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Theoretical Comparison of Branch Index Predictions using Different Models and Independent Permanent Sample Plots

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EXECUTIVE SUMMARY

Branches are important for trees in that they support the foliage required for photosynthesis and hence growth, but they constitute a defect from a timber perspective, with the diameter of branches determining the grade of logs and timber.

Two approaches have previously been developed for predicting branching characteristics of radiata pine. One approach (BIX models) predicts branch index directly at the stand level for different log height classes. The other approach (TreeBLOSSIM) predicts the branching pattern and branch development for individual trees. TreeBLOSSIM predictions may then be summarised to provide stand-level estimates of BIX for different log height classes.

The objective of this FFR project was to compare predictions of BIX from the two different modelling approaches.

Branch Index (BIX) was calculated for different log height classes using both the BIX models and TreeBLOSSIM, using an independent dataset. The independent dataset consisted of Permanent Sample Plots (PSPs) for which TreeD data were available for selected trees. This dataset was chosen as the TreeD provides a quantitative measure of branching characteristics of individual trees (though not BIX).

Graphs showing the predicted values of BIX indicate that the different models generally provide very similar estimates of BIX (generally within 2 cm).

A previous comparison of TreeBLOSSIM predictions with TreeD data at an individual tree level using a very similar set of PSPs indicated that the average branch diameter (averaged over the largest branch in each cluster) was predicted to within 2 cm for over 80% of the trees, and the maximum branch diameter was predicted to within 2 cm for over 50% of the trees. In many instances large differences in the prediction of the largest branch could be attributed to changes in leader and/or irregular spacing.

These results suggest that a “hybrid” approach where equations are based on an understanding of growth processes but are fitted using empirical data is an approach worthy of further research.

It is recommended that the development of TreeBLOSSIM be continued, as it is a more general “hybrid” model that can be summarised to provide estimates of BIX.

INTRODUCTION

Branches are important for trees in that they support the foliage required for photosynthesis and hence growth, but they constitute a defect from a timber perspective with the diameter of branches determining the grade of logs and timber. In this respect branches may be considered a “risk factor” associated with growing volume, as larger diameter trees tend to have larger branches, and branches over nominated diameters affect log grade.

Models that predict branching characteristics are therefore an important adjunct to growth models that predict volume. Two different models are available to predict branching characteristics of radiata pine (the BIX models and TreeBLOSSIM). These models were developed using different modelling philosophies and for different end-uses.

Branch Index (BIX) Models

The variable, branch index, is defined as the mean diameter of the largest four branches in a nominated log length where one branch comes from each quadrant¹. The field procedure¹ indicates that the quadrants should be defined with respect to magnetic North.

In collecting data for developing branch index models, it appears that sub-dominant and grossly malformed trees have been avoided¹.

There have been several iterations of equations for predicting branch index.

Iteration 1

The initial BIX model¹ was a national equation that predicted stand level BIX for the first three 5.5 m logs using the following variables:

- Stand mean DBH at age 20 years
- Site index
- Stand predominant mean height at time of last thinning before branch measurement
- Height from ground level to top of the log length

The equation was derived using data from 25 stands which did not contain genetically improved material¹.

Iteration 2

A revision of the above model² provided separate equations to predict the stand level BIX for the first three 5.5 m logs.

For log 1, BIX was predicted using the following variables:

- Initial stocking
- Stand mean DBH at age 20 years
- Height at final thinning or clearfelling (definition of height not specified)

For log 2, BIX was predicted using:

- Site index
- Stand mean DBH at age 20 years
- Height at final thinning or clearfelling (definition of height not specified)

For log 3, BIX was predicted using:

- Site index
- Stand mean DBH at age 20 years
- Rotation age
- Final stocking
- Height at final thinning or clearfelling (definition of height not specified)

These equations were derived using data from 40 genetically unimproved stands and covered a wider range of regimes than used in Iteration 1.

The equations and coefficients provided for log 2 and log 3 are the same as the code in STANDPAK.

The equation provided for log 1 is the same as the code in STANDPAK, but the coefficients are slightly different. No documentation has been found for the log 1 coefficients in STANDPAK.

Iteration 3

A regression model for predicting stand mean BIX in second logs of stands managed to a direct sawlog regime was developed for the Plantation Management Cooperative³. The predicted value applies only after the green crown height has risen above the top of the second log.

Second log BIX was predicted using:

- Stand mean DBH at age 20 years
- Site index
- Predominant mean height at time of last thinning
- GF factor

The model was developed using data from 26 stands covering a range of sites, stockings and seedlots.

This equation is included in STANDPAK with the GF factor set to 14.

Iteration 4

Equations that predict BIX for any log height class were developed in 1996⁴, but the equations have not previously been documented.

The model utilises the Second Log BIX Model (iteration 3) to predict BIX in the second log, and then adjusts this prediction to the butt log (log 1) and upper logs (logs 3 and higher) using the two variables final stocking (FSPH) and height of last thinning (HTTHIN). These equations were derived using all data available in 1996. There were data from 101 stands, mostly measured to the third log, but in some stands up to the fifth log.

The model predicts BIX in standard 5.5 m log height classes using the following steps:

- 2nd log BIX (BIX2) is predicted using the above 2nd Log BIX Model.
- 1st log BIX is predicted using:
$$BIX1 = BIX2 \times (1.61 - 0.947^{(FSPH/10)})$$
- Upper log (3rd and higher) BIX is predicted using:
$$BIX_{upper} = BIX2 \times (0.622 + 0.0361 \times HTTHIN + 0.000953 \times FSPH - 0.0000769 \times HTTHIN \times FSPH)$$

There is an override (in the software implementation) to the above equations which may reduce the predicted BIX. This override is particularly relevant for upper logs where the branches are still growing.

- MAXBIX is calculated for each log height class using:
$$MAXBIX = 1.41 \times SED^{0.543}$$

where SED is the mean small end diameter (cm) of the height class at the rotation end. This is derived in STANDPAK using a taper function.
- For each height class, if predicted BIX is greater than MAXBIX, then MAXBIX is used in place of predicted BIX

This override has not been included in the analysis below, which were carried out by directly implementing the BIX equation in SAS.

BLOSSIM Model

Note: BLOSSIM is the branch model, TreeBLOSSIM is the branch model linked to an individual tree distance-independent model.

The BLOSSIM model was designed and developed to link with both individual-tree distance-independent growth models and inventory data in order to grow inventory measurements forward in time. In addition it was designed to provide sufficient detail of branching patterns to be able to link with sawing simulators such as AUTOSAW¹³.

Development of a distance-dependent (spatially explicit) branch model was not appropriate at the time of development, as the growth models were distance-independent, but ability to map tree crowns using LIDAR data means that a distance-dependent approach to modelling should now be investigated, particularly as there is evidence that branch diameters are influenced by spacing in a given direction^{5,6}.

The BLOSSIM model can be classified as a “hybrid” model in that it considers the underlying structure and development of tree crown, but the model equations are derived using measured data. The model is hierarchical in structure in that there are functions at the following levels:

- The tree
- The annual shoot
- The branch cluster
- The branch

The functions at each level are:

Tree Level

- Probability that a tree has reached reproductive maturity (based on first occurrence of stem cones).
 - Stem cones were included in the model as they usually leave a hole in the stem.

Annual Shoot Level

- Number of branch clusters in an annual shoot.
- Relative position of branch clusters within the annual shoot.
 - These functions, together with branch angle enable the prediction of internode length. They are also relevant for sawing simulation.

Cluster Level

- Number of branches and stem cones in a cluster.
- Azimuthal location of branches and stem cones.
- Azimuth angle of largest branch.
 - These functions give the position of branches and stem cones, and are particularly relevant for sawing simulation.

Branch Level

- Branch potential.
- Branch diameter development through time.
- Branch angle.
- Occurrence of bark encasement due to branch mortality.
- Occurrence of bark trapped above a branch that is not due to branch mortality.
 - These functions provide estimates of branch diameter through time.

These functions have been linked with an individual-tree distance-independent growth model to create TreeBLOSSIM. There have been two main iterations:

- Version 1⁷

- This version was developed using a very small number of datasets.
- Version 3⁸
 - This version is designed for 850 seedlots only, and was developed using a larger number of datasets.

Trees with obvious malformations were avoided when collecting data for the development of the BLOSSIM functions. Within a site, sample trees were selected to cover a range of tree DBH.

Comments on Model Development

Models contain mathematical equations that predict one variable from one or more other variables. Models can be developed at different levels of complexity. Underlying any model is DATA, and the reliability of any model will depend on the coverage in the dataset and the way the mathematical equations have been constructed. A particularly important point to remember is that the reliability of a model outside the range of data used to build the model cannot be guaranteed, but a model that takes into account the underlying biology is more likely to perform better at the extremes than a regression model that takes no account of the biology.

The important differences between the BIX models and TreeBLOSSIM are outlined below:

- TreeBLOSSIM has taken the underlying biology of branch development into account and predicts the branching pattern at an individual tree level, whereas the BIX models are regression equations predicting stand level BIX from stand level variables.
- The database for the development of TreeBLOSSIM was from improved GF14 trees. The database for Iterations 1 and 2 of the BIX model was from unimproved stands. The database for Iterations 3 and 4 contained a mix of seedlots.
- There are regional coefficients for the TreeBLOSSIM model, but only national coefficients for the BIX models.
- The BIX models predict only the average diameter of four branches in a log (largest branch from each quadrant), whereas TreeBLOSSIM predicts all branches.
- Sub-dominant and grossly malformed trees were not included in the dataset used to develop the BIX models. (Trees included were classified as crop trees).
- Sub-dominant trees were included in the development of TreeBLOSSIM functions.
- Clusters with obvious malformations were excluded in developing TreeBLOSSIM functions.
- A recent examination of some TreeD images by C. Inglis in November 2009 indicates that crop trees may contain malformations that would have been excluded in the development of TreeBLOSSIM.

Previous Studies Examining the Performance of Branching Models

An SGMC project⁹ investigated the possibility of using TreeBLOSSIM to predict branching for the plots in the BIX database. However the relevant data were not available to run TreeBLOSSIM for plots in the BIX datasets.

The performance of TreeBLOSSIM itself has been tested extensively using TreeD¹¹. TreeD images are usually taken from one position for each selected sample tree. This gives a 180° view of the stem. Depending on the branch orientation with respect to the camera position, many of the branches originating on the hidden half of the stem will be visible on the image as the branch will extend past the stem. TreeD images have been analysed to provide the height to each cluster and the diameter of the largest branch in each cluster, as this is comparable with the branch data collected during inventory. BIX has not been extracted from TreeD images. It is not recommended because we do not know the orientation of North with respect to the TreeD image, and we do not know the position of the branch/stem junction for branches on the hidden half of the stem.

TreeD studies^{6,10} have provided datasets covering a range of site qualities, silvicultural treatments and levels of genetic improvement within each growth modelling region. Further datasets are required to provide a comprehensive dataset (see Appendix 1, Table 1). In general TreeBLOSSIM

performed well. By examining the TreeD images to determine the branches that gave large model residuals, it was identified that larger than expected branches occur when the tree stem is damaged, for example by wind, and there is a change in leader; and that larger than expected branches occur when the spacing is irregular. The latter issue could easily be resolved using distance-dependent modelling. However the former issue requires further research.

Approach Taken in the Current Study

The objective of this study was to compare the performance of the above BIX and TreeBLOSSIM branch models.

The approach taken was to predict stand level branch index using both the BIX models and TreeBLOSSIM for a series of Permanent sample Plots (PSPs) for which TreeD data were available.

The advantage of this approach is that, while we do not have BIX data for these PSPs, we do have an indication of how well TreeBLOSSIM predicts branching for selected trees in the PSP.

METHODS

Models Used

Version 3.1 of TreeBLOSSIM was used for this study. This gave identical estimates of branch diameter compared to Version 3.2 that is currently being implemented in Forecaster. The equations for predicting BIX were coded directly in SAS. This approach was selected as it provides a clean test of the equations.

As mentioned in the background, the documented and implemented equations for Inglis (1986) Log 1 BIX differ very slightly. These equations have been compared in this study. The documented equation is labelled as Log 1 Inglis. The implemented equation is labelled as Log 1 Atlas.

Data Used

Only PSPs planted with GF14 seedlots were used for this study, as the equations within TreeBLOSSIM are designed for this seedlot. Fifty-nine PSPs from 23 experiments¹² (Appendix 1) were selected. For each plot, several variables needed to be calculated and/or decisions made to enable the branch models to be run. These are discussed below.

Predicted Diameter at Breast Height at Age 20 years

As with any component of the branch index models, it was important to incorporate the best estimate for the variables within the model in order to obtain the most accurate branch index predictions.

There were a limited number of sites where the diameter at breast height was measured at exactly the age of 20 years. However, as there was information on diameter at breast height for several different ages, it was felt that applying a regression model to the data would be a suitable way of using the data to predict what the diameter at breast height would have been at age 20 years.

The information that was already available for each site was the mean diameter at breast height at a various range ages for each site. Linear and non-linear regression models were fitted to the data. On analysis, the non-linear regression models were shown to have the best fit with the data. A unique regression model was fitted to each site in order to increase the accuracy of the predictions being made.

The Shapiro-Wilk test appeared to show that the residuals of the data came from a normal distribution, thus satisfying the assumption of normality. The F-tests for the regression models all provided extremely strong evidence against the null hypothesis that age is not related to mean diameter at breast height with all of the p-values being less than 0.0001. The regressors within all of the models were shown to be significant with the exception of the intercepts of the sites FR8/0 25/14, FR54/0 22/14, FR54/0 29/15 and CY421/1 9/21.

