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Adjusting Branch Cluster Frequency for Genotype in the Branch Model BLOSSIM

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EXECUTIVE SUMMARY

Knots, the parts of branches that become encased in the stem, are a significant determinant of log and timber quality. Knots can adversely affect the strength, stability and appearance of wood products. In addition, the frequency of branch clusters on the stem influences the clear-cutting potential of the tree.

The branch model BLOSSIM, widely used in the industry in forecasting and inventory systems, currently cannot be adjusted for differences in branch habit related to the GFPlus branch habit rating of the seedlot.

BLOSSIM was originally developed under the auspices of the Stand Growth Modelling Cooperative to allow the prediction of branch development, including branch cluster frequency and branch diameter growth. A particular objective was to predict branch diameters at the end of the rotation from earlier inventory assessments of branch diameter.

BLOSSIM is currently incorporated in the software products FFR Forecaster and ATLAS Cruiser. The current version in FFR Forecaster (version 3.2) was developed using data collected from “850” / GF14 seedlots because this was a widely planted seedlot around the 1980s, and consequently would represent a large proportion of the trees currently being harvested. An older version of BLOSSIM is in ATLAS Cruiser.

The Radiata Pine Breeding Company (RPBC) has developed systems quantifying the likely development of improved radiata pine. They have developed breeding values and GFPlus ratings for different aspects of tree development. The branch breeding value and GFPlus branch habit score are measures of cluster frequency.

To enable BLOSSIM to simulate a wider range improved radiata pine, FFR funded a project to incorporate the branch breeding values and GFPlus branch habit scores into BLOSSIM.

BLOSSIM contains several functions predicting different aspects of branch development, two of which were considered to be influenced by branch breeding values. This study investigated whether branch breeding values influenced the number of growth units (branch clusters) in an annual shoot (annual height increment), and the relative length of these growth units. Both functions were revised.

The number of growth units in an annual shoot is now predicted as a function of branch breeding value, mean annual temperature, annual height increment and tree age. There was no justification for incorporating branch breeding value into the function predicting relative length of growth units. The function was modified to allow for greater variation in the length of growth units, which in turn will increase the variability in predicted internode lengths.

A new version of the linked stem and branch growth model TreeBLOSSIM (Version 4.0) was developed (for ease of testing) incorporating these modified functions. Predictions from TreeBLOSSIM Version 3.1 (equivalent to FFR Forecaster Version 3.2) and TreeBLOSSIM version 4.0 were compared with TreeD data for individual trees from Permanent Sample Plots (PSPs) covering a range of sites and branch breeding values. Version 4.0 gave better predictions for some but not all trees. The mean error for individual PSPs was generally within acceptable limits, with larger improvements being achieved for the long-internode seedlots.

The revised version (Version 4.0) of BLOSSIM will be implemented in FFR Forecaster. This will allow users to investigate the effect of different branch breeding values and GFPlus branch habit scores on the number and position of branch clusters, and therefore internode length.

The frequency of branch clusters on the stem is one of several branching factors that will influence the clear-cutting potential of the tree. For growers who wish to emphasise appearance products from clearcuttings this new addition to BLOSSIM supports improved examination of the trade-offs between growth and GFPlus branch habit scores.

As logs are generally graded on the basis of the largest branch in the log, further research is required to incorporate the influence of genetics on branch diameter growth. This will require incorporating GFPlus values for stem growth, as it is considered that branch development is influenced by the GFPlus rating for stem growth, not the GFPlus branch habit score. Previous analyses of TreeD data indicated that many of the largest branches on trees were in fact the result of stem damage (e.g. leader replacement) rather than part of the regular branching pattern. So a model to predict the probability of stem damage and how branches grow in response to such events also needs to be incorporated into BLOSSIM to produce realistic predictions of branching patterns.

In addition, BLOSSIM functions will be improved if larger and more comprehensive data sets are available for model development and testing. In particular it is recommended that:

- Further trees covering a greater range of genetic material and site conditions are destructively sampled to provide a comprehensive matrix of data points for model development.
- Further TreeD studies are carried out in GxExS trials to complete matrix of site qualities for which branching data are available. Such data would be used to test further releases of BLOSSIM and thus provide confidence in the model for a greater range of GxExS conditions.
- ATLAS Cruiser assessment of GxExS trials are carried out to determine real value of different seedlots. In addition such inventory data could be used to provide an estimate of the value loss through stem damage, and determine whether this value loss varied with seedlot.

INTRODUCTION

Background

Branch diameters are an important determinant of log grade. For this reason, branch diameters are visually estimated during forest inventory, and together with other factors are used to determine the log grade. Many forest inventories are carried out at mid-rotation, and a method was needed to predict how much branches would grow between mid-rotation and time of harvest. The branch growth model, BLOSSIM was developed for this purpose in the 1990s by the Stand Growth Modelling Cooperative.

Model Development Philosophy

The philosophy behind the BLOSSIM model was to develop a simple empirical model based on our botanical understanding of branch development in radiata pine.

Terminology

The following terminology is essential to understanding this report and the BLOSSIM model.

Annual Shoot

An annual shoot is the annual height extension in a year. For radiata pine growth models this is July to June. Each annual shoot contains a number of growth units.

Growth Unit

A growth unit is a section of an annual shoot.

The base of a growth unit is defined as the point of initiation of the highest branch in a branch cluster. The top of a growth unit is defined as the point of initiation of the highest branch in the next branch cluster.

Cluster Position

For this study, the cluster position is equivalent to the end of the growth unit.

Internode Length

The internode length is the section of clear timber between branch clusters at the time of measurement. As the lowest branches in a cluster tend to grow horizontally, and the upper branches grow at an angle to the stem, the internode length tends to decrease with increasing tree age.

BLOSSIM Model

The branching model BLOSSIM^[1,2,3,4] is based on a botanical description of stem branching patterns, and models those components that were considered important to the value of the tree at the end of the rotation. The linked stem and branch growth model is TreeBLOSSIM.

The specific aspects of branching incorporated into BLOSSIM are:

- The number of growth units formed in an annual shoot (annual height increment). This is equivalent to the number of branch clusters in an annual height increment.
- The relative length of the growth units within an annual shoot. As branch clusters are at the ends of growth units, this gives the relative position of branch clusters within the annual shoot, and together with other functions allows the calculation of internode length, an important determinant of clear-cutting potential.
- The number of branches and cones in each branch cluster.
- The azimuthal distribution of these branches and cones.

- The change in branch diameter through time (at a point adjacent to the stem but avoiding any nodal swelling).
- The angle of the branch from verticality, after each year of growth.
- When each branch dies – becomes bark encased.
- Whether bark is trapped above a live branch.

Three reasons for this approach were:

- Modelling the number of growth units (branch clusters) in an annual shoot allowed the branch growth model to be linked with tree growth models through the height growth function.
- The number of branch clusters is a selection trait in tree breeding programmes, so it should be relatively easy to adjust the model for different genotypes, provided that appropriate data were available.
- The level of detail was sufficient to “grow” or project inventory data forward in time and provide input to a sawing simulator such as AUTOSAW.

Version 3.1 of BLOSSIM (equivalent to version 3.2 in FFR Forecaster) was developed for “850” / GF14 seedlots, using data collected from destructively sampled trees^[4]. The performance of the model was then compared with data on cluster position and branch diameter extracted from TreeD images covering a far wider range of sites and seedlots^[3,5]. These comparisons indicated that the model predictions were generally realistic, but highlighted that the influence of stem damage needed to be incorporated within TreeBLOSSIM in order to more accurately predict the diameter of the larger branches that appeared to be the result of stem damage.

The Radiata Pine Breeding Company (RPBC) has developed genetic ratings for different aspects of tree development, including stem diameter growth, stem straightness and branching habit^[6]. There is no genetic rating for branch diameter growth. To modify BLOSSIM to predict the branching pattern of different improved radiata pine seedlots and/or clones, one needs to determine how the branch functions in BLOSSIM will be influenced by the different genetic ratings. In addition to the effects of genetic rating (G) on branching pattern, branching pattern is also influenced by silvicultural treatment (S) and environmental conditions (E) (including soil, average climate condition, and more severe individual climatic events such as wind events that damage the trees (D)).

The functions within BLOSSIM, which are classified into four levels, are listed below, together with a list of which of the above four components (G, S, E, D) are likely to influence that aspect of branching:

- Tree level
 - Probability tree is mature, i.e. able to produce stem cones (G, E)
- Annual shoot level
 - Number of growth units (clusters) in an annual shoot (G, E, D)
 - Relative length of growth units (position of clusters) in annual shoot (D?)
- Cluster level
 - Number of branches and stem cones (G)
 - Azimuth angle of branches and stem cones (G, D)
- Branch level
 - Branch growth through time (G, S, E, D)
 - Branch angle relative to stem (G, D)
 - Bark trapped above a live branch (G?, S?, D)
 - Branch mortality (E).

Of the branch functions mentioned above, it is considered that GFPlus branch habit scores primarily affect the number of clusters in an annual shoot, as GFPlus branch habit scores are derived from visual assessment of frequency of branch clusters. The GFPlus branch habit scores may also influence the relative position of clusters.

One may have the impression that trees with lower GFPlus branch habit scores (i.e. long internode trees) tend to have larger and steeper branches than trees with higher GFPlus branch habit scores. However, stem elongation (primary growth) and stem thickening (secondary growth) are controlled by different processes so one would not expect a genetic rating for primary growth to exert an influence on a secondary growth process. There is a genetic rating for stem diameter growth (a secondary growth process). It is therefore considered that the branch level functions, in particular branch growth, will be influenced by the GFPlus rating for stem diameter growth rather than the GFPlus branch habit score. Preliminary data supporting this view are shown in Appendix 2.

Objective

The objective of the current study was to incorporate branch breeding values and GFPlus branch habit scores into BLOSSIM.

The specific objectives of the study were:

- to develop revised equations to predict number and position of branch clusters within an annual shoot that incorporate the GFPlus scores for branching; and
- to develop a “reference” version of BLOSSIM prior to its implementation in FFR Forecaster and related ATLAS software.

METHODS

Dataset Selection

Two potential datasets were initially considered for this project:

- RPBC laser datasets, and
- TreeD datasets where cluster positions had been extracted.

As the research progressed, it was realised that there were major advantages in carrying out the study using a third dataset, namely:

- Destructively sampled datasets collected for BLOSSIM development.

In the end, the third dataset was used for this study. For completeness, the pros and cons of the different datasets are outlined below.

