.

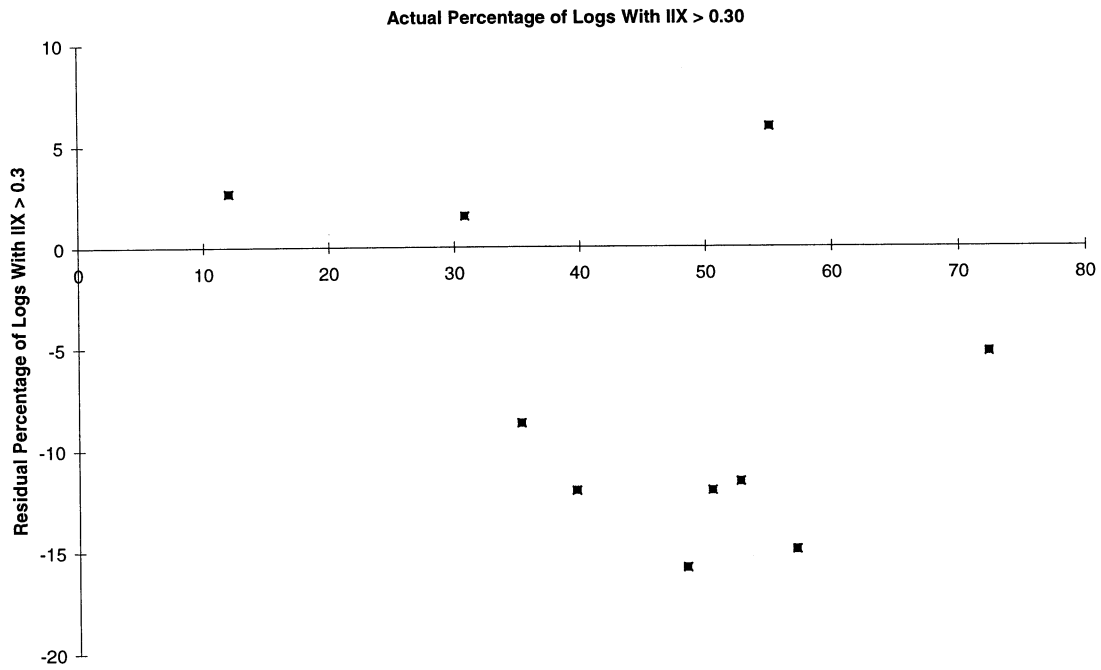


Figure 24: Errors in predicted percentage of logs with IIX > 0.30.