The R² values for all of the regression models were all shown to be at least 0.97, which indicates that at least 97% of the variation in diameter at breast height is explained for each site by these models. From this information it appears that these models will be fairly accurate in making predictions.

Initial Stocking

Initial stocking is a component of both the second iteration of the branch index model² and the TreeBLOSSIM model⁸. It was important to consider a consistent base value for initial stocking. There were two differing initial stocking values to choose from; nominal initial stocking, the stems per hectare that had been intended for each site, and actual stocking at first measurement. As these models were being developed for forestry companies, it was important to evaluate the effectiveness and the applicability of these models in the way that had been intended to be used commercially. As such, it was felt that it would be more suitable to use nominal initial stocking due to the accessibility of this variable for companies compared to the actual initial stocking.

Final Stocking

Final stocking was another variable used in Iterations 2 and 4 of the branch index model and the TreeBLOSSIM model⁸, so uniformity throughout the models was essential to producing practical results. There was a choice between using nominal final stocking, actual final stocking after thinning and the actual final stocking at last measurement. The decision was made to use the actual final stocking after thinning in the models. Again, it was important that the results obtained from this study reflect the results that would be obtained with commercial use in a company. Consequently, this decision was based on the assumption that the data for actual final stocking post-thinning would be more reasonable to use commercially, than actual final stocking at last measurement. Additionally it was felt that this variable would provide a more accurate and flexible branch index than nominal final stocking.

Mean Crop Height at Thinning

Mean crop height at final thinning is included in all the iterations of the branch index model. In this study there were several sites that had not been thinned. In this situation it was suggested that a default height of 20 metres be used¹. The decision to use 20 m instead of the actual height was based on commercial use of the branch index model and on maintaining similarities between the results that this report obtained and the results that the Inglis and Cleland model¹ intended to obtain.

Random Seed

The TreeBLOSSIM model⁸ uses a random seed which affects the generated outcome of the branch index.

In order to explore the effects and to check to see whether chosen seed of this model distorts the TreeBLOSSIM branch index result in any way, twenty other seeds were chosen to compare the branch index results against. The twenty seeds trialled were based on 7-digit prime numbers. Each seed was run through TreeBLOSSIM on a single site, keeping all other variables the same.

The results are displayed in Appendix 2, as side-by-side box plots. The random seeds all appear to produce a similar mean value of BIX for the plot and a similar range in BIX values across individual trees. This indicates that one simulation using the supplied random seed is appropriate and does not appear to distort the branch index results within the TreeBLOSSIM model.

RESULTS

Comparison of BIX Predictions

The BIX models predict a plot level value directly. TreeBLOSSIM predicts branching patterns for each tree. These were summarised to give a BIX value for each log on each tree and then a mean BIX was calculated for the plot. This approach enabled BIX models and TreeBLOSSIM to be compared. The predicted values of BIX are presented according to region and log, with the graphs demonstrating the similarities and differences between the different models for each site (PSP) considered (see Appendix 3). As the silviculture varies between sites (PSPs), the important points to examine on the graphs are whether the predicted BIX is similar for each site, and the consistency of model performance across sites within a region.

The graphs show predictions using 3 different models.

Predictions from TreeBLOSSIM are labelled:	Tree Blossim
Prediction from Iteration 2 of the BIX models are labelled:	Inglis
Predictions from Iteration 3 or 4 of the BIX models are labelled:	PM

For Log 1 there is an additional model labelled “Atlas”. This uses the same model formulation as Iteration 2 (Inglis) but the coefficients are those implemented in Atlas software. The predictions are essentially identical. It is recommended that the documented coefficients be implemented in ATLAS software.

One would not expect different models to give identical answers. The graphs (Appendix 3) indicate that in general there are only small differences (approx. 2 cm) in the predicted BIX for a given site (PSP). Overall, there was a tendency for all the models to fluctuate in the same direction from site to site, showing that the general trends of these models were very similar. These results are pleasing to see, given the different philosophies used in model development, but not unexpected as measurements of radiata pine branch diameter are the basis for all three models – though the databases and the selection criteria for measuring a tree are different.

For log 1, the PM model often predicts larger values of BIX. This is particularly noticeable for the Hawke’s Bay, Clays, Central North Island, and Southland Regions. This model is interesting in that initial stocking is not used to predict BIX. TreeBLOSSIM model tends predict lower values of BIX. This is particularly noticeable in the Clays, Nelson and Central North Island Regions. One possible reason may be that TreeBLOSSIM was developed using GF14 (‘850’ breed) data; this breed is expected to have smaller branch index than unimproved trees¹⁴.

For log 2, all three models produce similar results.

For log 3, all three models produce similar results. TreeBLOSSIM predictions tend to be slightly lower in the Hawke’s Bay and Nelson Regions.

Notes on Comparison of TreeBLOSSIM with TreeD Data

Graphs⁶ (reprinted in Appendix 4) provide a high level summary of the comparison of TreeBLOSSIM predictions with TreeD data for 259 trees from 54 PSPs with a GF rating of 14, and includes most of the PSPs used in the current study. Two cm was considered an acceptable difference considering measurement and modelling error. Appendix 4, Figure 1 shows that for the majority of trees, TreeBLOSSIM predicts the average branch diameter to within 2 cm. (The bar charts labels are the mid-point value for each bar, the boundaries for the bars are the midpoint value between the adjacent labels). Appendix 4, Figure 2 shows that for over 50% of the trees, TreeBLOSSIM predicts the maximum branch diameter to within 2 cm. The maximum branch diameter is predicted to within 6 cm for approximately 80% of the trees. Examination of the tree images has indicated that many of the large differences are the result of some stem defect, rather

than being part of the regular branching pattern of the tree. These large branches also impact on the mean value for a given tree. Taking these factors into account, it is considered that TreeBLOSSIM has provided realistic predictions of regular branching patterns, but it is acknowledged that it does not predict large branches that are the result of malformation.

CONCLUSION

Two approaches have previously been developed for predicting branching characteristics of radiata pine. One approach (BIX models) predicts branch index directly at the stand level for different log height classes. The other approach (TreeBLOSSIM) predicts the branching pattern for individual trees. These may then be summarised to provide estimates of BIX for log height classes.

This study compared predicted BIX for different log height classes for a set of independent Permanent Sample Plots (PSPs) for which TreeD data were available for selected trees, to provide an indication of branching. Graphs showing the predicted values of BIX from the individual models indicate that the models generally provide very similar estimates of BIX (generally within 2 cm).

A summary of TreeBLOSSIM predictions with TreeD data indicate that TreeBLOSSIM predictions are generally realistic, but that it does not predict large branches caused by stem defects.

These results suggest that a “hybrid” approach where equations are based on an understanding of growth processes but are fitted using empirical data is an approach worthy of further research.

It is recommended that the development of TreeBLOSSIM be continued as it is a more general “hybrid” model that can be summarised to provide estimates of BIX. Further development of TreeBLOSSIM should include the ability to predict the occurrence of stem damage and how branches respond to stem damage. Other enhancements would be to provide better prediction of internodal material, by modifying the function predicting the relative position of branch clusters in an annual shoot (mean positions are calculated at present); and making the model distance-dependent to allow for irregular spacing patterns. Further data collection for function development and testing is also recommended given the small datasets available.

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APPENDICES

Appendix 1. Sites used to compare radiata pine branch models

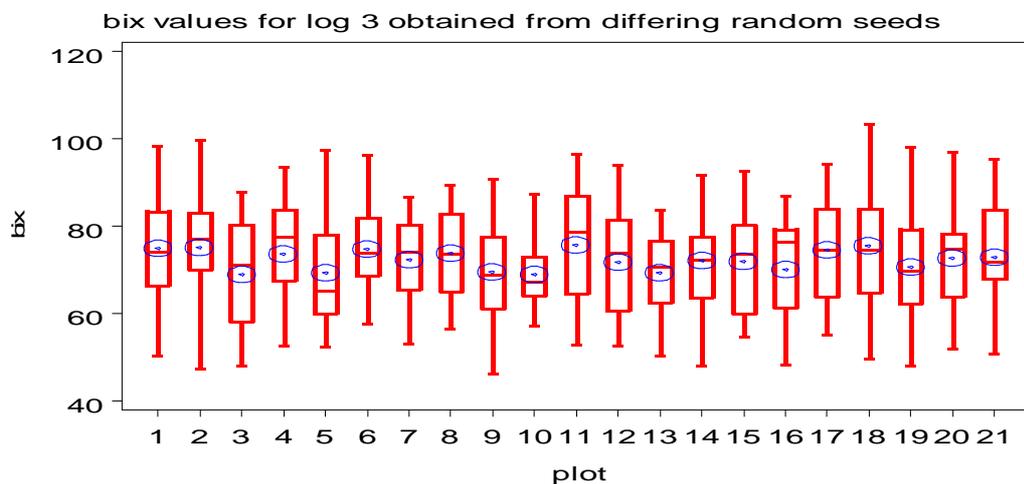
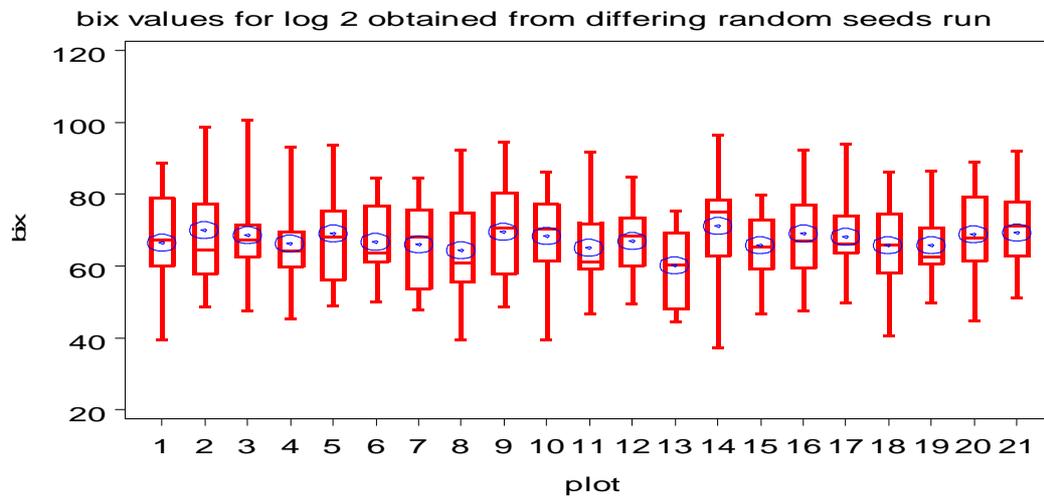
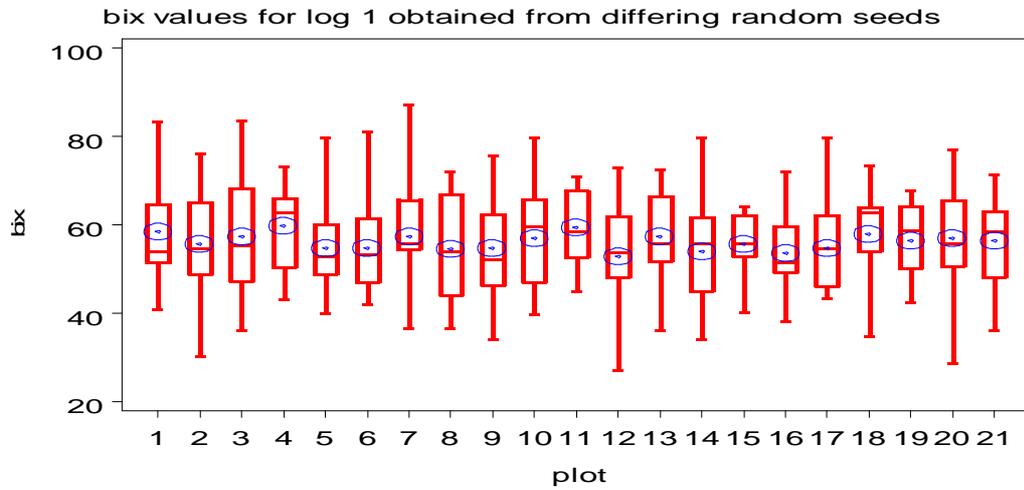
Table 1. Radiata pine experiments used in this study according to site quality and growth modelling region as defined by the Stand Growth Modelling Cooperative¹¹.

Site Quality → Growth Modelling region ↓	Low	Medium	High	High Basal Area
Clays		FR121/1	FR121/4	FR54
Sands	AK1058	AK1056 FR7		
Central NI		FR121/2 FR8	RO2103/1	
Hawke's Bay	WN364	WN364	WN364	WN377
Nelson	NN529/1	NN530/2	FR121/13	
Canterbury	CY597	CY421/1		
Southland		SD682		SD564/1

Table 2. Radiata pine experiments and PSPs used in this study according to site quality and growth modelling region as defined by the Stand Growth Modelling Cooperative¹¹.