RPBC Laser Datasets

Laser measurements of cluster frequency were previously collected from two sites covering 50 open-pollinated families^[7]. The main disadvantage of these datasets was that there were no data on annual height growth that could be used to determine annual height increments, which is what BLOSSIM requires.

TreeD Data Datasets

TreeD data were previously collected for 23 sites covering a range of silviculture treatments and seedlots. The TreeD data provides:

- position of branch clusters for a section of the stem, and
- diameter of the largest branch visible on the image for each cluster.

These data were considered more appropriate than the RPBC laser datasets in that the data were collected from Permanent Sample Plots, and height growth data were available. However it was still necessary to develop a methodology to assign the clusters measured by TreeD to an annual shoot. Such a methodology was developed, but the assumptions that needed to be made, and the errors that resulted from these assumptions, were considered too great to justify its use in model development.

Destructively-sampled Datasets

These datasets were collected for the development of BLOSSIM, and have the advantage that annual shoot lengths were determined from ring counts below and above each cluster.

Using these datasets for model development had the advantage that it left the TreeD data sets free for testing model improvements.

Overall, these destructively-sampled datasets were considered the most appropriate to use for this study.

Approach taken to Incorporate Genetic Parameters within BLOSSIM

Plants are sold on the basis of GFPlus ratings, which are in turn calculated from the underlying breeding values developed, and IP owned by, the Radiata Pine Breeding Company (RPBC).

For this study, and as approved by the RPBC, the approach taken was to explicitly incorporate breeding values into the BLOSSIM functions. Within FFR Forecaster, the user will be able to input either branch breeding value or GFPlus branch habit score. For users who do not have access to breeding values, the GFPlus rating will be converted to breeding value using a RPBC supplied conversion.

Prediction of Number of Clusters within an Annual Shoot

A mathematical equation that predicts the number of clusters in an annual shoot from branch breeding values and other variables was developed using the following steps:

- Plotting raw data in a variety of ways to investigate the relationships between different variables.
- Fitting appropriate equations to each combination of site and breeding value.
- Investigating how predicted coefficients varied with breeding values and site variables.
- Fitting one equation to the whole dataset that incorporated breeding values and site variables.
- Investigating the performance of the single equation.

Prediction of Relative Position of Clusters within an Annual Shoot

BLOSSIM Version 3.1 contained a look-up table that predicted the end-position of each branch cluster within the annual shoot. This look-up table contained the observed mean values for each cluster in an annual shoot with a given number of growth units. The wide variability in observed branching patterns between annual shoots and trees resulted in predicted cluster positions being fairly evenly distributed within an annual shoot. Consequently, BLOSSIM Version 3.1 lacked the ability to predict some of the longer internodes observed in the field.

Therefore, two aspects were investigated:

- Whether the relative positions of clusters within an annual shoot were influenced by branch breeding values.
- Approaches that would allow for more variation in the predicted growth unit lengths.

RESULTS

Note: larger versions of the Figures that follow are provided in Appendix 1. Smaller graphs that accompany the text are useful for quickly comparing patterns across groups of graphs.

Number of Clusters within an Annual Shoot

Model Developed

Branch breeding values were available for 16 of the 19 destructively-sampled datasets (Figure 1 and Table 1). The datasets were collected from sites covering a wide range of mean annual temperature. The range of branch breeding values was greatest in the Central North Island (mean annual temperature of approximately 11 degrees). There were few trees with branch breeding values below -2.0.

The observed number of clusters in an annual shoot varied between one and 10 with a mean value of 3.5. As with previous analyses, the number of clusters in an annual shoot is influenced more by annual shoot length than by the tree age when the annual shoot was formed, so the initial analyses used annual shoot length as the dependent variable.

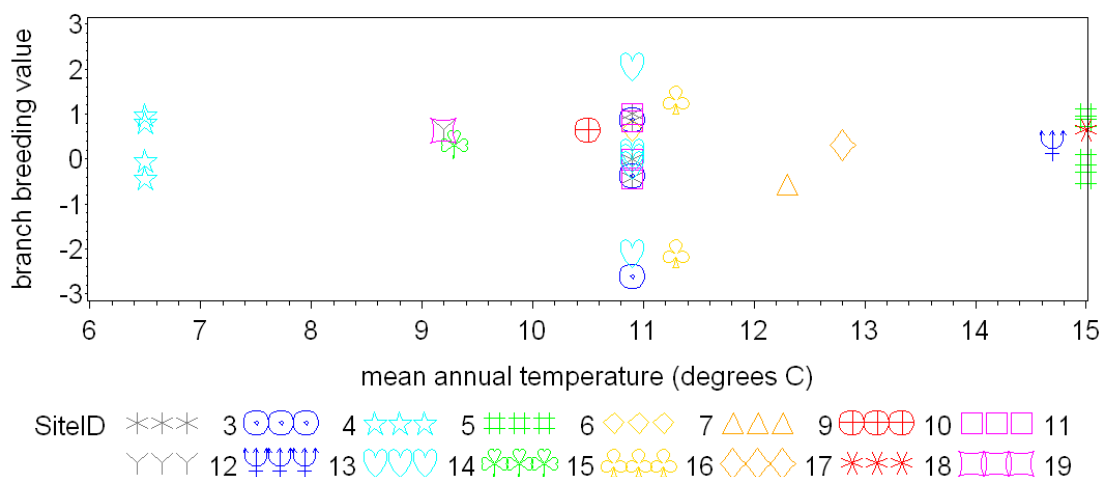


Figure 1: Distribution of data across branch breeding values and mean annual temperature.

Table 1: Forest location for destructively-sampled datasets.

SiteID	Forest
3	Kaingaroa
4	Kaingaroa
5	Taringatura
6	Woodhill
7	Kaingaroa
9	Wairau North
10	Eyrewell
11	Mawhera
12	Golden Downs
13	Riverhead
14	Kaingaroa
15	Golden Downs
16	Shellocks
17	Mohaka
18	Woodhill
19	Golden Downs

A number of different equations forms were investigated, and their performance assessed to ensure that they behaved realistically across a logical range of input values. The most appropriate equation (Eqn. 1) was selected based on the correlation between residuals and predicted values, and the performance of the equation.

$$\text{Clustersperyear} = 1.0 + (f \times AT + g \times BBV) \times \exp(-\exp(a - b \times SL)) \times (1.0 - \exp(-c \times AGE)) \quad (1)$$

Where:

Clustersperyear is the number of branch clusters formed during one year
AT is the mean annual temperature in degree C
BBV is the branch breeding value
SL is the annual shoot length in m
AGE is the tree age in years.

The predicted coefficients are:

$a=0.9484$
 $b=0.5677$
 $c=0.1345$
 $f=0.8397$
 $g=1.0658$

Model Performance

The performance of this model (Eqn. 1) was assessed by predicting the number of clusters for a range of annual shoot lengths, tree age, mean annual temperature and branch breeding value (see Figure 2). As there are four independent variables, these graphs provide the average values across the points simulated, and illustrate that the number of clusters increases:

- Approximately linearly with annual shoot length.
- To an asymptote with increasing tree age. The simulation has been run to age 62 to illustrate the effect of growing radiata pine longer than the current rotation length. Botanically, it is expected that the number of clusters would decrease to zero with increasing age, but we do not have any data for very old radiata pine to determine the shape of such a curve. Until such data are available, an asymptotic curve is the logical model.
- Very slightly with branch breeding value and mean annual temperature.

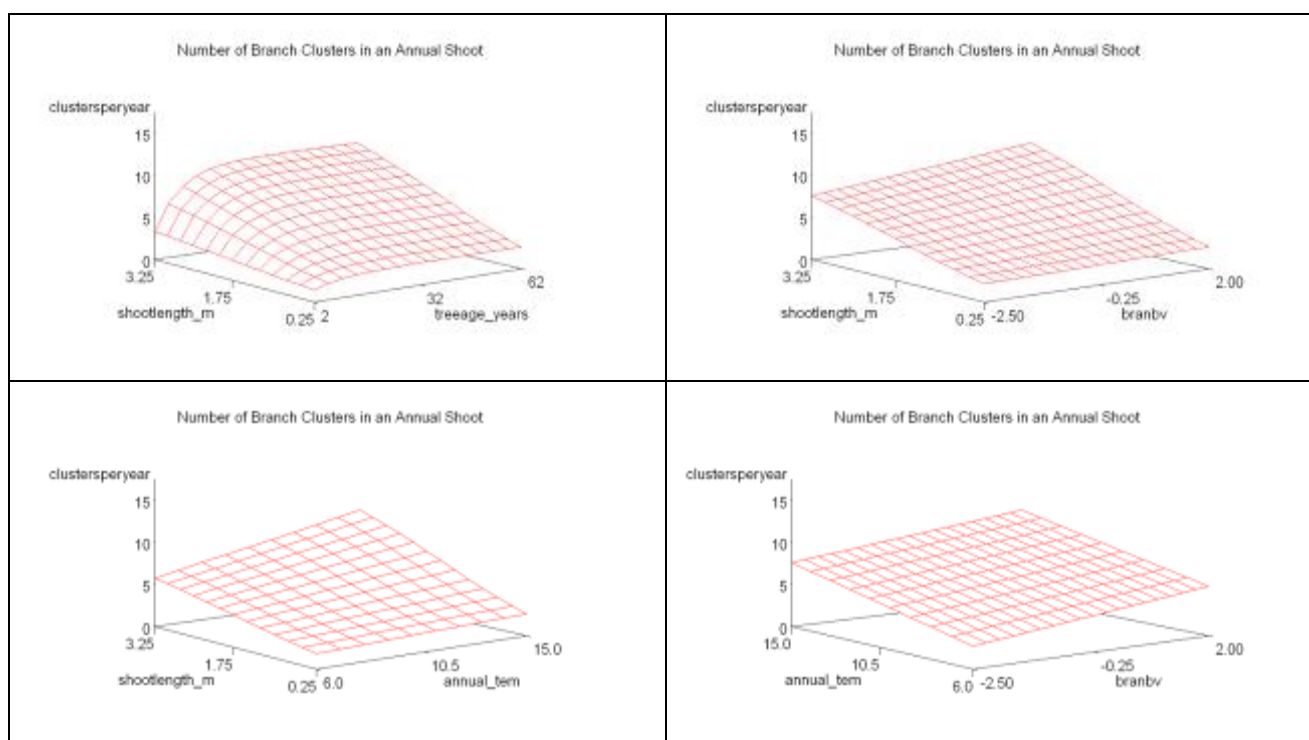


Figure 2: Performance of the equation for predicting the number of branch clusters in an annual shoot.