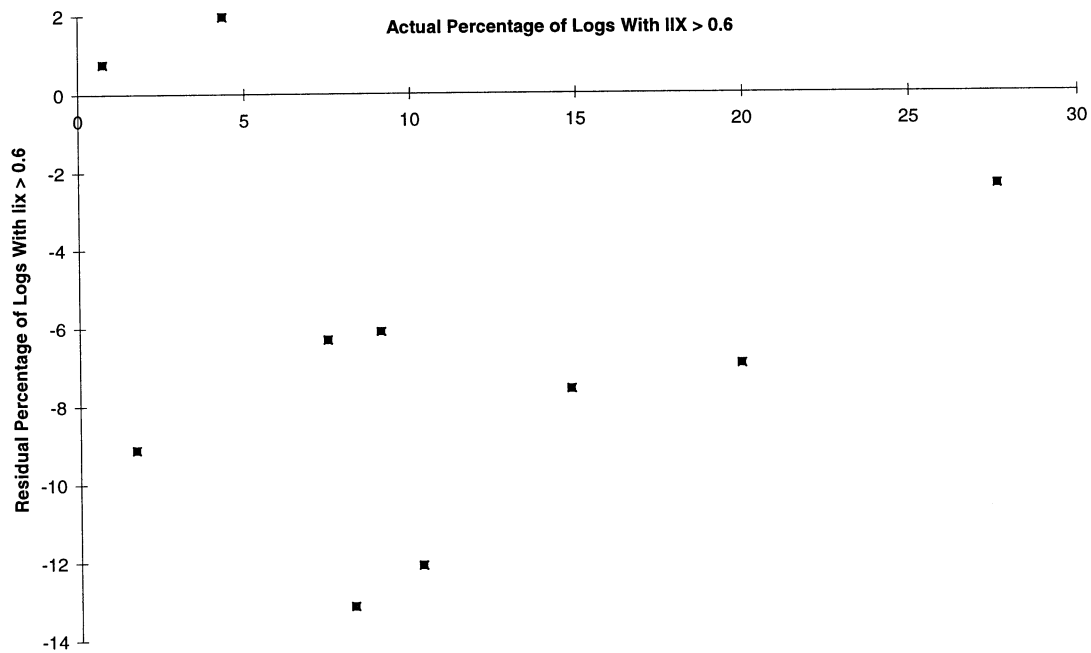


Figure 25: Errors in predicted percentage of logs with IIX > 0.60.

Based on the residual plots of estimates of mean IIX for logs with $0 < \text{IIX} \leq \text{threshold}$, the error in predicting mean IIX for logs where the *threshold* is set at 0.15 is ± 0.014 , ± 0.02 for a *threshold* of 0.30, and ± 0.05 for a *threshold* of 0.60.

Effect of Silviculture on Prediction of Individual Log IIX

Silvicultural practice, in particular stocking, has not been identified as having an effect on MIL or IIX (Siemon *et al.* 1976; Tombleson, Grace & Carson 1990; Grace & Carson 1992). Knowles and Kimberley (1992), however, using a clear cutting index which expresses the proportion of log length which is knotty, found this index decreased with increasing stocking on both forest and farm sites, ie., the amount of clear cuttings increased with increasing stocking. The potential effect on internode lengths of low stockings grown on farm sites, may influence the relationship between MIL and IIX and estimates of the percentages of logs in different groupings. To test this influence, data from two farm sites (Table 9) for which internode length measurements were made on low stocked trees was used to validate the models developed. Table 9 clearly shows low MIL and IIX for the lower final stockings compared with the higher final stockings on these two farm sites.

Table 9: Initial and final crop stockings, number of logs measured, site average internode length (MIL), and site average internode index (IIX) for individual locations.

Site	Initial Stocking (stems/ ha)	Final Stocking (stems/ ha)	No. of Logs	MIL	IIX
Tikitere	≥ 1000	≥ 200	16	0.35	0.22
	500	95	13	0.26	0.06
Whatawhata	≥ 800	≥ 183	8	0.31	0.17
	400	91	12	0.22	0.03

Internode length measurements from the two farm sites were used to predict site mean IIX, percentage of logs with $IIX=0$, $IIX > 0.15$, $IIX > 0.30$, $IIX > 0.60$, and the mean IIX for the logs with $0 < IIX \leq threshold$ with the *thresholds* being set as 0.15, 0.30 and 0.60. The error in predicting site mean IIX (Table 10) using Equation 8 does not appear to be different between farm sites with low or high final stockings. The model appears to over-predict the percentage of logs with $IIX=0$ by up to 25% on both low and high stocked sites (Table 10). Estimates of the percentage of logs with $IIX > threshold$ appears to be greatly under-estimated for the higher final stockings, by up to 37%. This is likely to be an artefact of the shorter internode lengths for low stocked trees resulting in a low percentage of logs with $IIX > threshold$. There was no bias in estimates of mean IIX of logs in the different aggregation classes.

Table 10: Residuals (actual - predicted) for high final stockings (> 183 stems/ ha) and low final stockings (95 stems/ ha) on two farm sites, Tikitere and Whatawhata.

Final Stocking	Location	IIX	% logs ($IIX=0$)	% logs ($IIX > 0.15$)	% logs ($IIX > 0.30$)	% logs ($IIX > 0.60$)
High	Tikitere	0.08	-21.5	14.8	18.5	0.0
	Whatawhata	0.08	-17.6	16.3	37.5	0.0
Low	Tikitere	0.02	-22.8	6.1	0.0	0.0
	Whatawhata	0.03	-25.0	0.0	0.0	0.0

Effect of Genetic Improvement on Prediction of Individual Log IIX

While a single equation to predict IIX from MIL is implemented in Standpak, the derivation of 4 equations by Woods and Carson (1988) for different sites and genetic material suggests that the MIL/ IIX relationship may vary for genetic material. An exploration of the effect of genetic improvement on the models developed was therefore carried out.