Growth Modelling Region	Site Quality	Experiment	PSPs considered	Age(years) when TreeD data collected	Report summarising TreeD analysis
Clays	High	FR121/4	6/12	14	SGMC 135
Clays	Medium	FR121/1	4/12	16	SGMC 142
Clays	High BA	FR54	10/12, 15/13, 22/14, 29/15	16	SGMC 133
Sands	Medium	AK1056	2/11, 5/12, 3/13, 9/14, 8/15, 4/16, 1/17	27	SGMC 116
Sands	Medium	FR7	4/21 10/22 23/13, 27/24, 35/25, 43/26	20	FFR R09
Sands	Low	AK1058	8/41	24	SGMC 120
Central NI	High	RO2103/1	10/51	24	SGMC 120
Central NI	Medium	FR121/2	4/12	17	SGMC 148
Central NI	Medium	FR8	10/12, 20/13, 25/14, 34/15	17	SGMC 133
Hawke's Bay	Very High	WN364	5/1	23	SGMC 134
Hawke's Bay	High	WN364	4/3	23	SGMC 134
Hawke's Bay	Medium	WN364	3/3, 6/1, 7/1, 8/1	23	SGMC 134
Hawke's Bay	Low	FR121/3	5/12	16	SGMC 142
Hawke's Bay	Low	WN364	2/3	23	SGMC 134
Hawke's Bay	Very low	WN364	1/2	23	SGMC 134
Hawke's Bay	High BA	WN377	6/41	24	SGMC 120
Nelson	High	FR121/13	7/12	15	SGMC 142
Nelson	Medium	NN530/2	6/31	24	SGMC 120
Nelson	Low	NN529/1	6/31, 3/32, 5/33, 4/34, 1/35, 7/36, 8/37	27	SGMC 116
Canterbury	Medium	CY421/1	9/21	24	SGMC 120
Canterbury	Low	CY597	13/24, 15/21, 9/22, 10/23, 14/25, 11/26, 12/27	26	SGMC 117
Southland	Medium	SD682	5/51, 11/41, 14/31	26	SGMC 137
Southland	High BA	SD564/1	5/61	24	SGMC 120

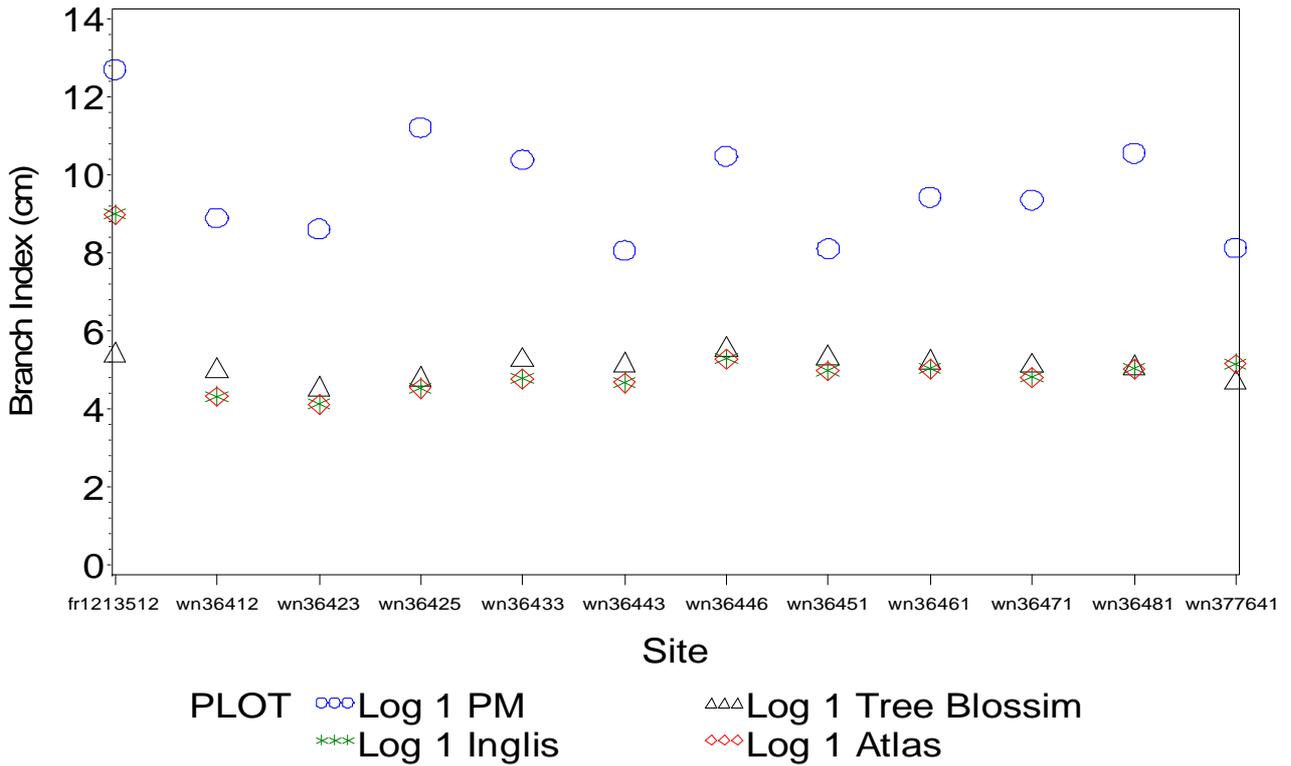
Appendix 2. Effect of different random seeds on the prediction of tree level BIX values (in mm).



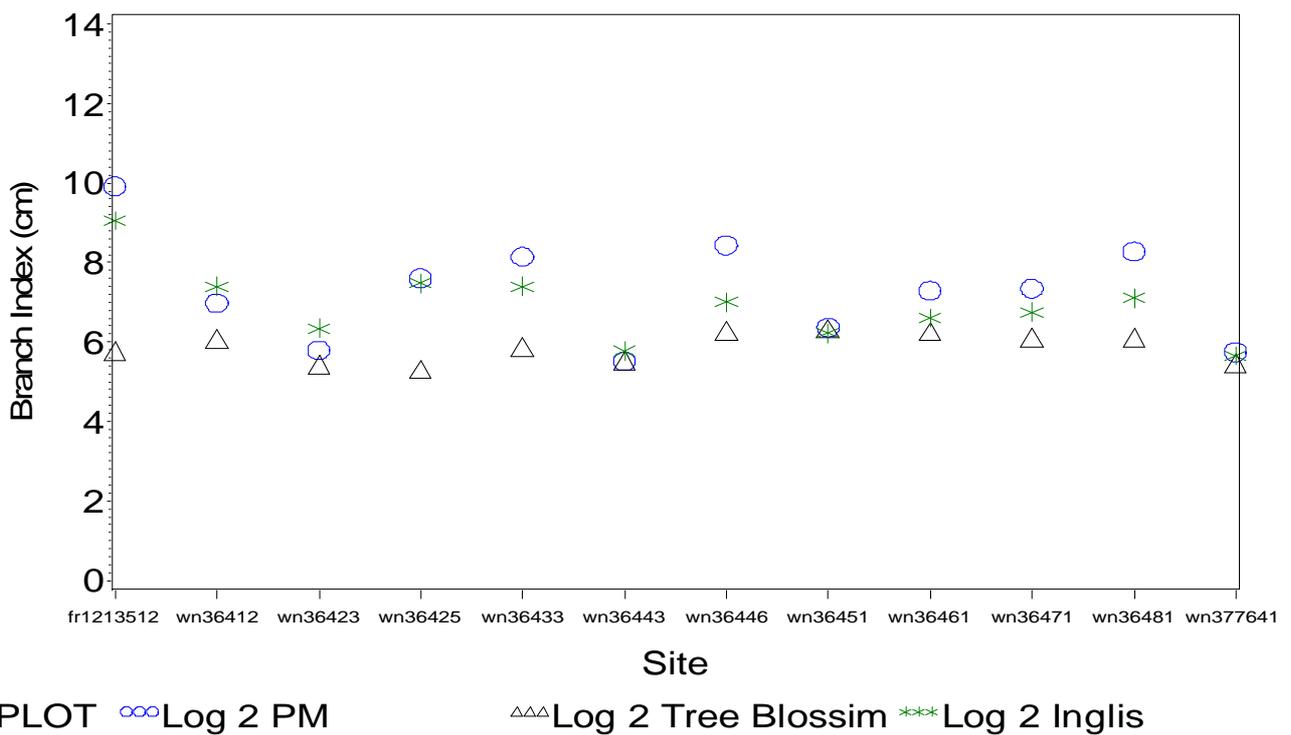
Appendix 3. Stand level predictions of BIX using different models for the different growth modelling regions.

HAWKE'S BAY REGION

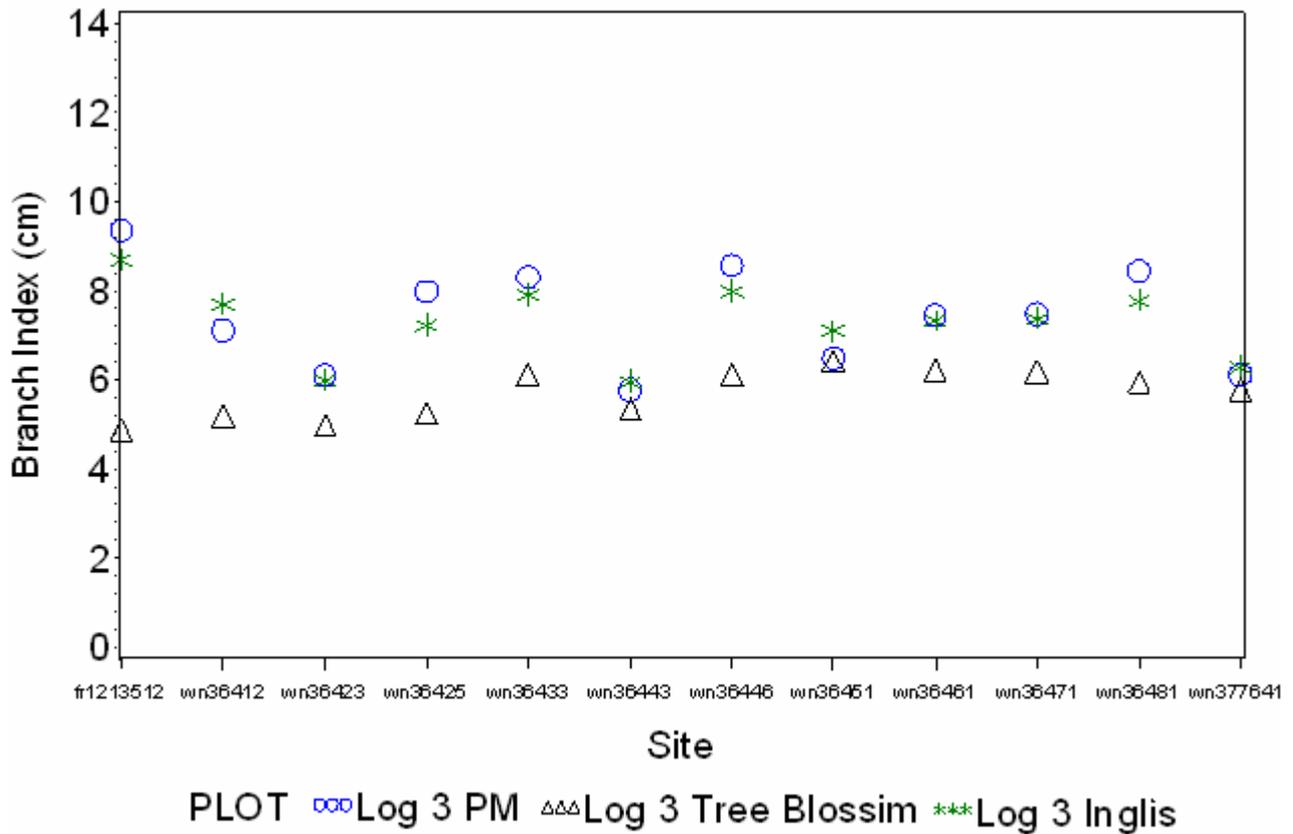
Predicted Log One Branch Index Results for the Hawkes Bay Region