Relative Position of Clusters within an Annual Shoot

In the destructively-sampled dataset, the number of clusters within an annual shoot varied between one and 10. For a given site, the number of annual shoots with a given number of clusters can be very small. For this reason a look-up table was included in previous versions of TreeBLOSSIM to predict the relative position of clusters within an annual shoot. A very much larger dataset would be needed to develop a probabilistic model that predicted the observed variation in the data.

In this study, relative growth unit length was examined in order to develop an approach to incorporate more variability into BLOSSIM predictions of growth unit length. Relative growth unit lengths were plotted in two ways: (1) ranked by position in annual shoot, and (2) ranked by relative length within the annual shoot. Annual shoots with two and four clusters have been chosen to illustrate the approach (see Figure 3).

When the relative lengths of growth units were plotted versus observed position in the annual shoot, there was a lot of variation but little difference in mean relative length with respect to position in the annual shoot, and no obvious differences between sites (the data points for the different sites are not clearly separate) (see Figure 3).

When the growth units were ordered by relative length, the mean relative length varied with position, but there were no obvious differences between sites (the data points for the different sites are not clearly separate) (see Figure 3).

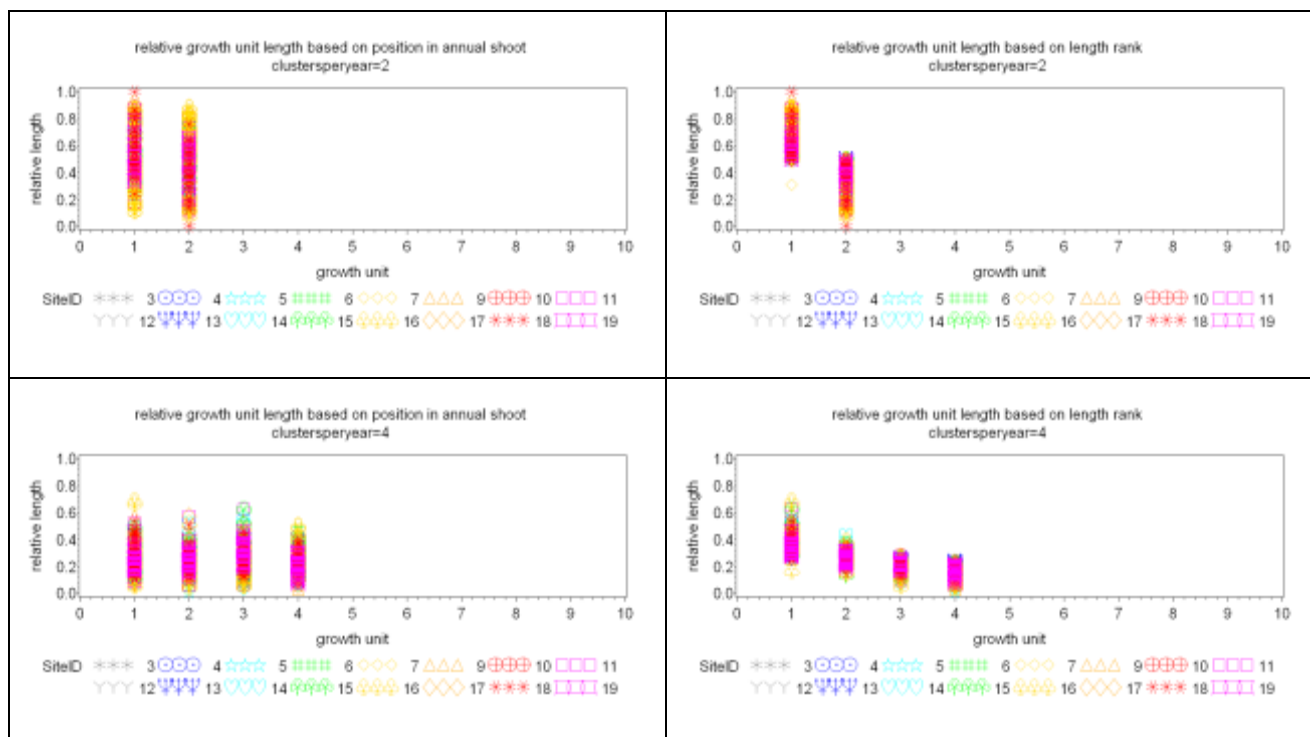


Figure 3: Relative length of growth units for annual shoots with two (top line) or four clusters (bottom line), with growth units ranked by position in annual shoot (left) or relative growth unit length (right).

The second approach (ranking by relative length within the annual shoot) provided more variation in relative growth unit length, and was selected for implementation. It was implemented by assuming the longest growth unit was at the base of the annual shoot and the shortest was at the top. This pattern is botanically realistic, but it is not obvious in the radiata pine data. Possible reasons for this include the fact that autumn extension is considered to be a head-start on the next-year's growth; leader changes also impact on observed patterns.

The influence of branch breeding value on relative growth unit length was investigated for annual shoots with two and four growth units. The relative length of the longest growth unit in each annual shoot was plotted against breeding values (see Figure 4). There was little variation with breeding value (i.e. relative length is approximately constant with increasing breeding value). Consequently there is no justification for incorporating breeding values into this function at the present time. The assumption should be re-checked when further data are available.

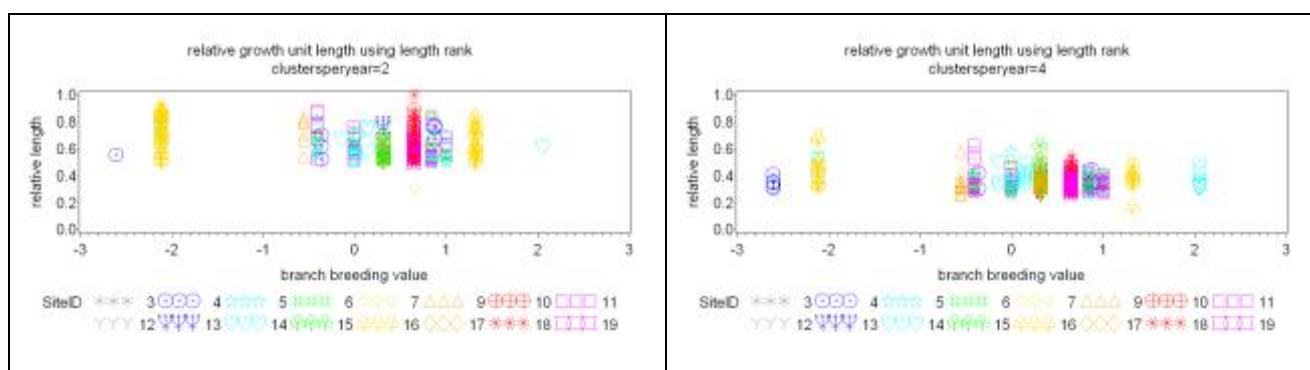


Figure 4: Observed relationship between relative growth unit length for first growth unit when ranked by length and branch breeding value for annual shoots with two (left) or four clusters (right).

In previous versions of BLOSSIM, the position of branch clusters was determined from a look-up Table. The position of the branch cluster corresponds to the end of the growth unit. For BLOSSIM Version 4.0, it was decided to maintain the look-up table, but assume the longest growth unit

occurred first in every annual shoot. Botanically, this is what you would expect, but it is not obvious in the radiata pine data. This approach will bring more variation to predicted growth unit and internode lengths. The revised look-up table is shown below (Table 2). For example, if an annual shoot was 1 m long and contained two growth units, the end of the first growth unit would be at 0.65 m, and the end of the second growth unit would be at 1 m.

Table 2: Look-up table for relative position of ends of growth units.

No. Clusters	1	2	3	4	5	6	7	8	9
Relative position for ends of growth units									
1	1.0								
2	0.65	1.0							
3	0.46	0.77	1.0						
4	0.36	0.63	0.84	1.0					
5	0.28	0.51	0.71	0.87	1.0				
6	0.24	0.44	0.62	0.77	0.89	1.0			
7	0.22	0.40	0.55	0.69	0.81	0.92	1.0		
8	0.22	0.38	0.53	0.65	0.77	0.87	0.94	1.0	
9	0.18	0.32	0.45	0.56	0.66	0.76	0.85	0.93	1.0

Performance of TreeBLOSSIM Version 4.0

TreeBLOSSIM Version 4.0 was run for selected Permanent Sample Plots (PSPs) from one trial in each of five growth modelling regions. These were trials selected as they contained a long-internode seedlot and TreeD data had previously been collected:

- FR7, Woodhill
- FR121/1, Tungrove
- FR121/2, Kinleith
- FR121/13, Golden Downs
- SD682, Dean.

Suitable data were not available for the other growth modelling regions. As with previous studies the difference in number of branch clusters per metre was calculated on an individual tree basis. The difference in number of branch clusters per metre from Version 4.0 was compared to the differences from Version 3.1.

Figure 5 shows the differences between actual and predicted clusters per metre for individual trees. The mean values for a given GFPlus rating for branch habit and model version are joined by a line. An assumption was made that an 'acceptable' model prediction is within 0.5 clusters per annual shoot. With an annual shoot length of 1.5 m, the acceptable error is within 0.33 clusters per metre, marked by horizontal lines at -0.33 m and 0.33 m. If the annual shoot length was 1 m, then an acceptable error would be between -0.5 and 0.5 m. Most of the mean values are within 0.33 m, suggesting that the model performance is acceptable (Figure 5). The performance of Version 4.0 is often, but not consistently, a slight improvement over Version 3.1. The improvement is particularly noticeable for the long-internode seedlots (low GFPlus values). This is a satisfying result given that there were few trees with low branch breeding values in the dataset used to develop the revised equations. The smaller differences between the two model versions for seedlots with higher breeding values are not unexpected, as TreeBLOSSIM Version 3.1 was designed for multinodal seedlots.

The fact that Version 3.1 contained regional functions for number of clusters per annual shoot, whereas Version 4.0 contains only one function that incorporates variability between sites through mean annual temperature, is a possible reason for the poorer performance of Version 4.0 in some instances.

Difference between TreeD and TreeBLOSSIM predictions for number of clusters per m for versions 3.1 and 4.0 for seedlots with different GFPlus rating for branch habit. Lines join the mean value for each seedlot and each version.

Assuming an acceptable model prediction is within 0.5 clusters per annual shoot and an annual shoot length of 1.5 m, then the acceptable error is within 0.33 clusters per metre, marked by horizontal lines at -0.33 m and 0.33 m.