Non-Seed Orchard Seedlots

Comparison of the models' prediction ability was made using data from the two sites for which internode length data from both seed orchard (GF14) and non-seed orchard (GF7) seedlots were made, Omataroa and Rotoehu (Table 11).

Table 11: Number of logs measured, average internode length (MIL), and site average internode index (IIX) for GF7 and GF14 seedlots at Omataroa and Rotoehu.

GF	Location	No. of Logs	MIL	IIX
7	Omataroa	38	0.44	0.35
	Rotoehu	88	0.43	0.27
14	Omataroa	70	0.47	0.39
	Rotoehu	94	0.45	0.27

There is no clear bias in mean IIX prediction and mean IIX of logs in the different aggregation classes for either GF7 or GF14 seedlots at Omataroa or Rotoehu (Table 12). There appears to be a greater difference in estimates of percentages of logs with $IIX > threshold$ between the two sites than between the different genetic material (Table 12).

Table 12: Residuals (actual - predicted) for GF7 (non-seed orchard) and GF14 (seed orchard) genetic material at Omataroa and Rotoehu.

GF	Location	IIX	% logs (IIX=0)	% logs (IIX > 0.15)	% logs (IIX > 0.30)	% logs (IIX > 0.60)
7	Omataroa	0.08	-15.4	16.1	1.3	-8.2
	Rotoehu	0.07	-2.9	-2.1	-0.6	-5.5
14	Omataroa	0.02	-10.0	22.4	28.5	4.9
	Rotoehu	-0.02	-0.3	3.9	-2.7	0.2

Long Internode Seedlots

Models fitted for Tawhai (Figure 26) and Dusky (Figure 27) have unusual parameter estimates (Appendix I) and slightly larger RMSE (Table 5) which may be a reflection of the highly uninodal habit of trees at these sites, resulting in few logs with IIX of 0, and a large number with IIX greater than 0.8. Comparison of internode length data for uninodal¹ (Figure 28) and multinodal (Figure 29) seedlots on one site, Ngatira, was used to identify the influence of the long internode habit on the IIX/ MIL relationship (Tables 13 and 14). The parameter estimates for Dusky and Tawhai forests, and for the Ngatira long internode material suggest separate models should be used for the prediction of IIX. A number of sites, for example Longwood, while having large MIL and IIX do not have model forms which differ from those for more multinodal sites. Separate models may, therefore, be useful for the three data sets discussed, but not as a general rule for all long internode sites or material.