Predicted Log Two Branch Index Results for the Hawkes Bay Region



Predicted Log Three Branch Index Results for the Hawkes Bay Region

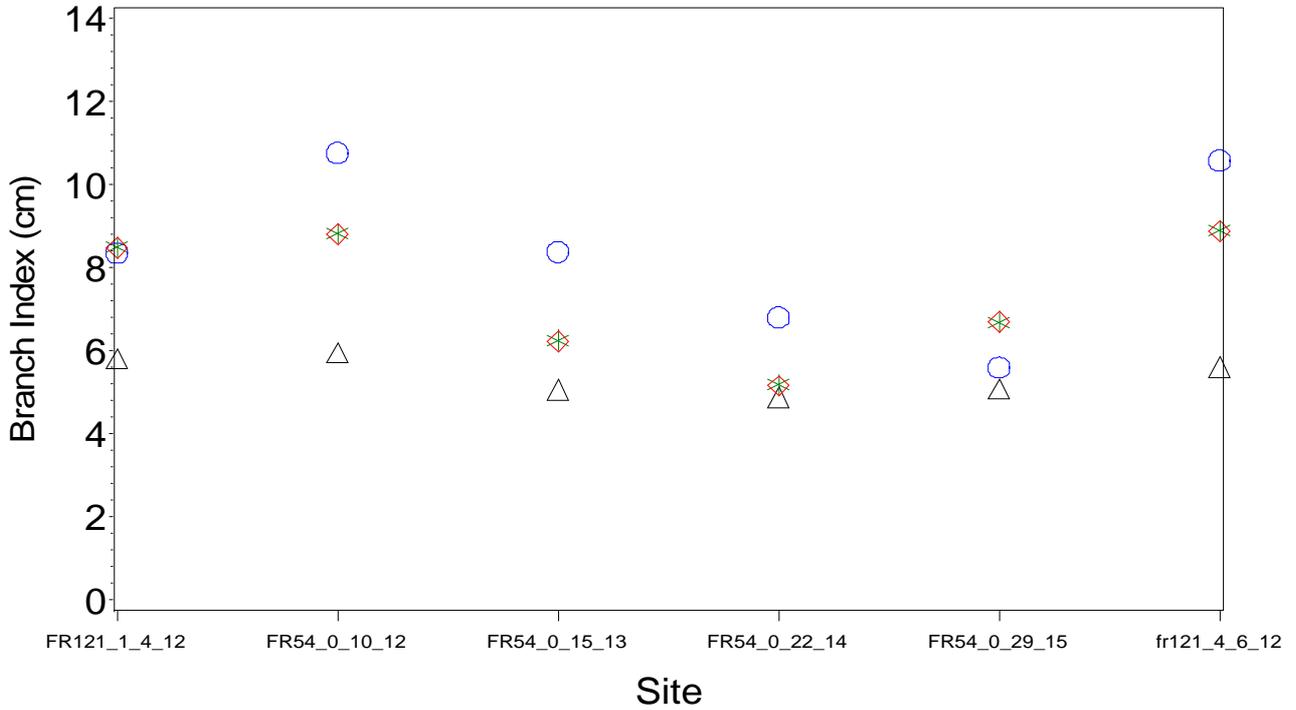


Explanation of labels on graphs

Label on graph	Explanation
Log 1 PM	BIX for log 1 calculated using BIX model Iteration 4 (developed for Plantation Management Cooperative)
Log 1 TreeBlossim	BIX for log 1 calculated by summarising individual tree predictions from TreeBLOSSIM
Log 1 Inglis	BIX for log 1 calculated using documented equation for Iteration 2
Log 1 Atlas	BIX for log 1 calculated using Atlas implementation of Iteration 2 (slightly different from documented equation)
Log 2 PM	BIX for log 2 calculated using BIX model Iteration 3 (developed for Plantation Management Cooperative)
Log 2 TreeBlossim	BIX for log 2 calculated by summarising individual tree predictions from TreeBLOSSIM
Log 2 Inglis	BIX for log 2 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation
Log 3 PM	BIX for log 3 calculated using BIX model Iteration 4 (developed for Plantation Management Cooperative)
Log 3 TreeBlossim	BIX for log 3 calculated by summarising individual tree predictions from TreeBLOSSIM
Log 3 Inglis	BIX for log 3 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation

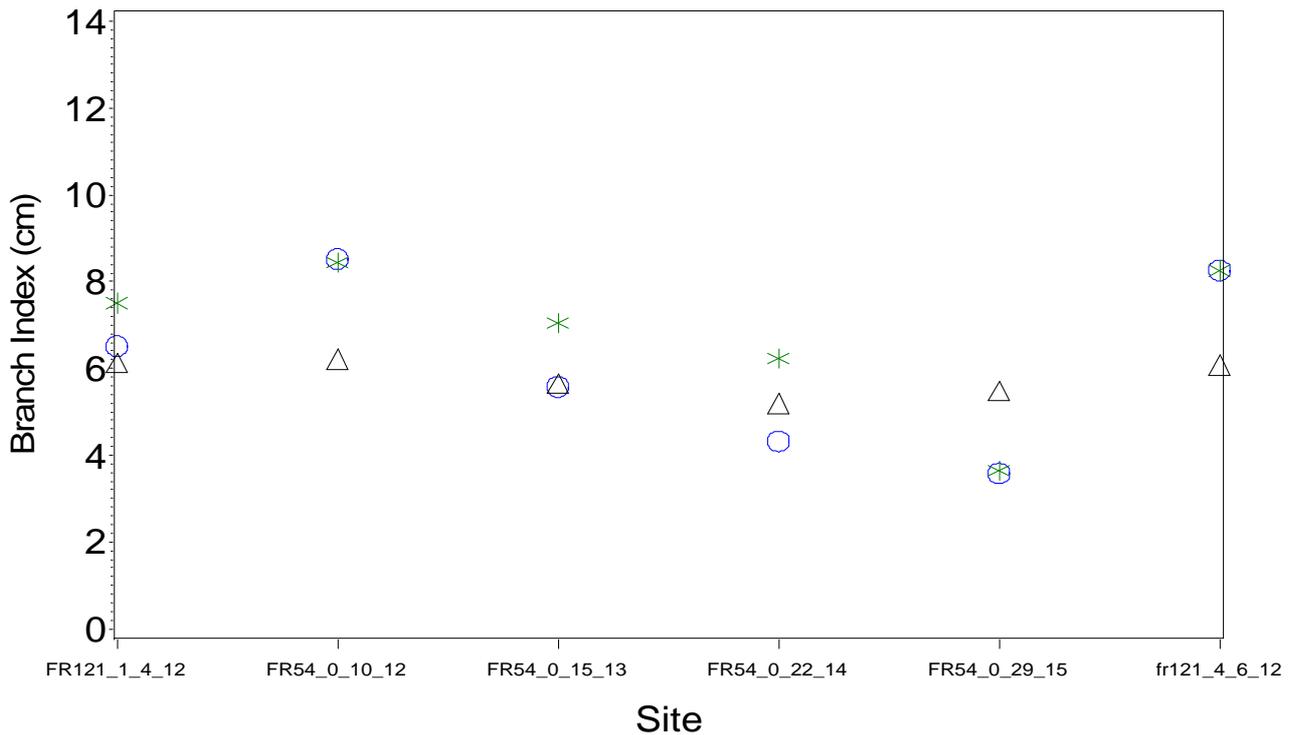
CLAYS REGION

Predicted Log One Branch Index Results for the Clays Region



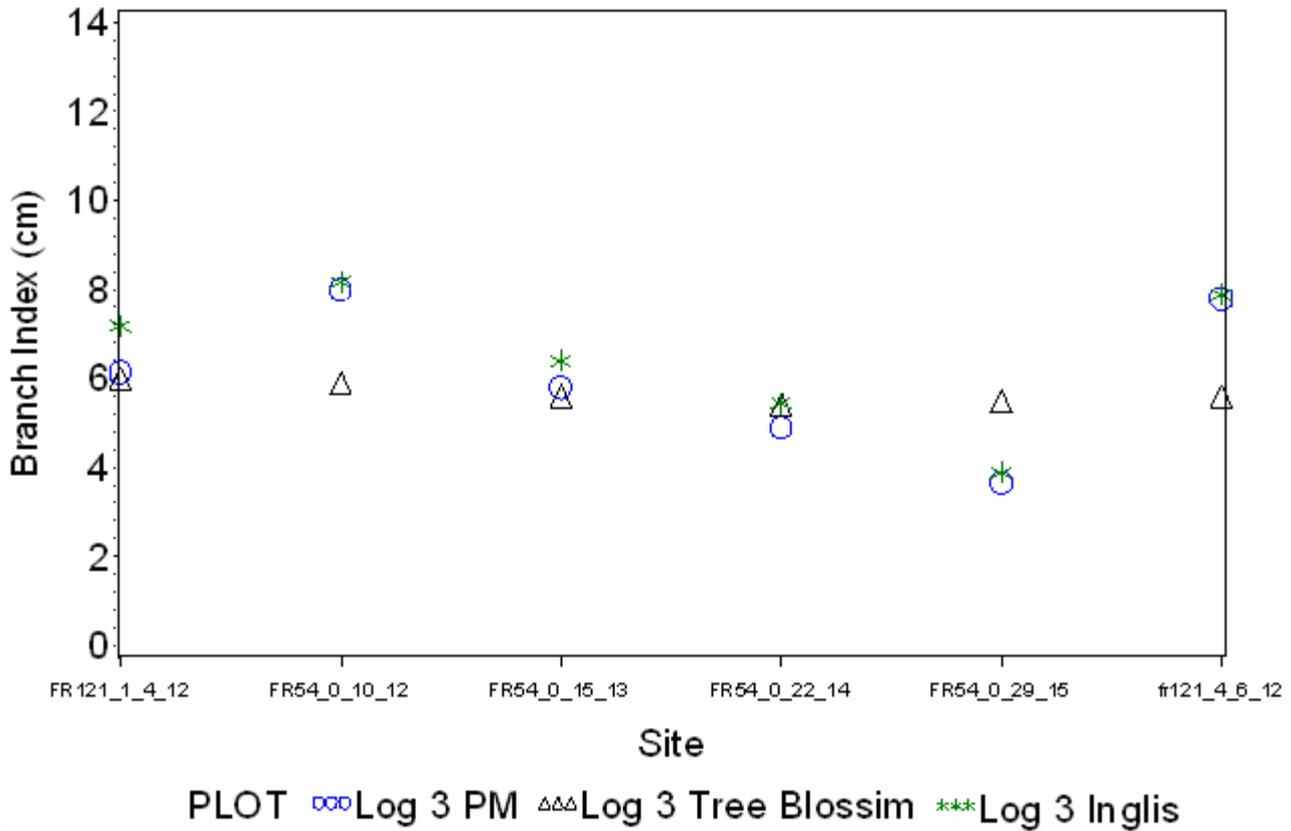
PLOT ○○ Log 1 PM △△ Log 1 Tree Blossim
 - Log 1 Inglis ◇◇ Log 1 Atlas

Predicted Log Two Branch Index Results for the Clays Region



PLOT ○○ Log 2 PM △△ Log 2 Tree Blossim *-* Log 2 Inglis

Predicted Log Three Branch Index Results for the Clays Region

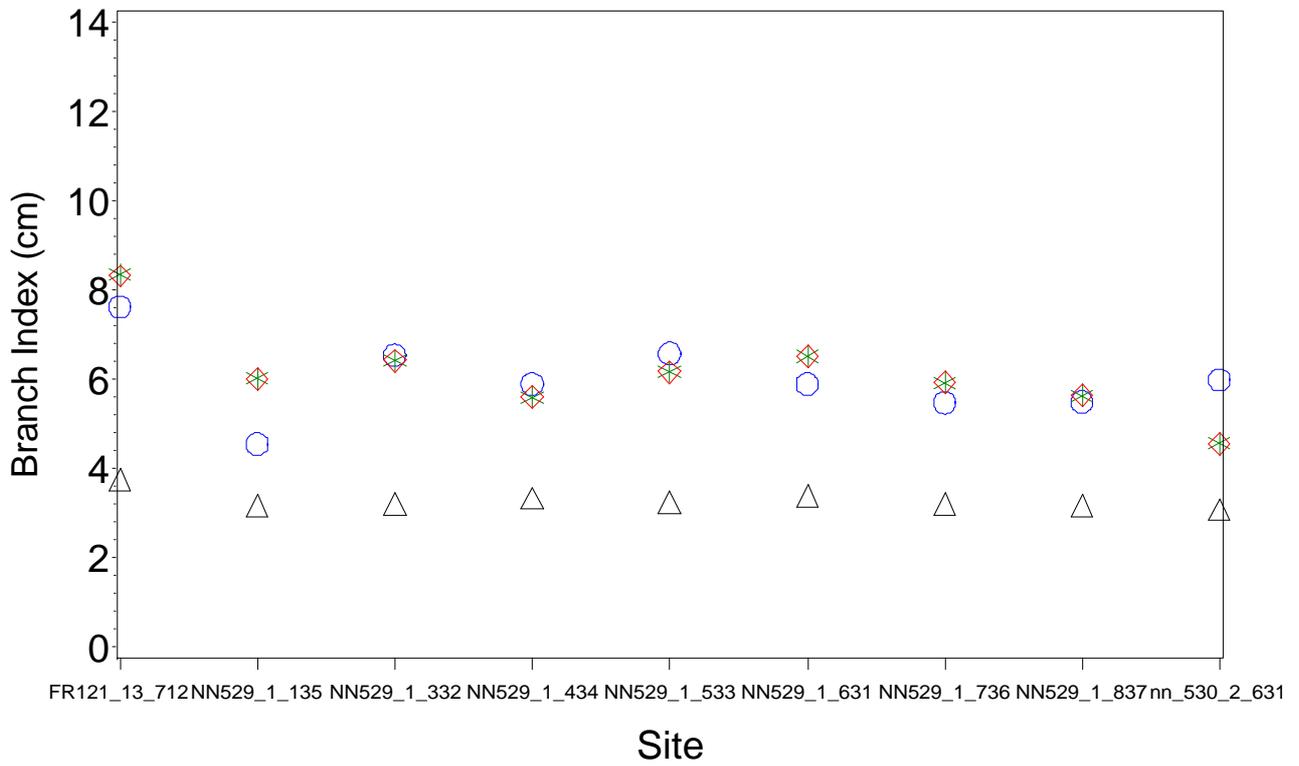


Explanation of labels on graphs

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Log 1 PM	BIX for log 1 calculated using BIX model Iteration 4 (developed for Plantation Management Cooperative)
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Log 3 Inglis	BIX for log 3 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation