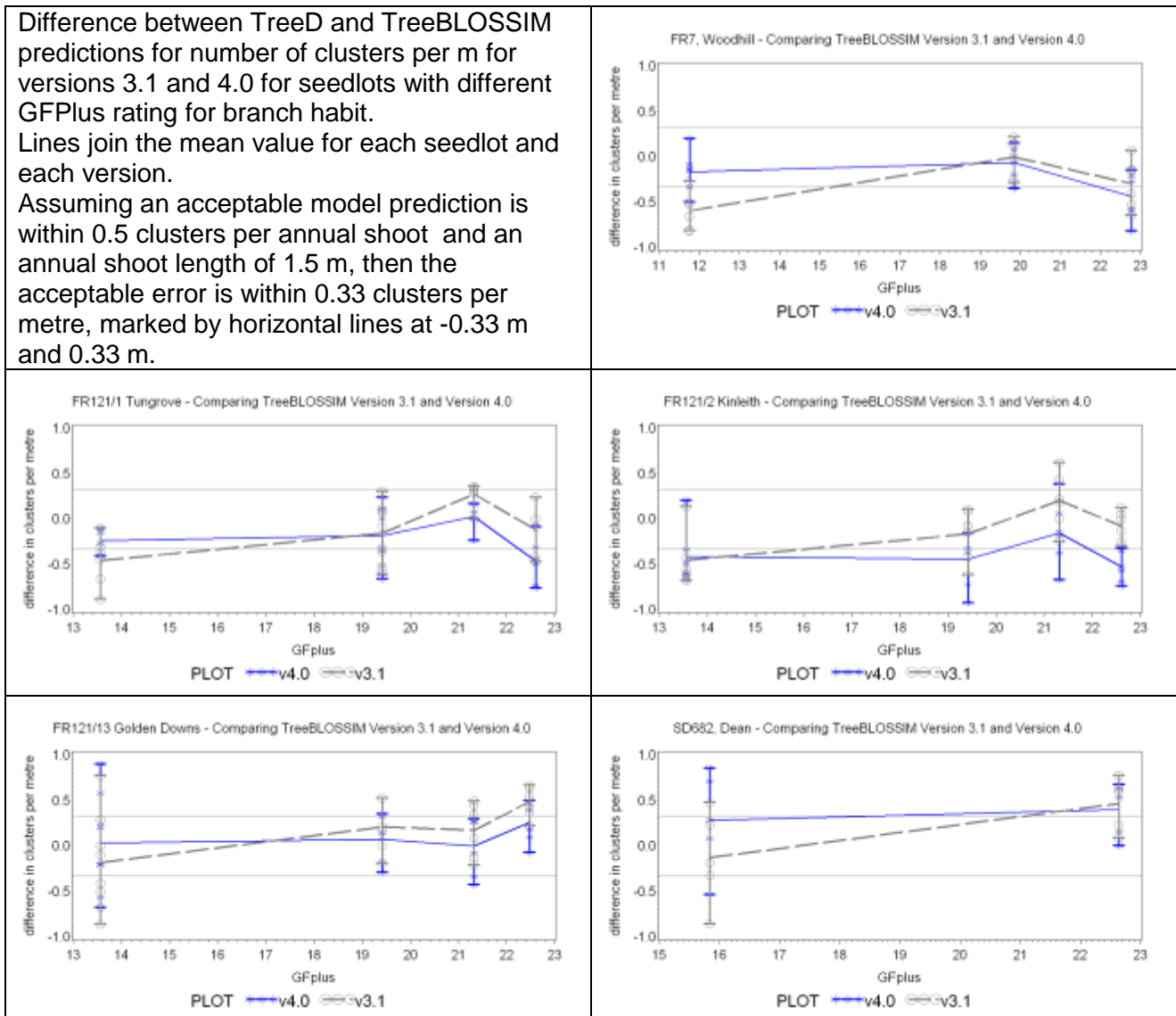


Figure 5. Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1.

CONCLUSION

Branch breeding values and mean annual temperature have been incorporated within the BLOSSIM function predicting the number of branch clusters in an annual shoot. Initial tests indicate that the incorporation of branch breeding values has improved the predictions of number of clusters, particularly for long-internode seedlots (i.e. low GFPlus branch habit scores).

TreeBLOSSIM Version 4.0 has been provided to ATLAS programmers for implementation in FFR Forecaster. The revised version in FFR Forecaster will allow the user to input branch breeding values and/or GFPlus branch habit scores. This will allow the impact of branch breeding values / GFPlus branch habit scores on the location of branch clusters to be investigated. Other functions within BLOSSIM (in particular branch angle and branch diameter growth) will need to be modified to fully account for the influence of genetics on internode length.

The predictions from Version 4.0, should be considered the “best case” scenario, as BLOSSIM does not predict the effects of damage (e.g. leader loss) on branching characteristics of an individual tree. Previous tests using TreeD^[3] have indicated that leader loss impacts on branching patterns, especially the occurrence of large branches.

Further improvements to BLOSSIM could be made by:

- Destructively-sampling more trees covering a greater range of genetic material and site conditions to provide a comprehensive matrix of data points for model development.
- Carrying-out further TreeD studies in GxExS trials to complete a matrix of site qualities for which branching data are available. Such data would be used to test further releases of BLOSSIM and thus provide confidence in the model for a greater range of conditions than used for model development.
- Carrying out ATLAS Cruiser assessment of GxExS trials to determine real value of different seedlots. In addition this would provide an estimate of the value loss through stem damage and whether this value loss varied with different seedlots.
- Incorporating the influence of genetics on other functions within BLOSSIM, in particular the influence of genetics on branch growth.
- Incorporating the probability of stem damage and its affect on branch development into TreeBLOSSIM.

ACKNOWLEDGEMENTS

Paul Jefferson and RBPC for allowing the incorporation of branch breeding values into BLOSSIM.
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APPENDICES

APPENDIX 1 – Large Graphs for Figures

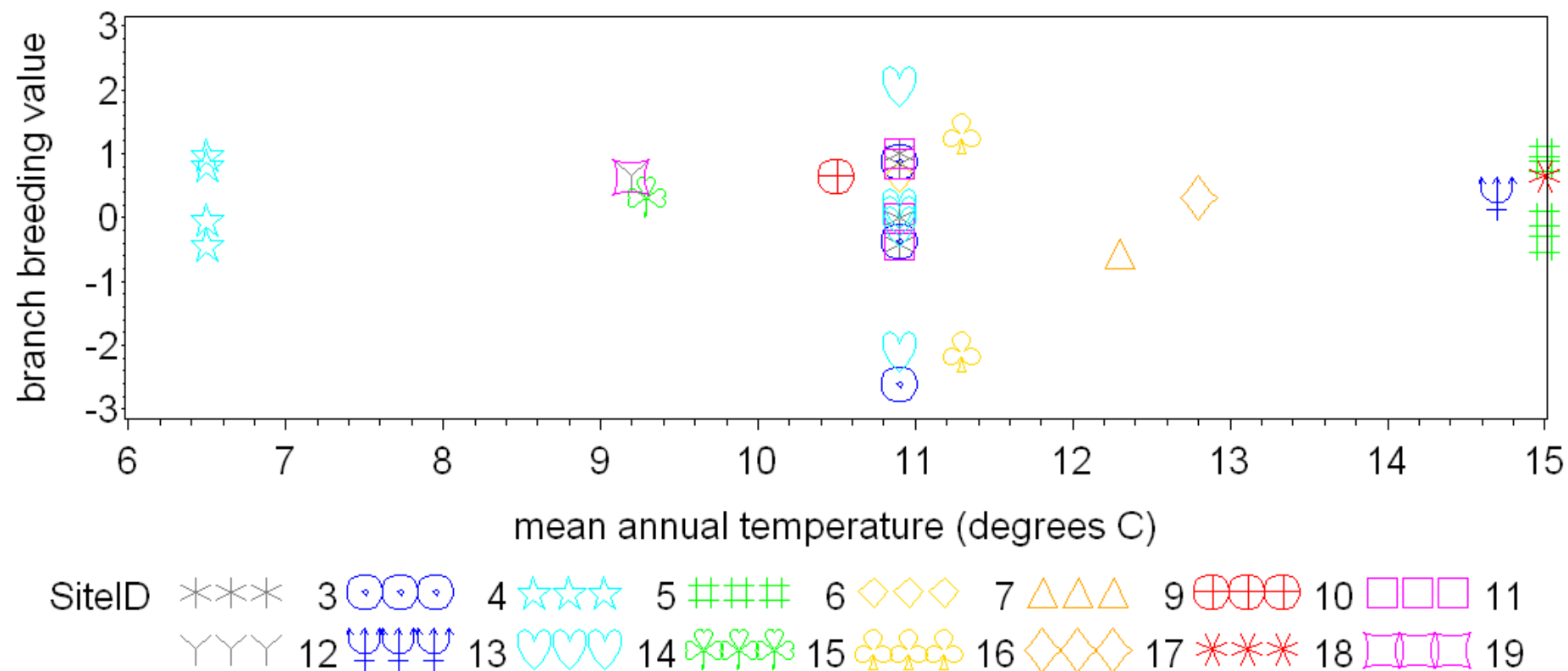


Figure 1: Distribution of data across branch breeding values and mean annual temperature.