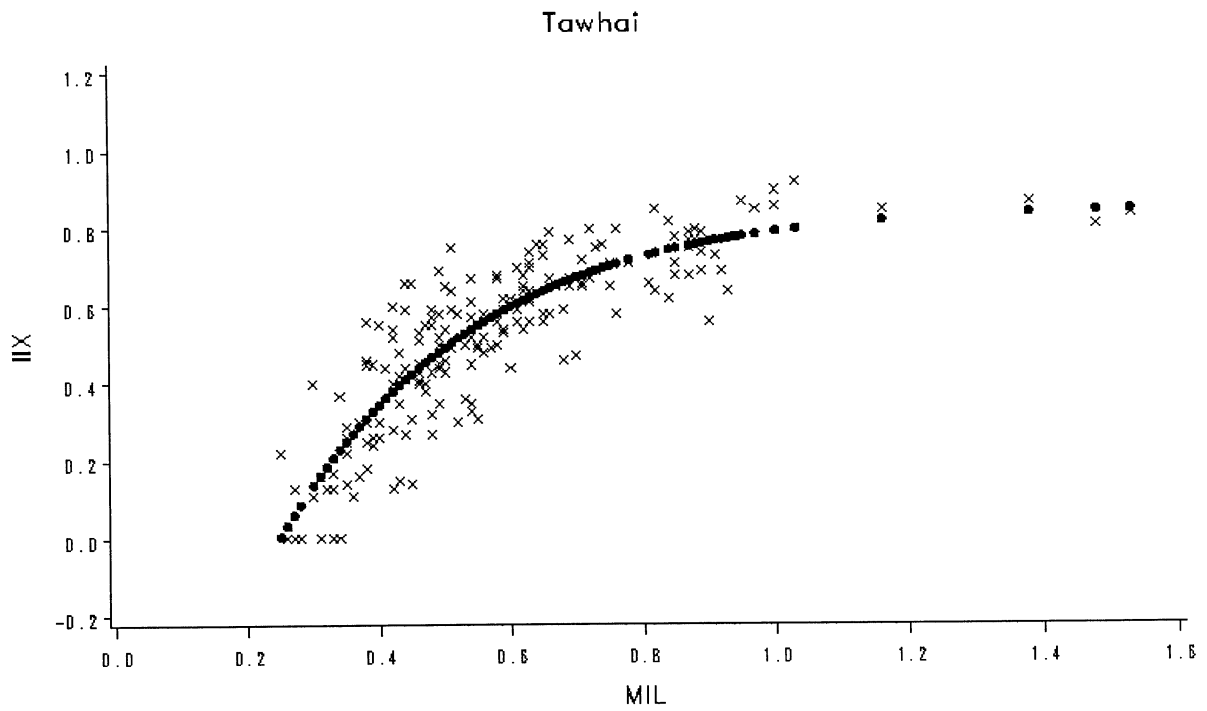


Figure 26: Logistic sigmoidal curve fitted to individual log MIL and IIX data from Tawhai.