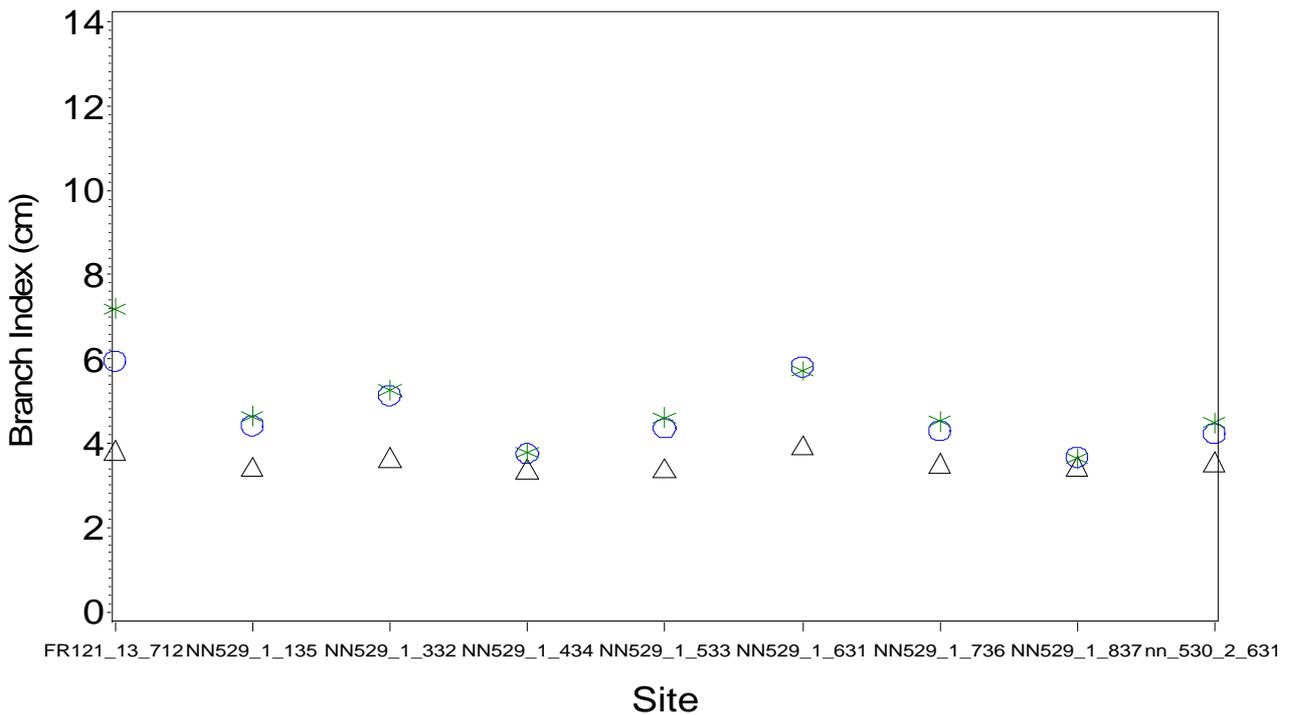
NELSON REGION

Predicted Log One Branch Index Results for the Nelson Region



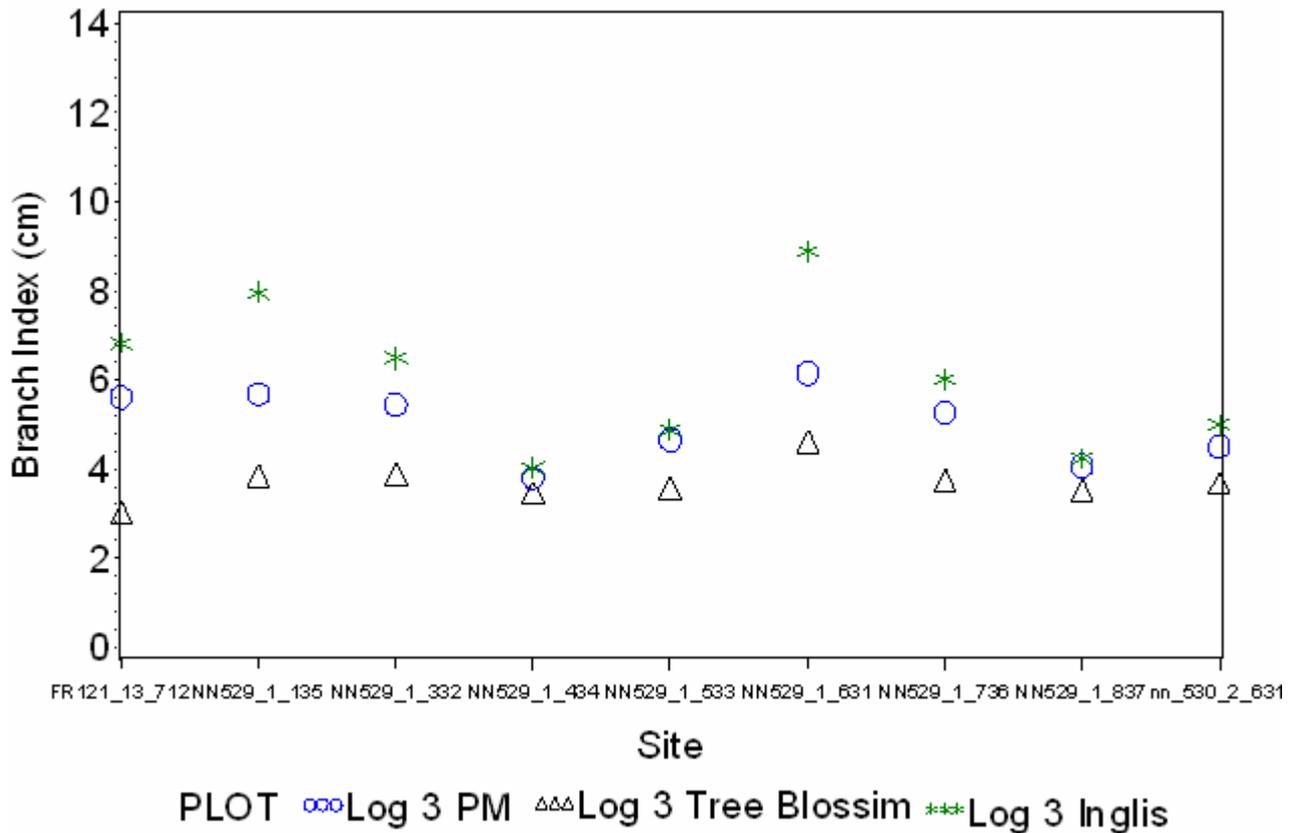
PLOT ○○ Log 1 PM △△ Log 1 Tree Blossim
 *** Log 1 Inglis ◇◇ Log 1 Atlas

Predicted Log Two Branch Index Results for the Nelson Region



PLOT ○○ Log 2 PM △△ Log 2 Tree Blossim *** Log 2 Inglis

Predicted Log Three Branch Index Results for the Nelson Region

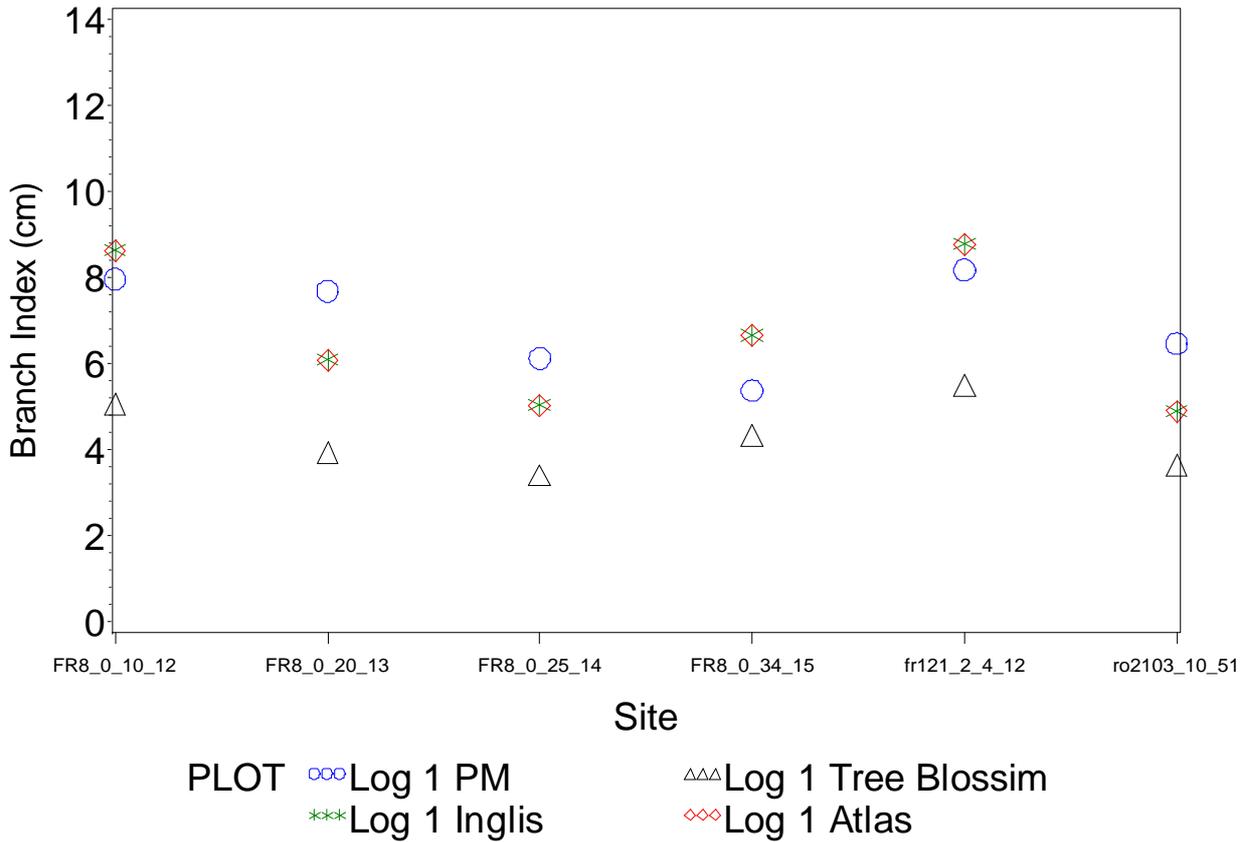


Explanation of labels on graphs

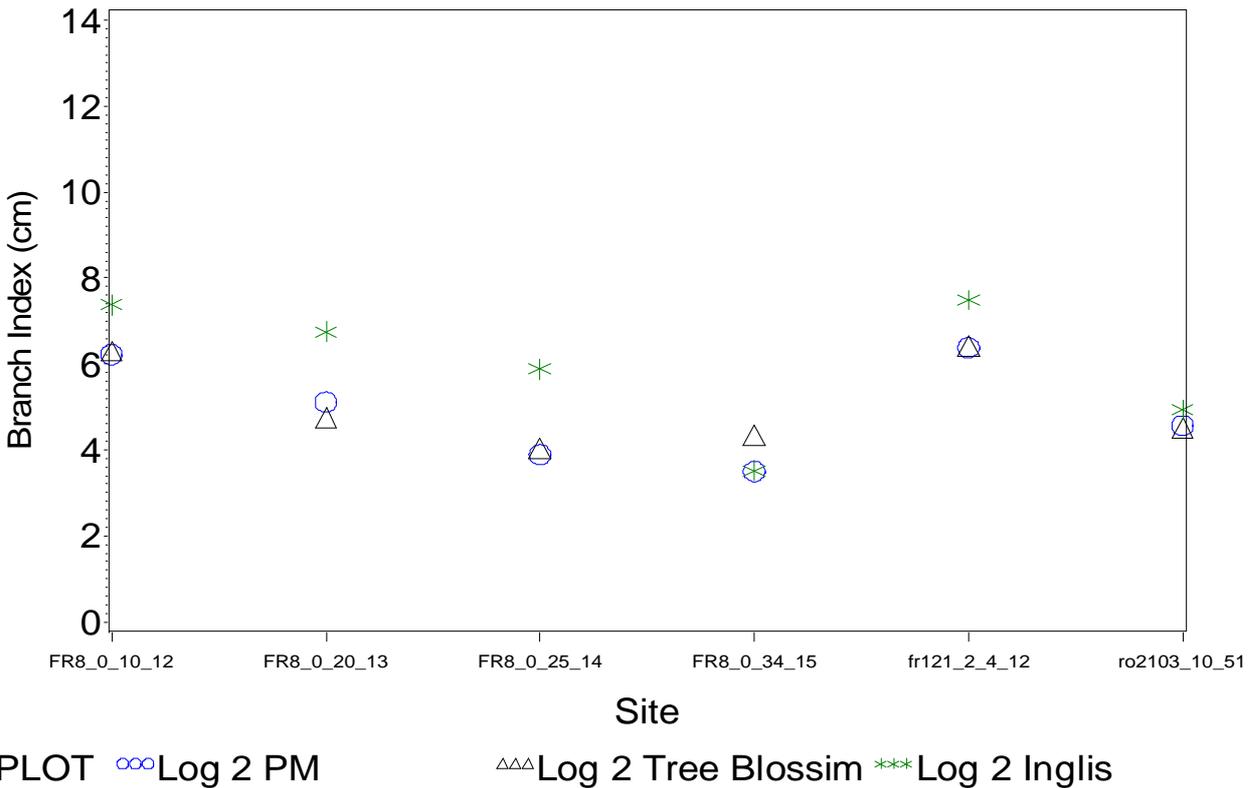
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Log 3 Inglis	BIX for log 3 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation

CENTRAL NORTH ISLAND REGION

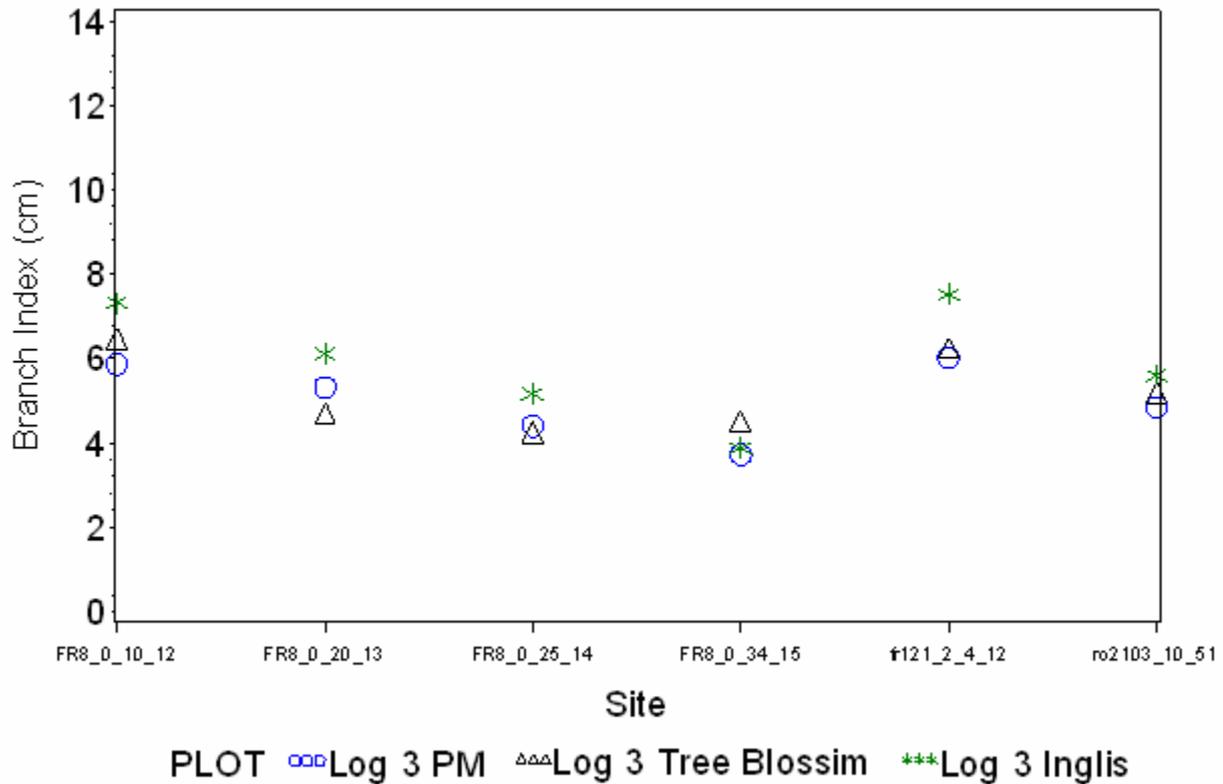
Predicted Log One Branch Index Results for the Central North Island Region



Predicted Log Two BRach Index Results for the Central North Island Region



Predicted Log Three Branch Index Results for the Central North Island Region

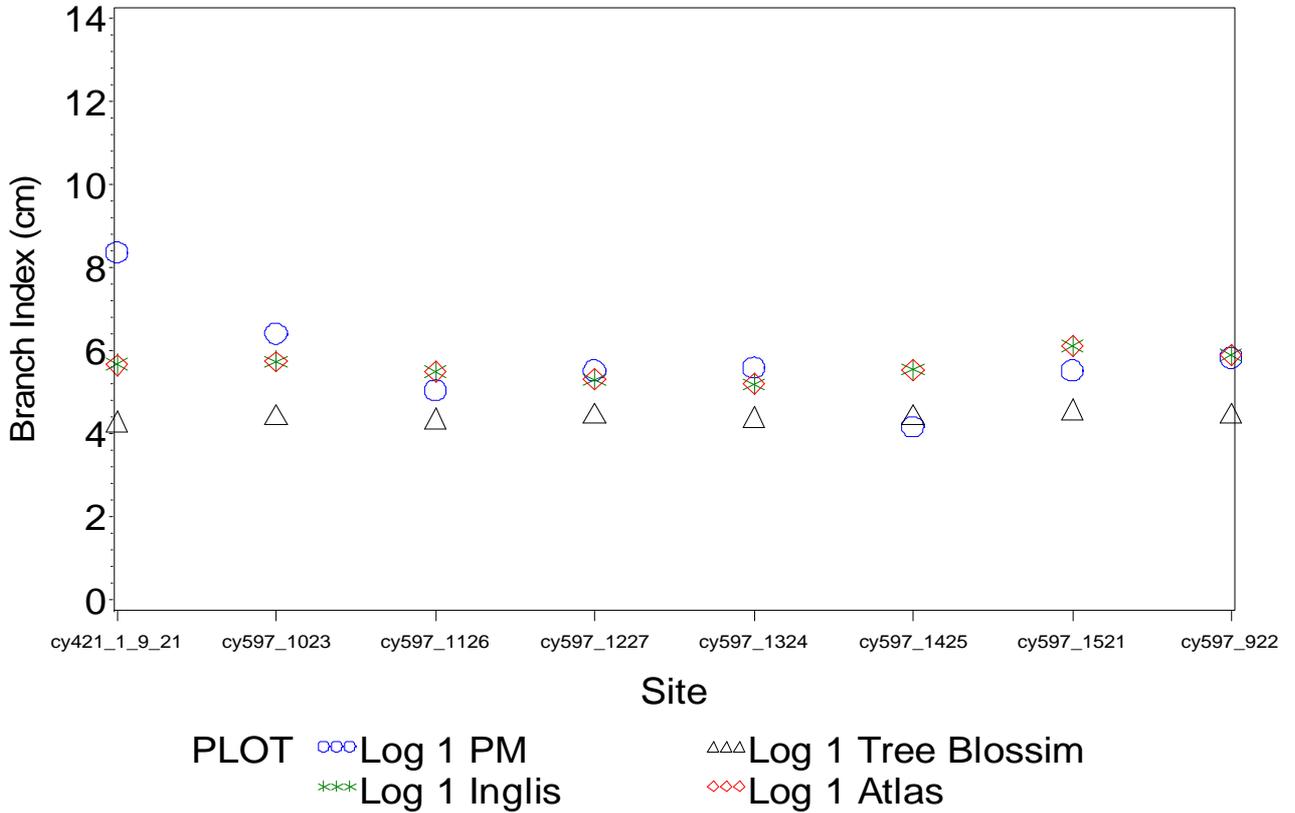


Explanation of labels on graphs

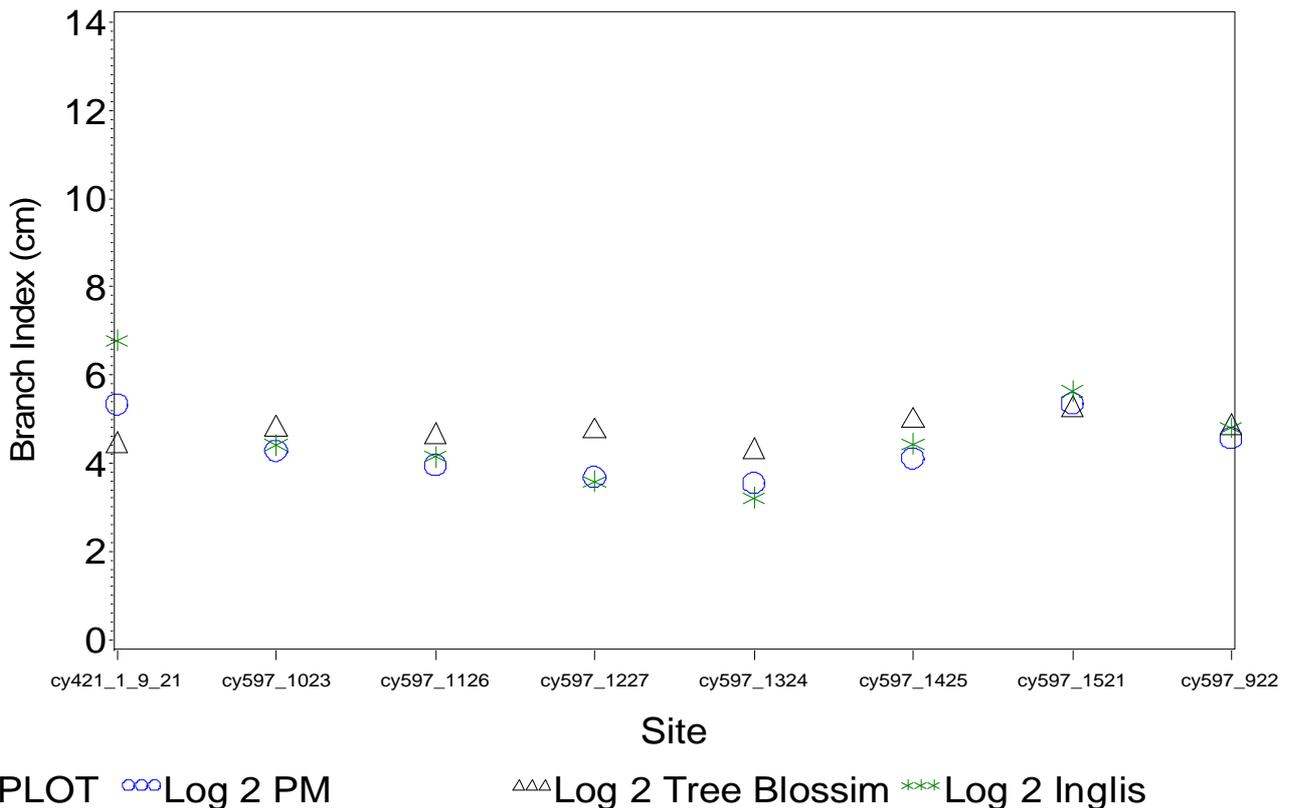
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Log 1 TreeBlossim	BIX for log 1 calculated by summarising individual tree predictions from TreeBLOSSIM
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Log 3 Inglis	BIX for log 3 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation

CANTERBURY REGION

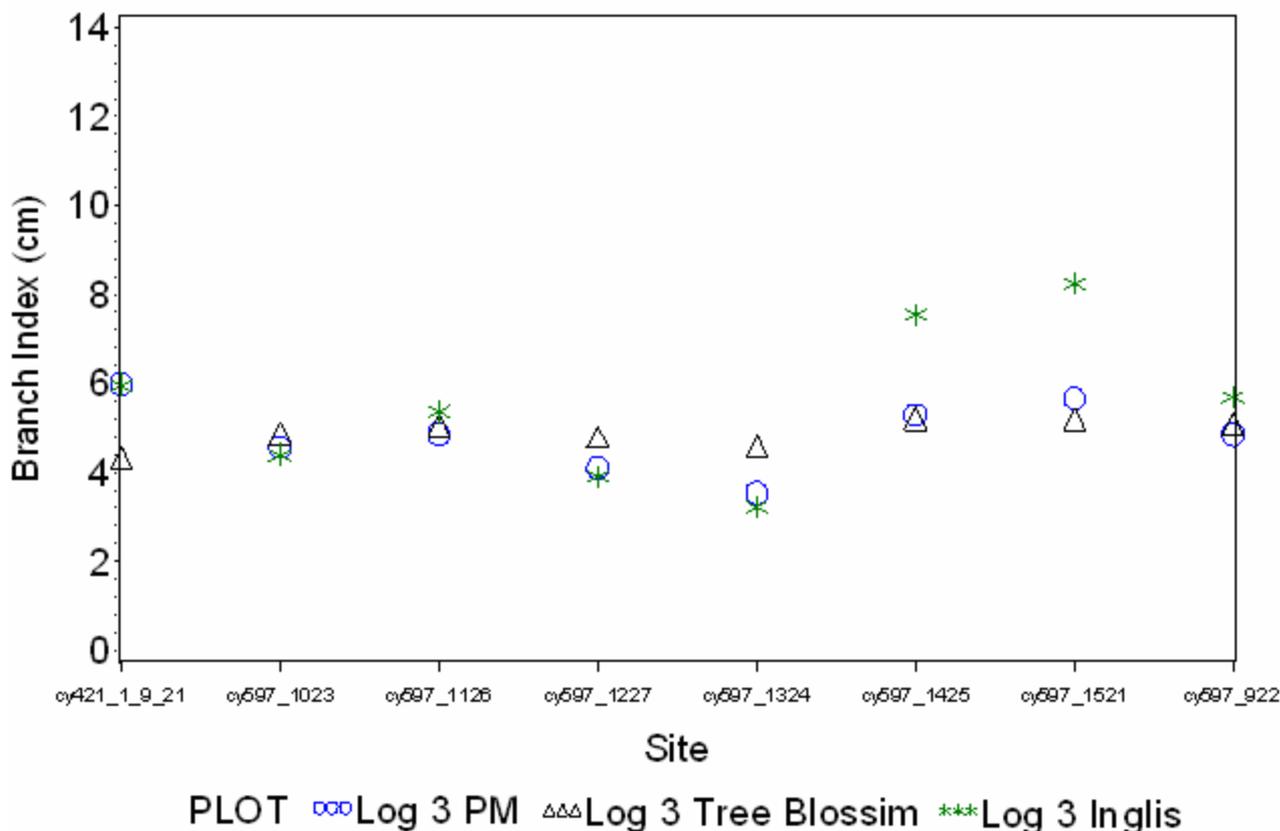
Predicted Log One Branch Index Results for the Canterbury Region