Number of branch clusters in an annual shoot

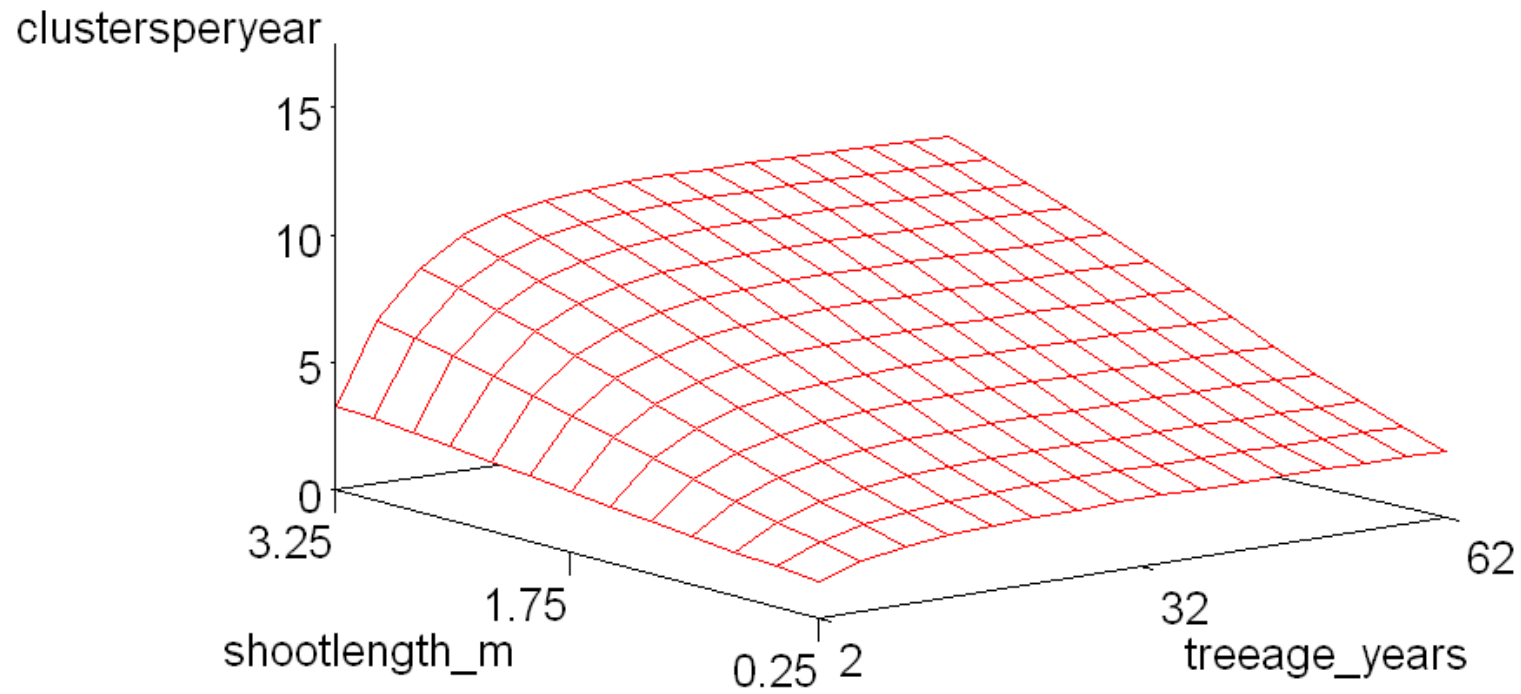


Figure 2a: Predicted number of branch clusters in an annual shoot – influence of shoot length and tree age.

Number of branch clusters in an annual shoot

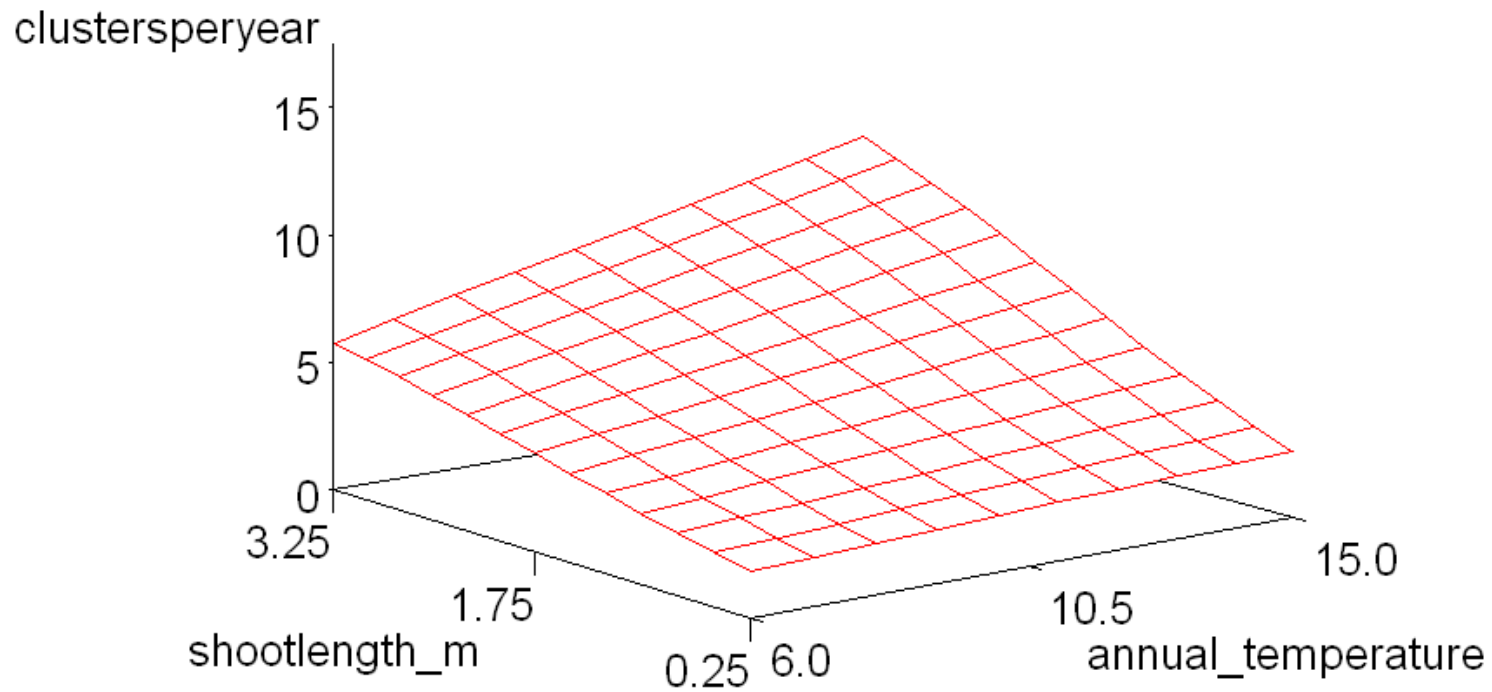


Figure 2b: Predicted number of branch clusters in an annual shoot – influence of shoot length and mean annual temperature.

Number of branch clusters in an annual shoot

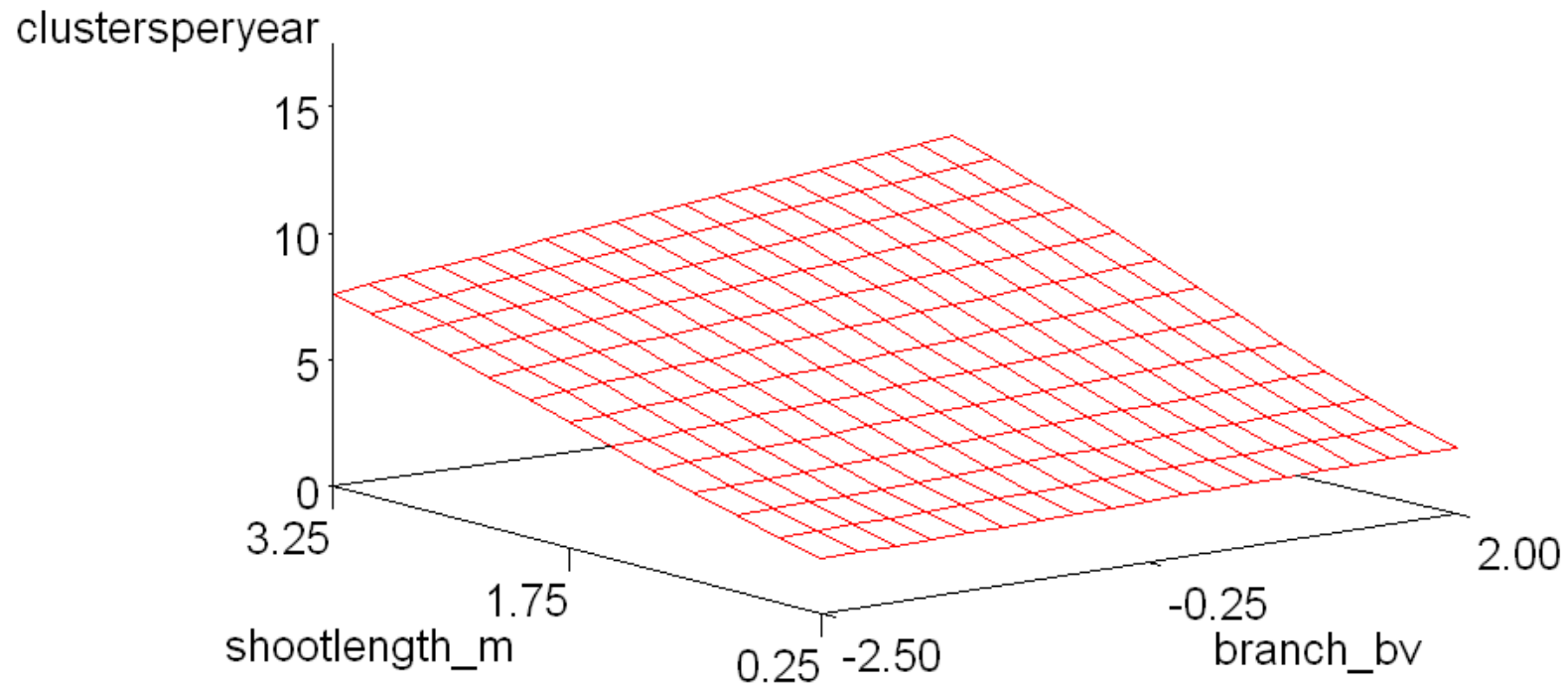


Figure 2c: Predicted number of branch clusters in an annual shoot – influence of shoot length and breeding value.