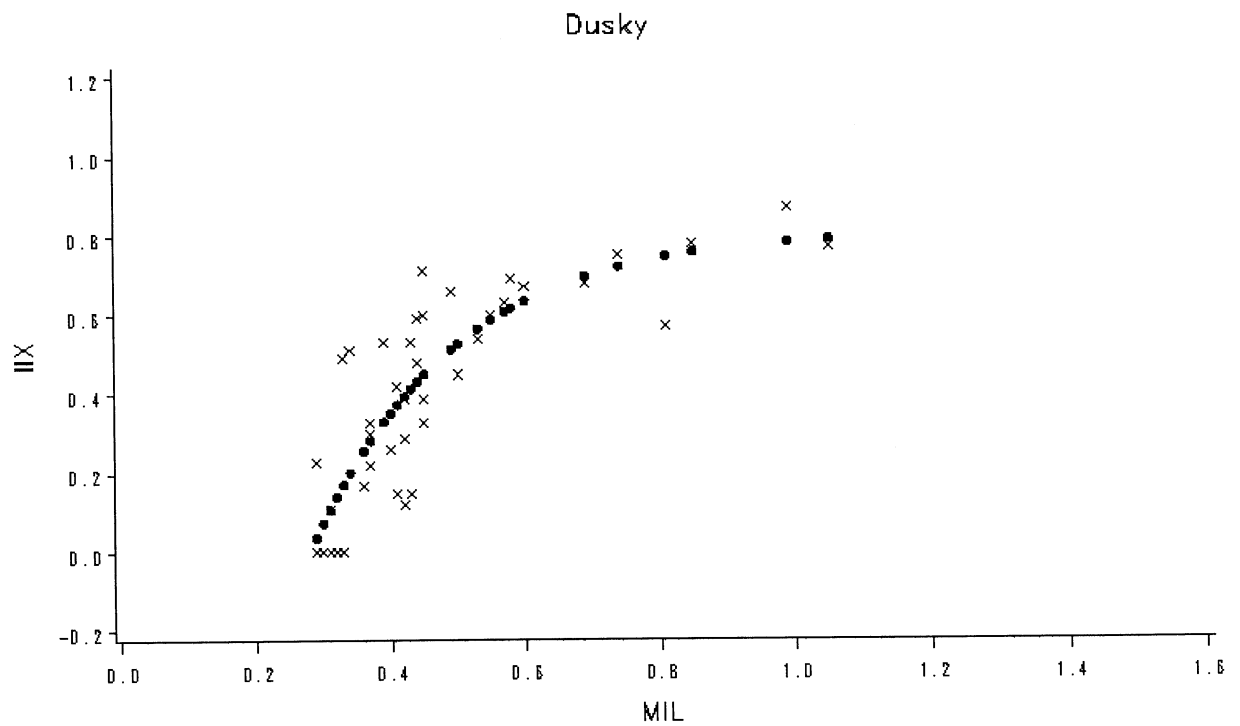


Figure 27: Logistic sigmoidal curve fitted to individual log MIL and IIX data from Dusky.

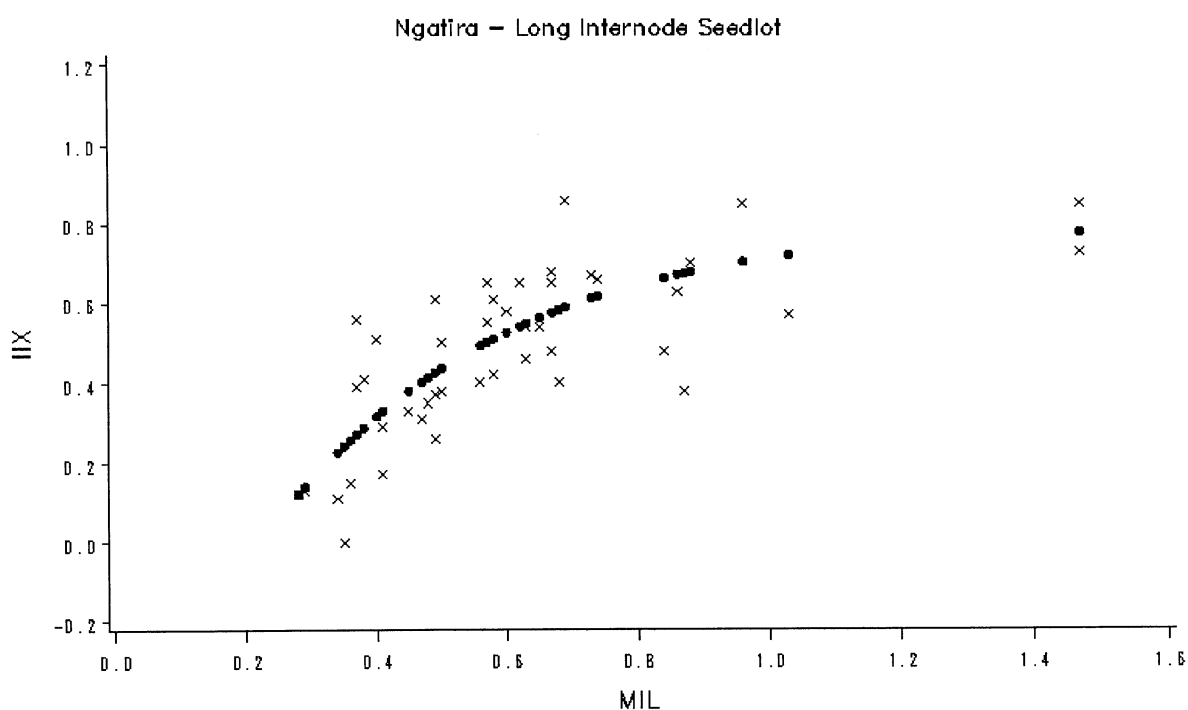


Figure 28: Logistic sigmoidal curve fitted to individual log MIL and IIX data from a long internode seedlot at Ngatira.