Predicted Log Two Branch Index Results for the Canterbury Region



Predicted Log Three Branch Index Results for the Canterbury Region

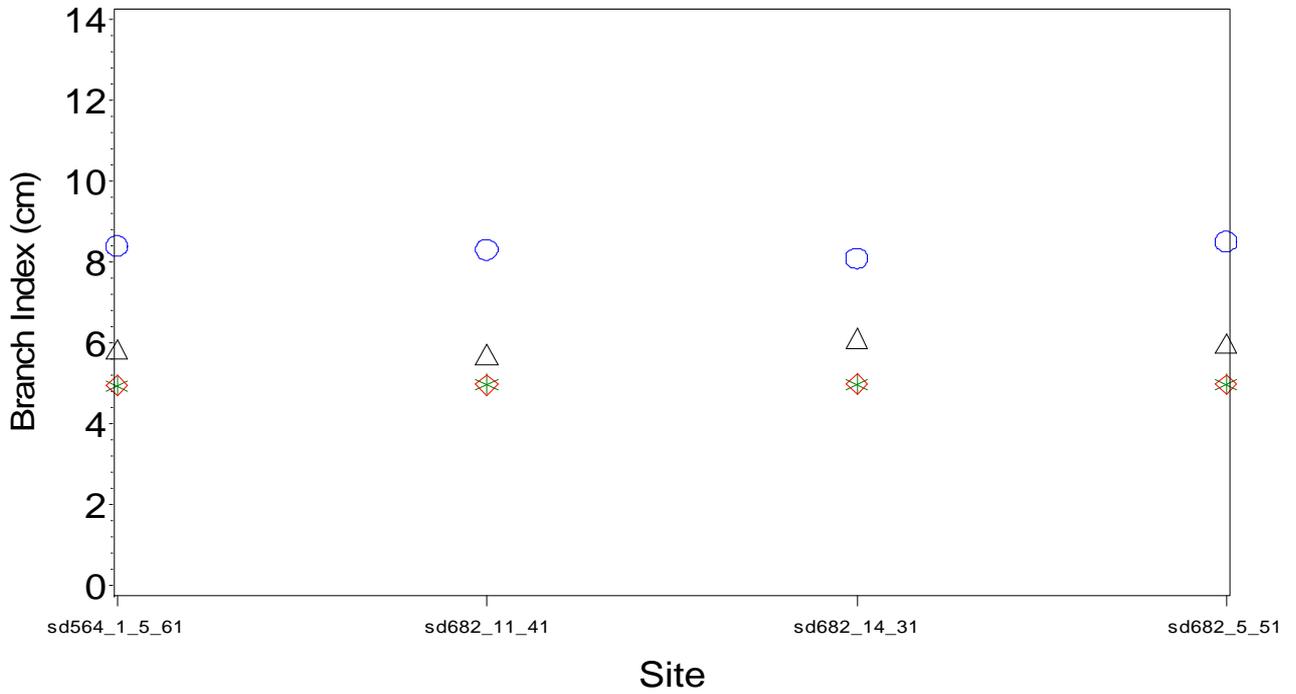


Explanation of labels on graphs

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Log 1 PM	BIX for log 1 calculated using BIX model Iteration 4 (developed for Plantation Management Cooperative)
Log 1 TreeBlossim	BIX for log 1 calculated by summarising individual tree predictions from TreeBLOSSIM
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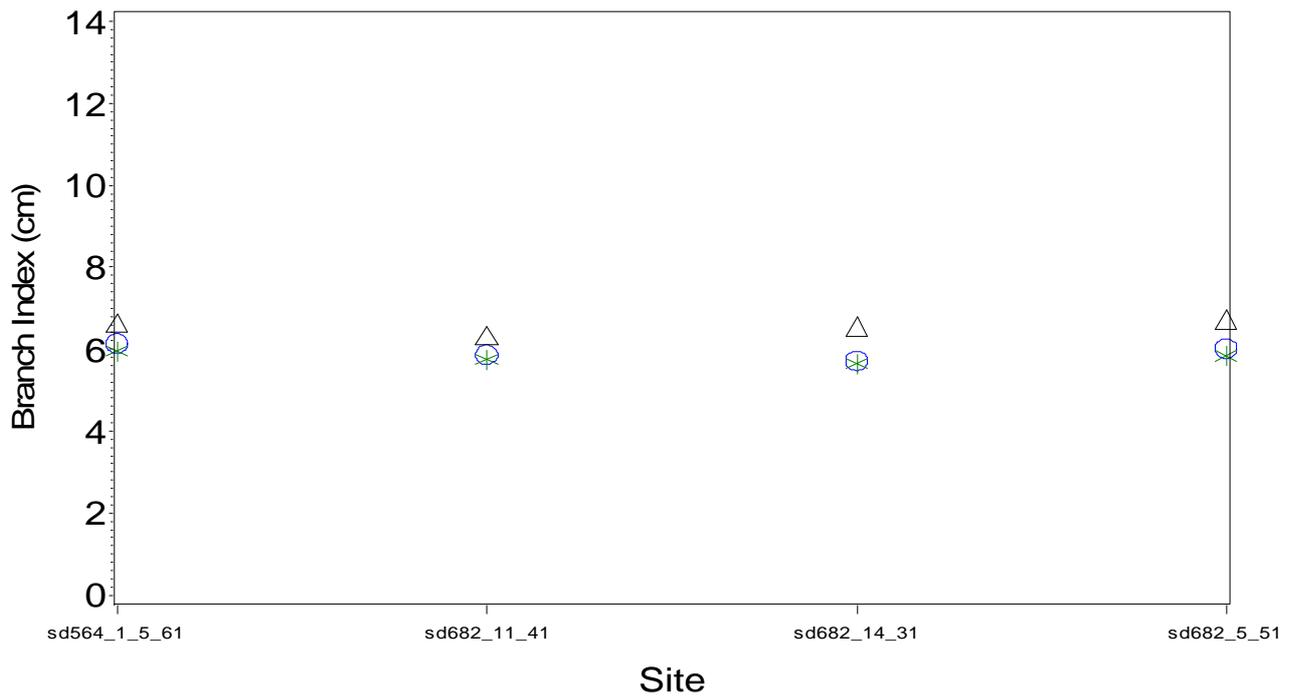
SOUTHLAND REGION

Predicted Log One Branch Index Results for the Southland Region



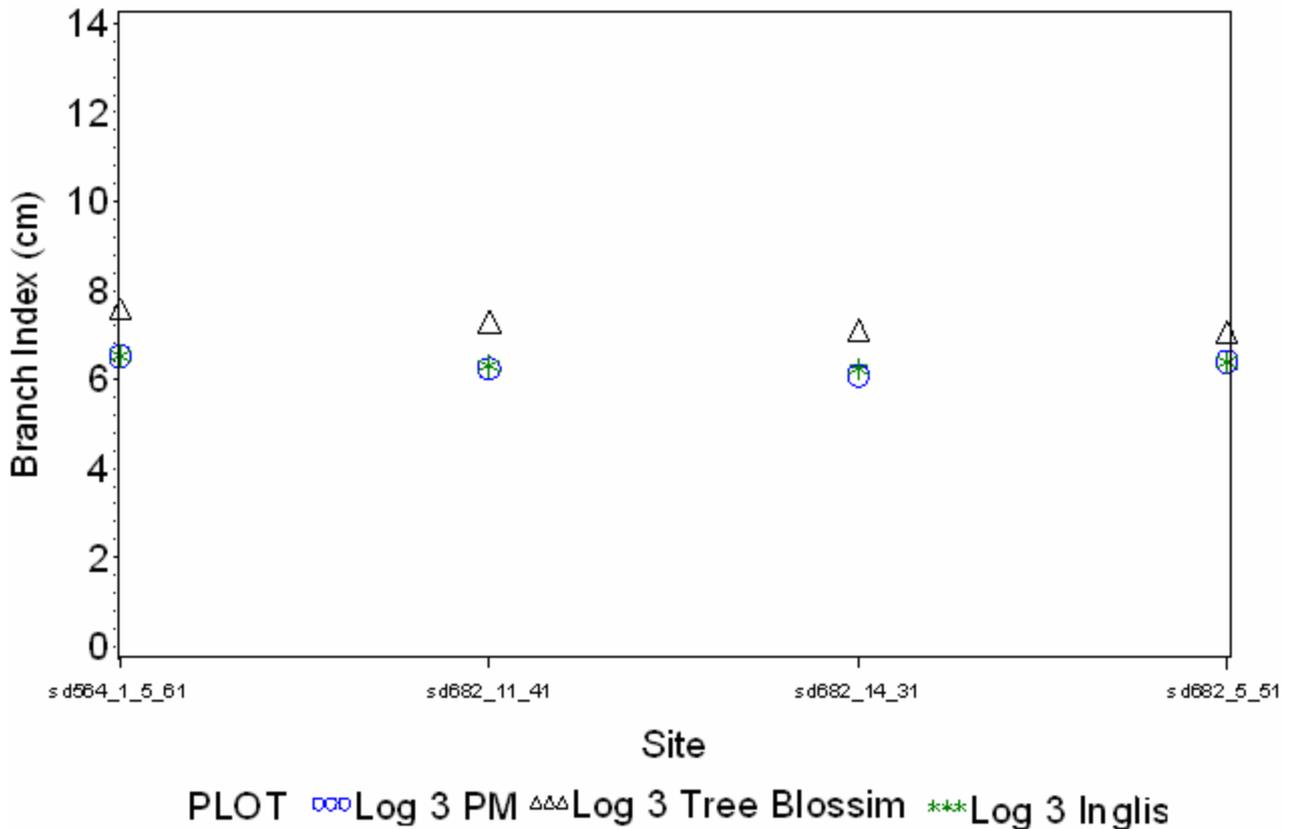
PLOT ○○ Log 1 PM △△ Log 1 Tree Blossim
 ** Log 1 Inglis ◇◇ Log 1 Atlas