Number of branch clusters in an annual shoot

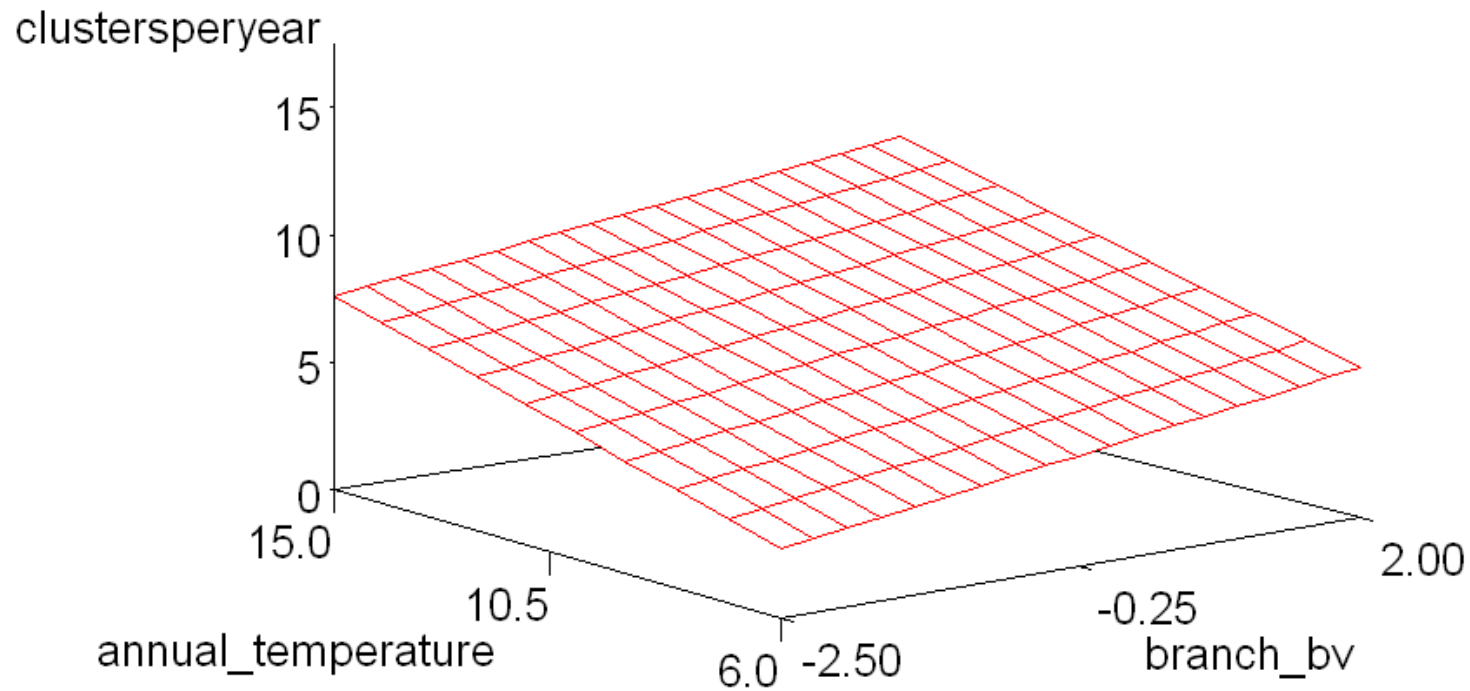


Figure 2d: Predicted number of branch clusters in an annual shoot – influence of mean annual temperature and branch breeding value.

relative growth unit length based on position in annual shoot
clustersperyear=2

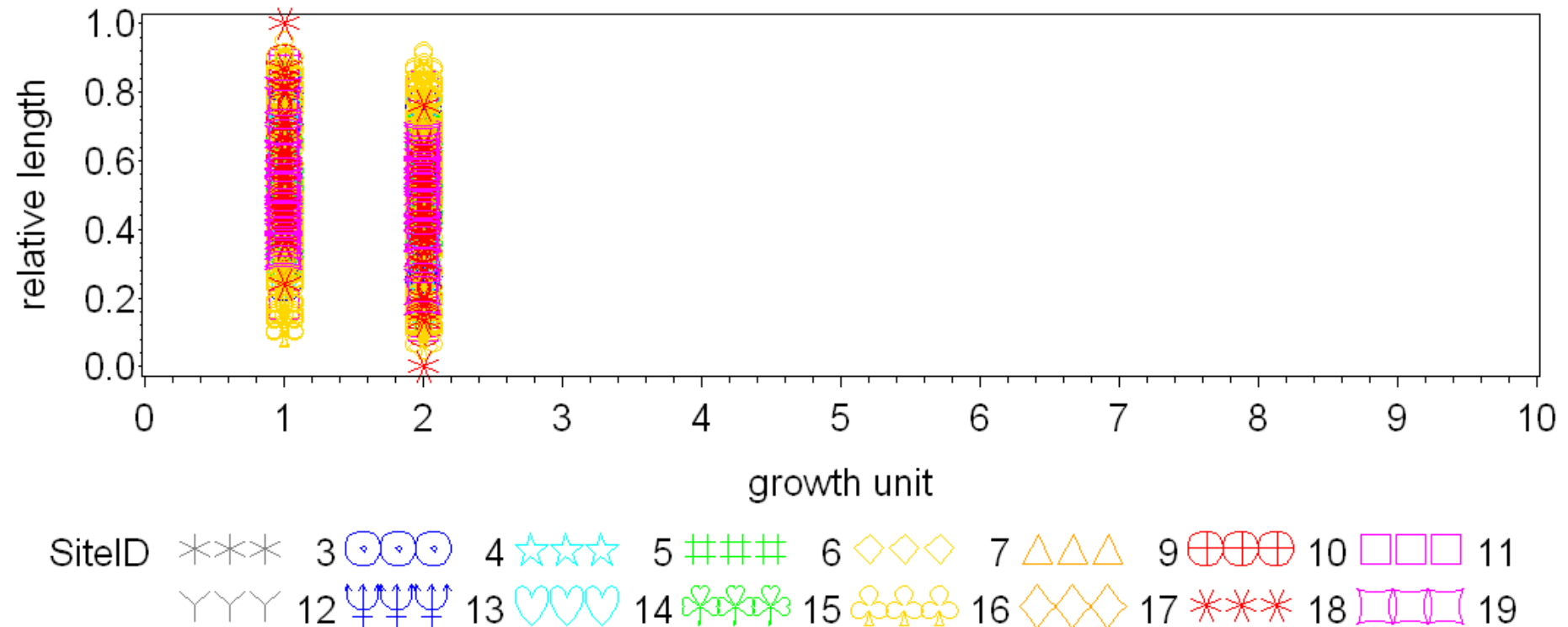


Figure 3a: Relative length of growth units for annual shoots for annual shoots with two clusters and growth units ranked by position.

relative growth unit length based on position in annual shoot
clustersperyear=4

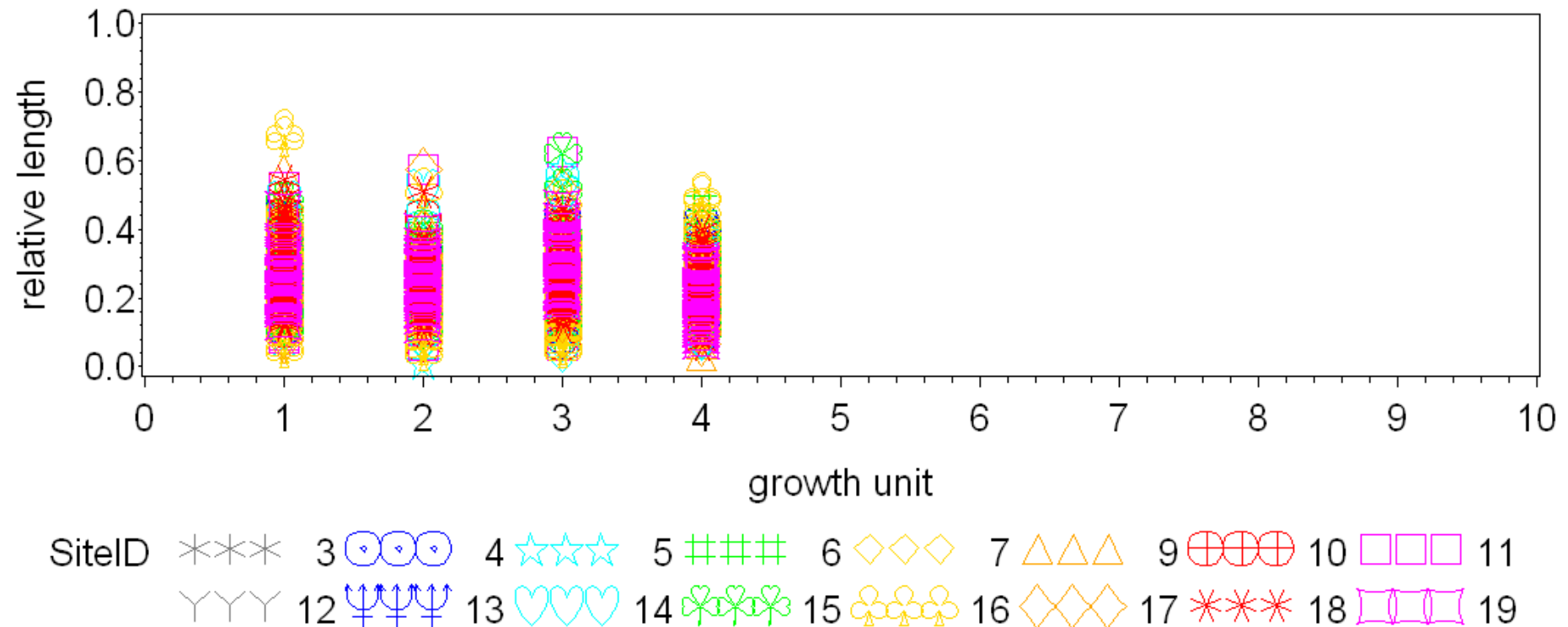


Figure 3b: Relative length of growth units for annual shoots with four clusters and growth units ranked by position.