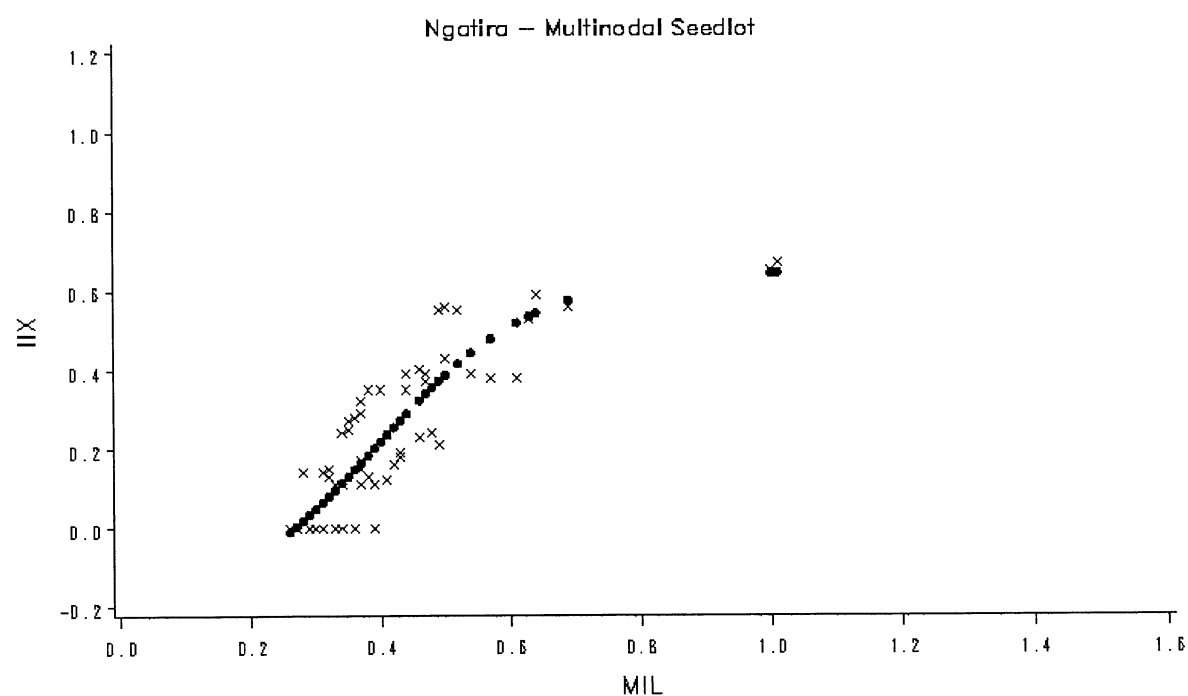


Figure 29: Logistic sigmoidal curve fitted to individual log MIL and IIX data from a multinodal seedlot at Ngatira.

There is no clear bias in mean IIX prediction, and mean IIX of logs in the different aggregation classes for either the long internode or multinodal material at Ngatira (Table 14).

Table 13: Number of logs measured, average internode length (MIL), and site average internode index (IIX) for long internode and multinodal seedlots at Ngatira.

	No. of Logs	MIL	IIX
Long Internode ¹	46	0.67	0.49
GF14	59	0.42	0.23

Table 14: Summary statistics and residuals (actual - predicted) for long internode and GF14 (multinodal) genetic material at the Ngatira farm site.

	IIX	% logs (IIX=0)	% logs (IIX > 0.15)	% logs (IIX > 0.30)	% logs (IIX > 0.60)
Long Internode ¹	-0.04	-8.7	-11.0	2.5	3.3
GF14	-0.01	-0.1	3.2	-1.4	-2.6

CONCLUSION

The development of a MIL/ IIX relationship using a logistic sigmoidal model derived from nationally aggregated data increased the accuracy of IIX prediction, particularly at high and low levels of MIL. Using the extended branch habit database a three-way distribution was refitted to the internode length data, and additional predictive equations developed to allow users to define a *threshold IIX* for grading. Simple regression equations were also developed to enable prediction of percentage of logs, and mean IIX of those logs, greater than a user-defined *threshold IIX*. The models developed appear to be reasonable predictors of site mean IIX, and mean IIX for aggregations of logs in the three-way distribution. Validation of the models using an independent data set showed that there is no bias in estimates of the percentage of logs with $0 < \text{IIX} \leq \text{threshold}$. All the models for estimating mean IIX, and percentages and means of logs with $\text{IIX} > \text{threshold}$ were not biased by stocking or genetic improvement. The models developed are to be incorporated into Standpak to enable users to predict log IIX from their own estimates of stand MIL.