Predicted Log Two Branch Index Results for the Southland Region



PLOT ○○ Log 2 PM △△ Log 2 Tree Blossim ** Log 2 Inglis

Predicted Log Three Branch Index Results for the Southland Region

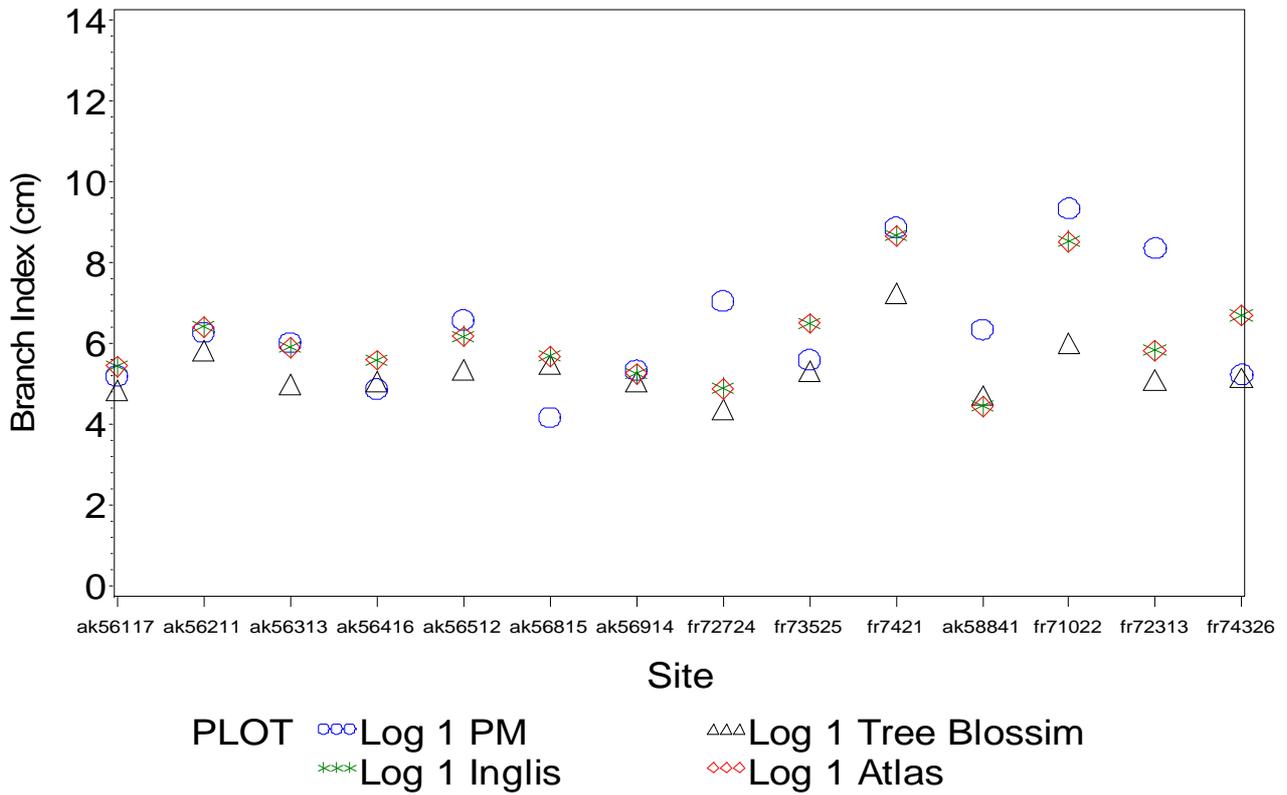


Explanation of labels on graphs

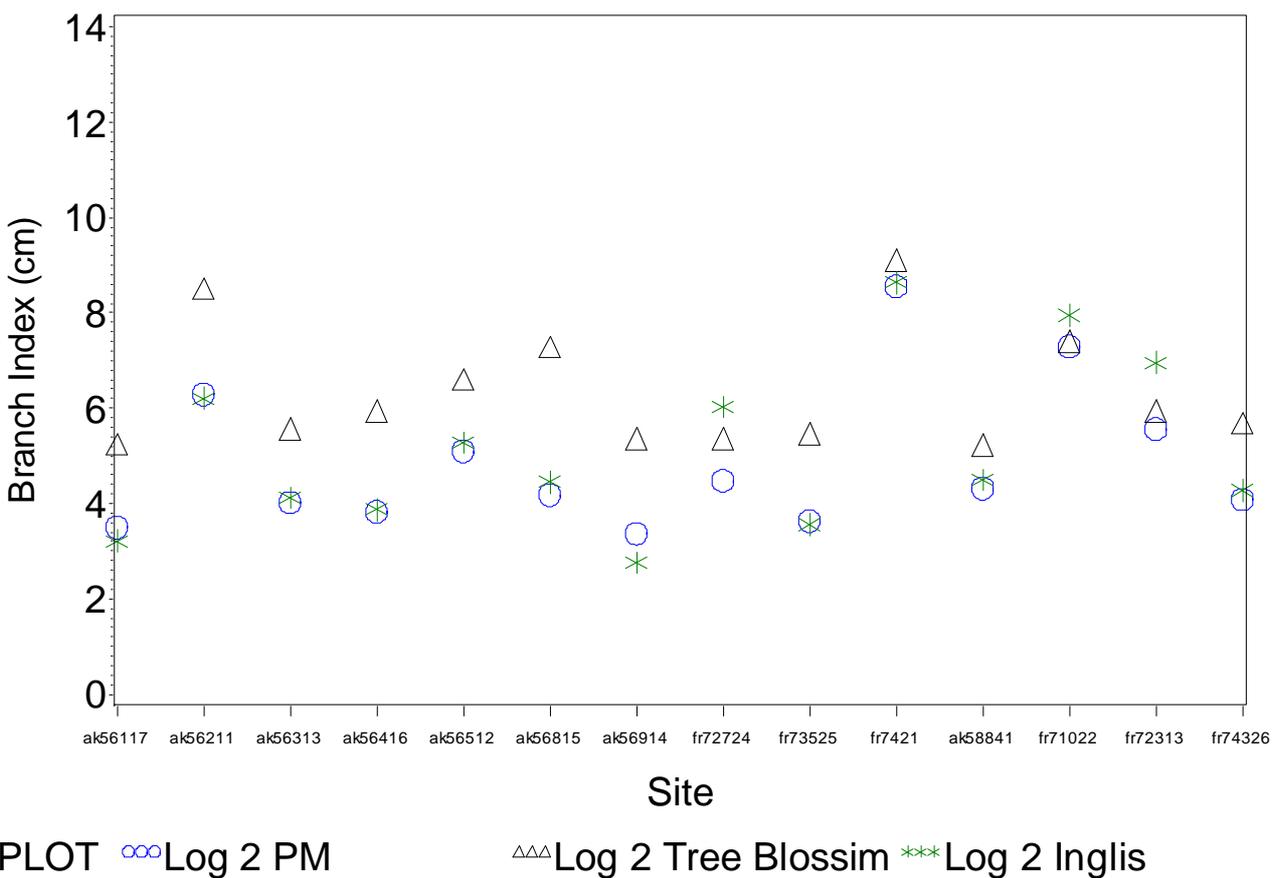
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Log 3 Inglis	BIX for log 3 calculated using documented equation for Iteration 2 which is the same as the ATLAS implementation

Sands Region

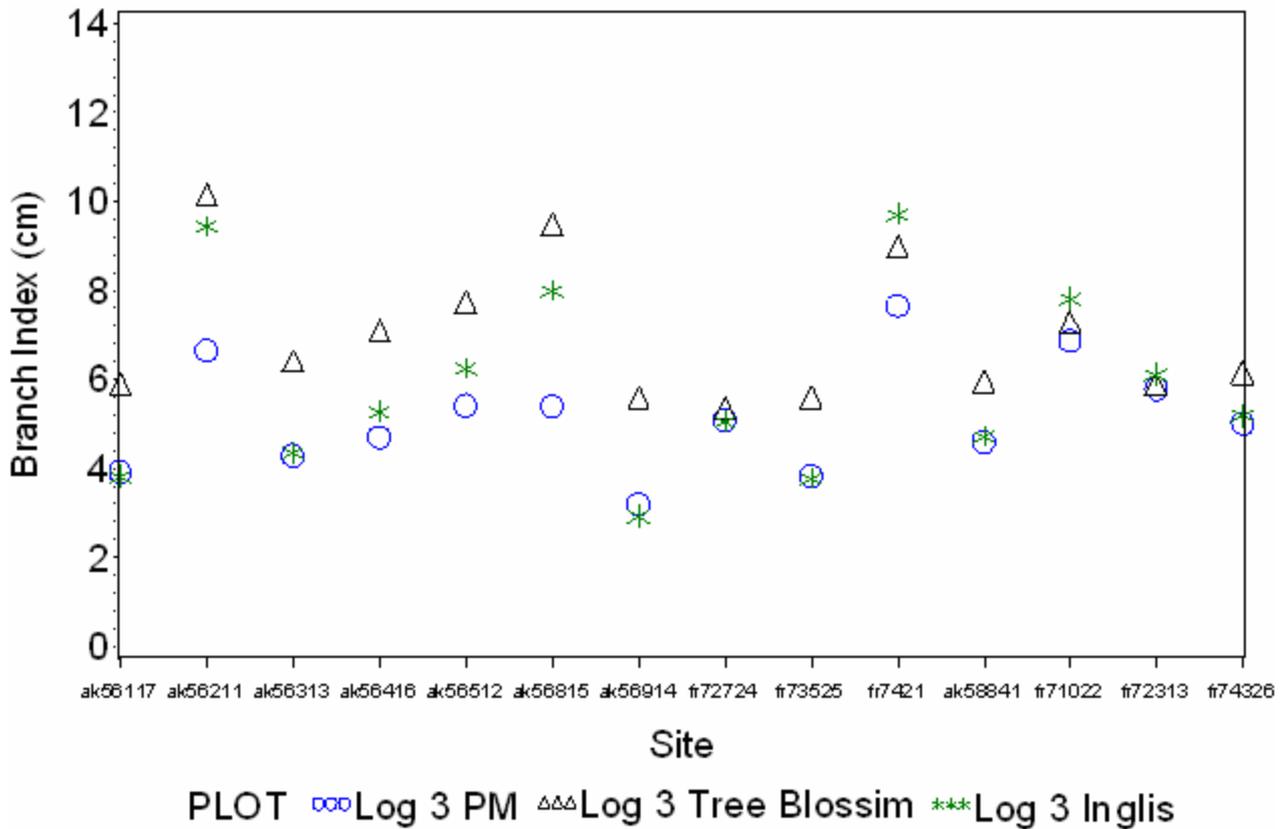
Predicted Log One Branch Index Results for the Sands Region



Predicted Log Two Branch Index Results for the Sands Region



Predicted Log Three Branch Index Results for the Sands Region



Explanation of labels on graphs

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Log 1 PM	BIX for log 1 calculated using BIX model Iteration 4 (developed for Plantation Management Cooperative)
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Appendix 4. Comparison of TreeD data with TreeBLOSSIM predictions

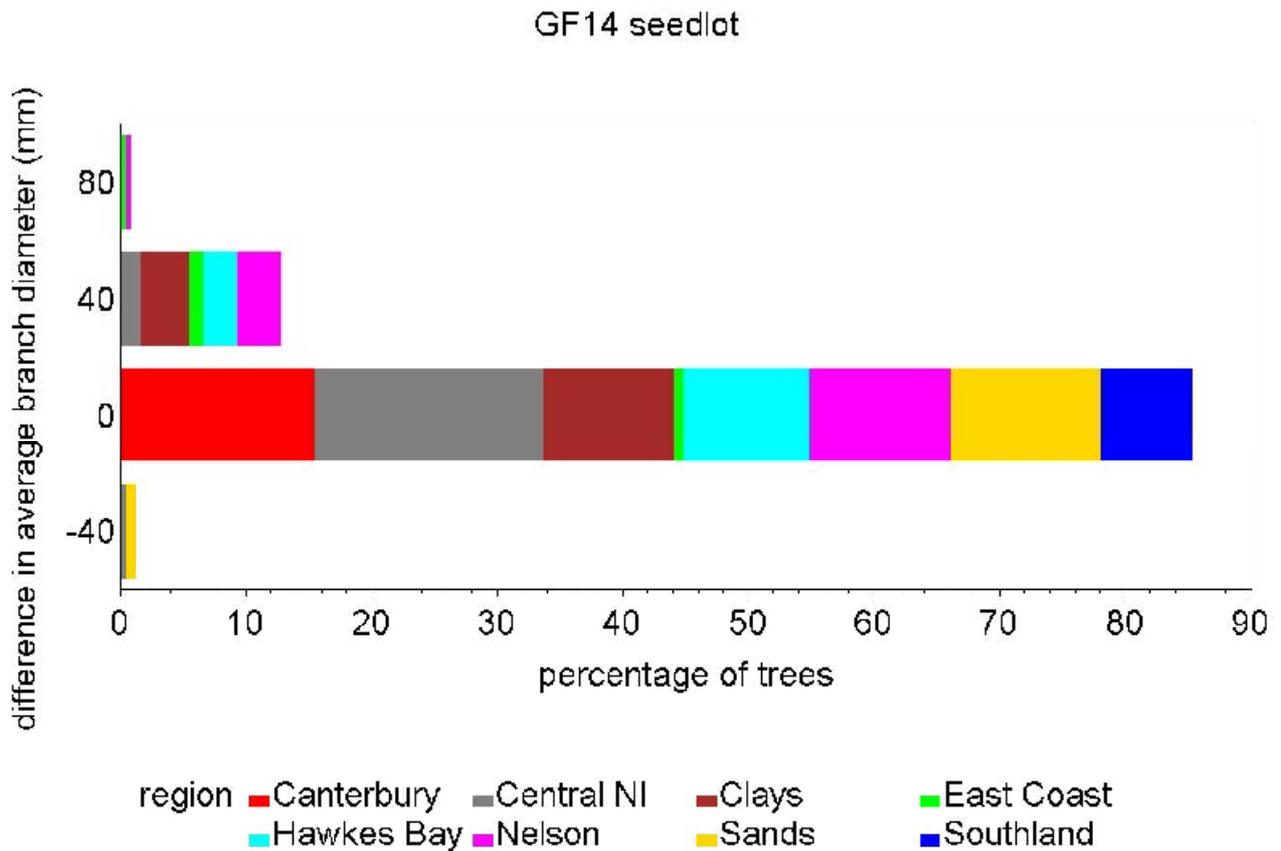


Figure 1. Difference between average branch diameter as measured by TreeD and average branch diameter as predicted by TreeBLOSSIM for different growth modelling regions. Note: The average branch diameter was calculated using largest branch in each cluster.

GF14 seedlot

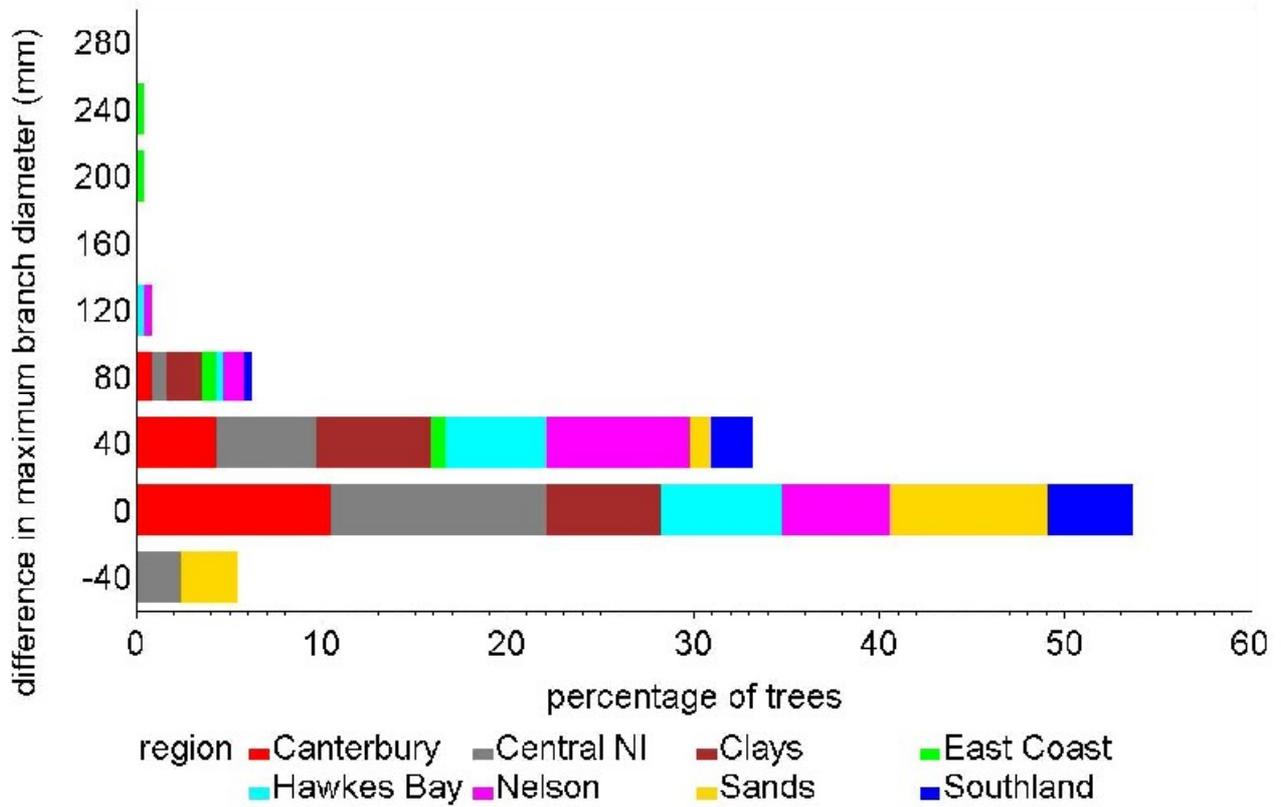


Figure 2. Difference between tree maximum branch diameter as measured by TreeD and tree maximum branch diameter as predicted by TreeBLOSSIM for different growth modelling regions.