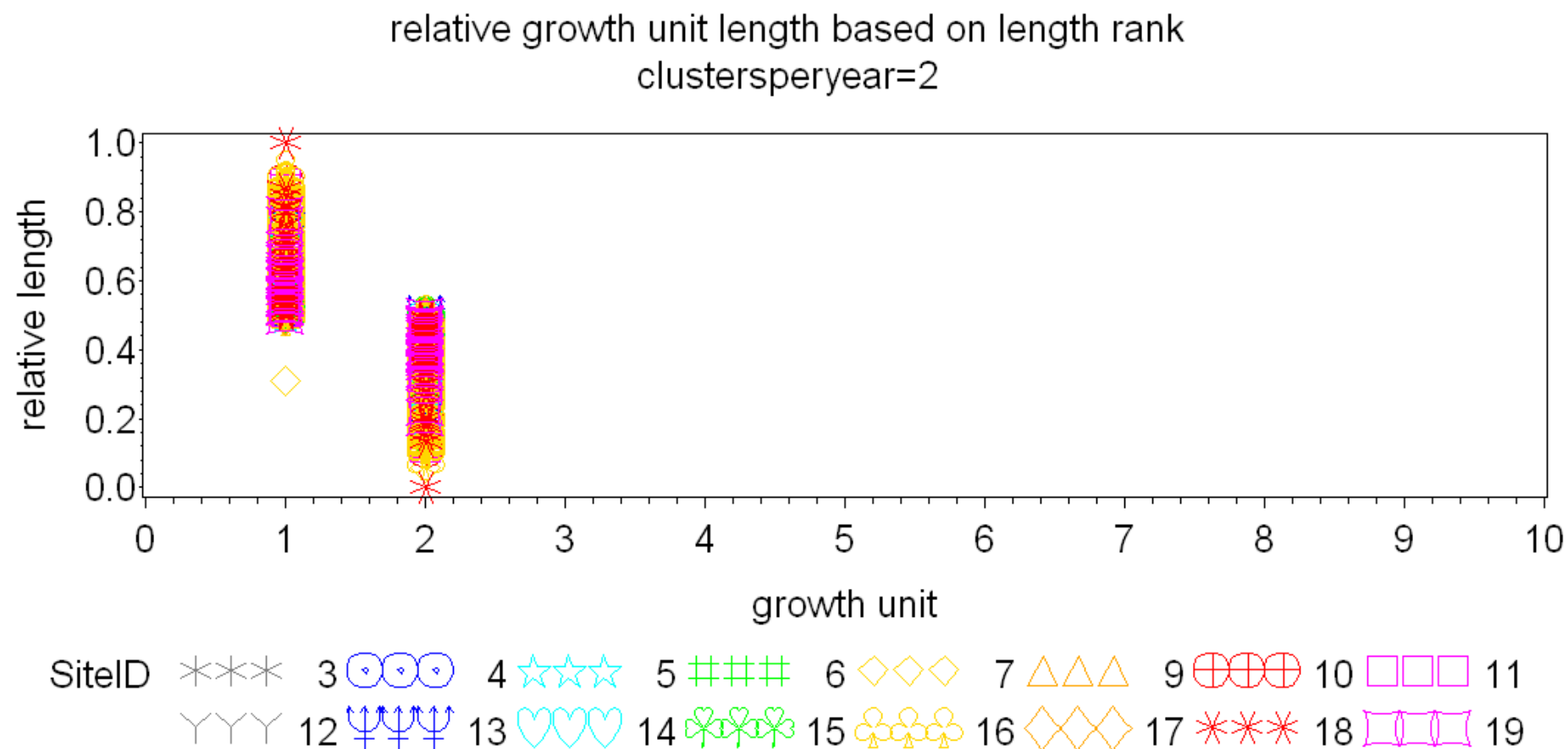
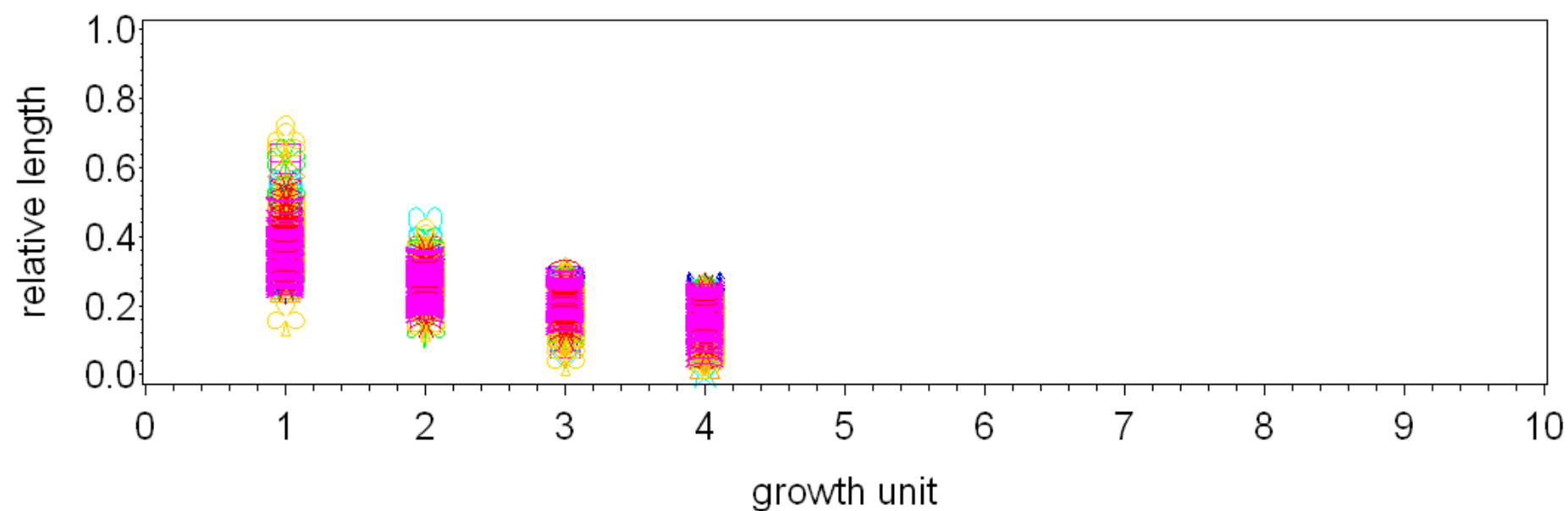


Figure 3c: Relative length of growth units for annual shoots for annual shoots with two clusters and growth units ranked by length.

relative growth unit length based on length rank
clustersperyear=4



SiteID *** 3    4    5    6    7    9    10    11
   12    13    14    15    16    17    18    19

Figure 3d: Relative length of growth units for annual shoots for annual shoots with four clusters and growth units ranked by length.

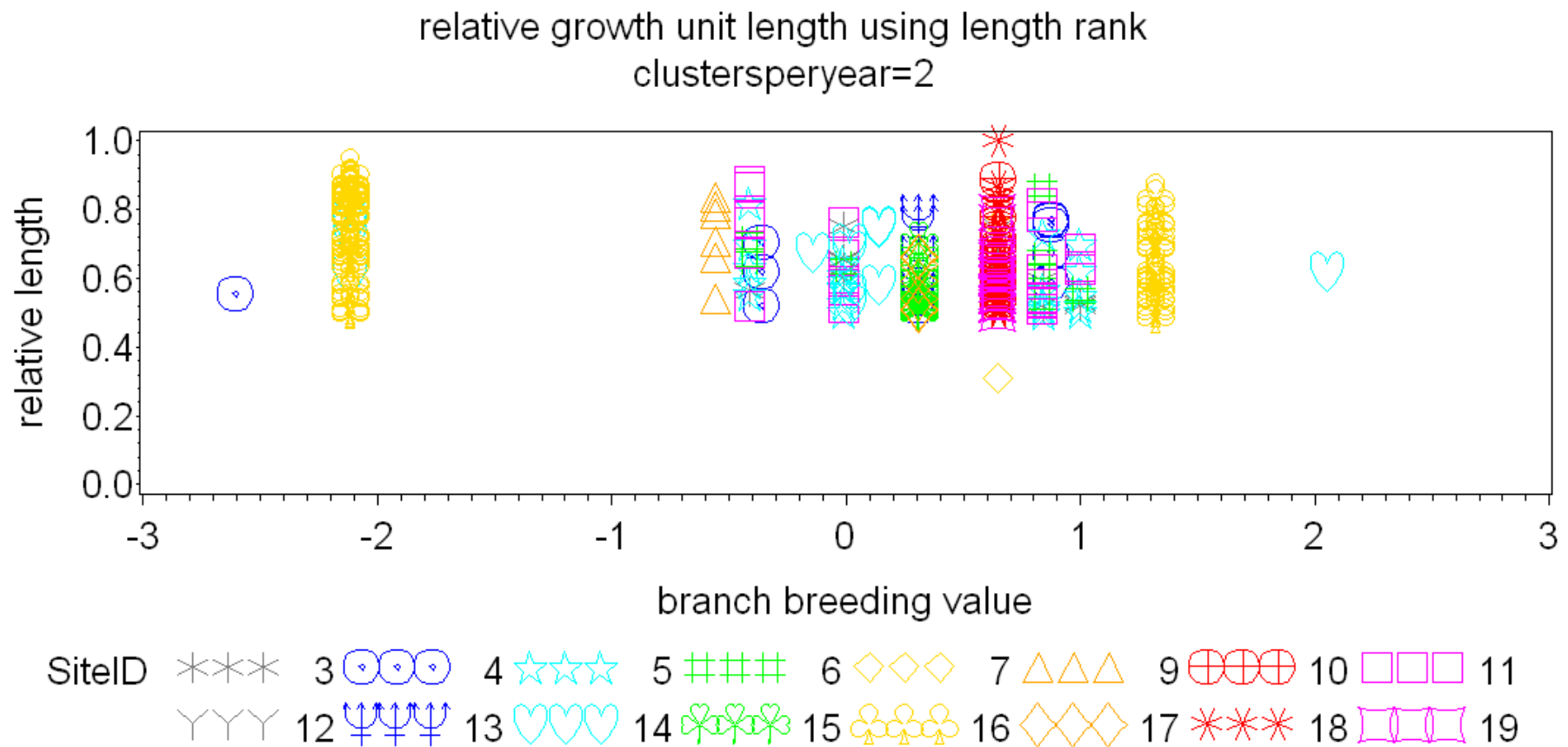


Figure 4a: Relationship between relative growth unit length for first growth unit when ranked by length and branch breeding value for annual shoots with two clusters.