ACKNOWLEDGMENTS

Firstly thanks must be given to Craig Treloar and Graeme Young of Fletcher Challenge Forests for suggesting this study be undertaken. Abbey Straker provided comments on several drafts of this report, invaluable assistance with analysis, and carried out the extraction of data from the branch database. Leith Knowles made a number of useful comments on the draft report. Jenny Grace developed many of the initial concepts explored in this study.

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APPENDIX I: LOGISTIC SIGMOIDAL MODEL PARAMETER ESTIMATES

Region	Location	Site Type	α	β	γ	λ	R ²
Auckland							0.70
	Aupouri	forest	-5.51	11.45	0.05	0.64	0.65
	Whangapoua	forest	-3.56	6.31	-0.08	1.00	0.80
	Whatawhata	farm	-94.51	260.93	0.03	0.33	0.84
	Woodhill	forest	-2.92	7.25	-0.14	0.67	0.59
Rotorua							0.71
	Goudies	forest	-9.01	20.92	0.05	0.52	0.90
	Kaingaroa	forest	-4.00	9.23	-0.08	0.68	0.73
	Matea	forest	-4.83	11.42	-0.07	0.81	0.80
	Ngatira (LI) ¹	farm	2.23	2.93	-14.23	15.03	0.65
	Ngatira (GF14)	farm	-3.21	8.12	-0.23	0.88	0.74
	Northern Boundary	forest	-2.94	7.06	-0.13	0.84	0.69
	Omataroa	forest	-3.69	7.34	0.10	0.65	0.63
	Rotoehu	forest	-5.31	12.03	-0.02	0.64	0.74
	Tarawera	forest	-5.93	12.34	0.09	0.58	0.68
	Tikitere	farm	-5.50	13.30	-0.02	0.60	0.70
	Waimihia	forest	-2.87	6.87	-0.13	0.88	0.56
	Waratah	forest	0.03	1.95	-2.12	3.39	0.65
	Whakarewarewa	forest	0.26	2.54	-2.85	4.02	0.72
Hawkes Bay							0.77
	Gwavas	forest	-4.14	9.99	-0.07	0.72	0.81
	Mohaka	forest	-4.42	9.65	-0.03	0.70	0.75
Wellington							0.74
	Ngaumu	forest	0.09	3.49	-2.27	3.14	0.72
	Waitarere	forest	-6.68	17.72	-0.01	0.48	0.73
Nelson							0.71
	Golden Downs	forest	-4.77	9.63	0.01	0.78	0.71
Westland							0.75
	Mawheranui	forest	-4.42	8.46	0.21	0.54	0.66
	Nemona	forest	-2.12	6.33	-0.29	0.99	0.66
	Tawhai	forest	4.00	3.41	-109.55	110.41	0.77
	Waimia	forest	-3.81	9.73	-0.09	0.72	0.67
Canterbury							0.76
	Ashley	forest	-2.20	6.07	-0.32	1.05	0.86
	Geraldine	forest	-4.24	9.77	-0.02	0.68	0.77
	Hanmer	forest	2.38	3.45	-17.04	17.73	0.61
Southland							0.75
	Beaumont	forest	-1.95	6.01	-0.56	1.40	0.80
	Berwick	forest	-3.67	8.64	-0.07	0.78	0.72
	Dusky	forest	3.00	4.81	-62.51	63.32	0.70
	Hokonui	forest	-4.15	10.51	-0.24	0.97	0.89
	Longwood	forest	-5.60	12.77	0.03	0.73	0.61
	Otago Coast	farm	-10.42	22.65	0.13	0.46	0.77
	Otago Coast	forest	-1.27	5.23	-0.85	1.64	0.77
	Slopedown	forest	-3.18	7.37	-0.12	0.90	0.85
National Model			-3.32	7.76	-0.12	0.84	0.74