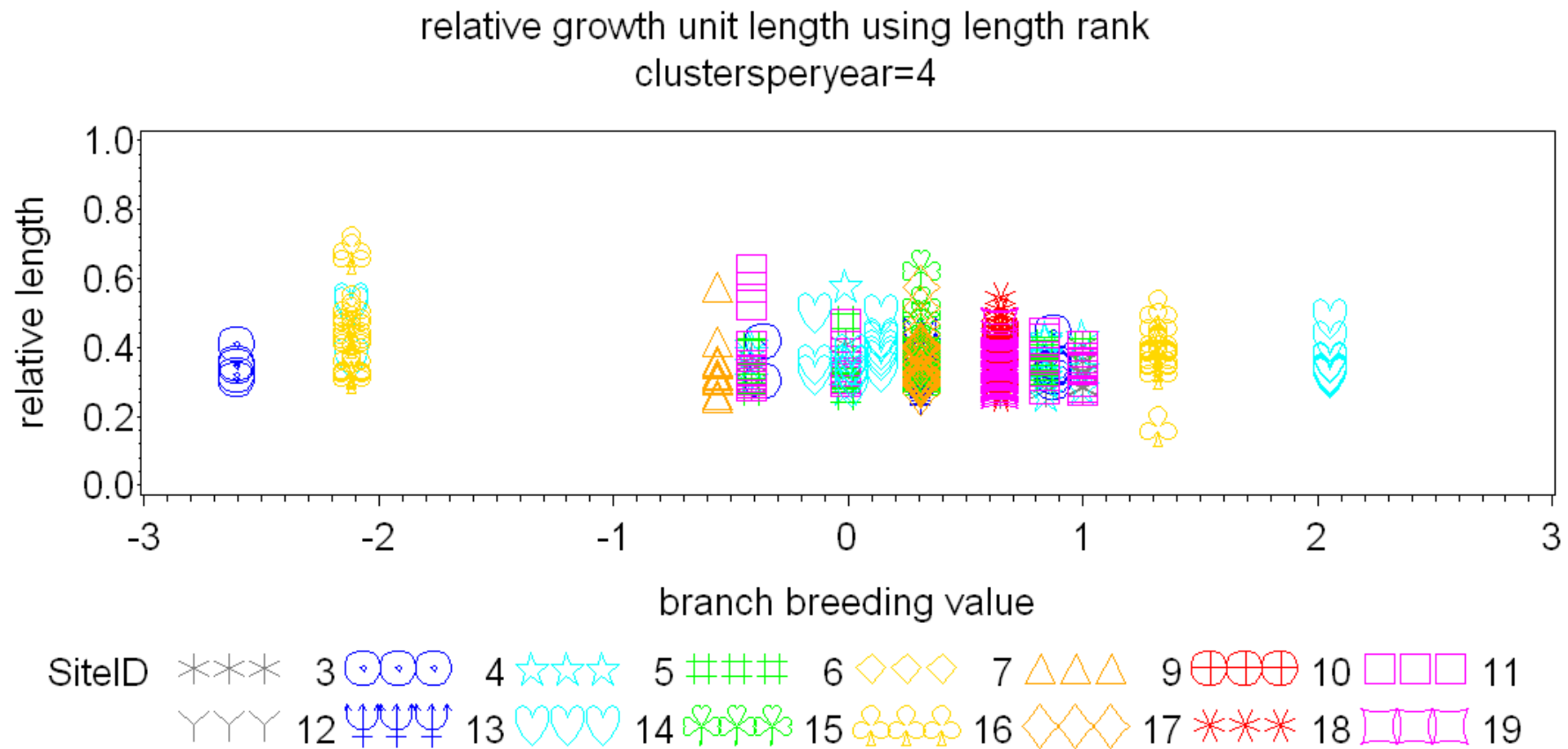


Figure 4b: Relationship between relative growth unit length for first growth unit when ranked by length and branch breeding value for annual shoots with four clusters.

FR7, Woodhill - Comparing TreeBLOSSIM Version 3.1 and Version 4.0

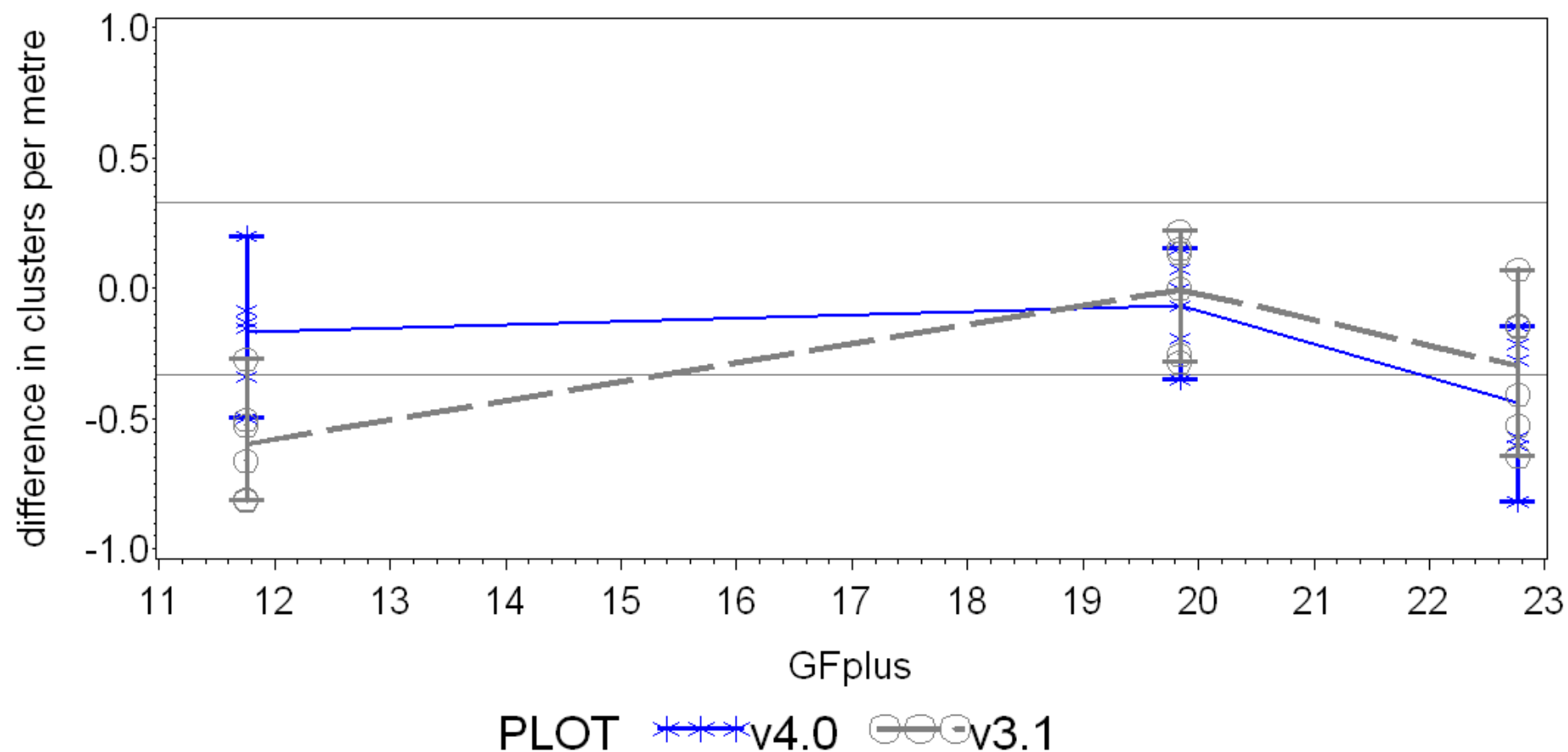


Figure 5a: Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1 for FR7, Woodhill.

FR121/1 Tungrove - Comparing TreeBLOSSIM Version 3.1 and Version 4.0

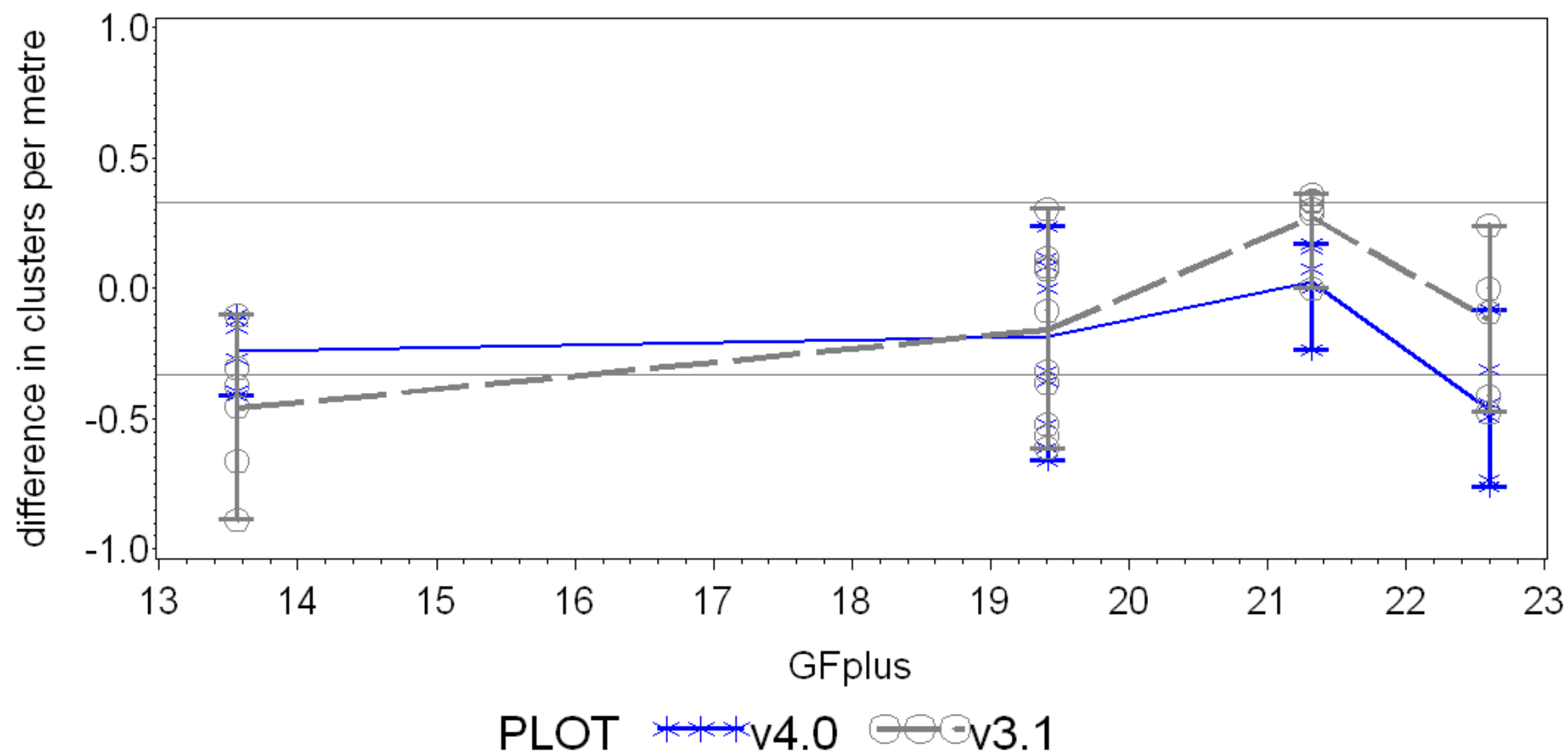


Figure 5b: Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1 for FR121/1, Tungrove.

FR121/2 Kinleith - Comparing TreeBLOSSIM Version 3.1 and Version 4.0

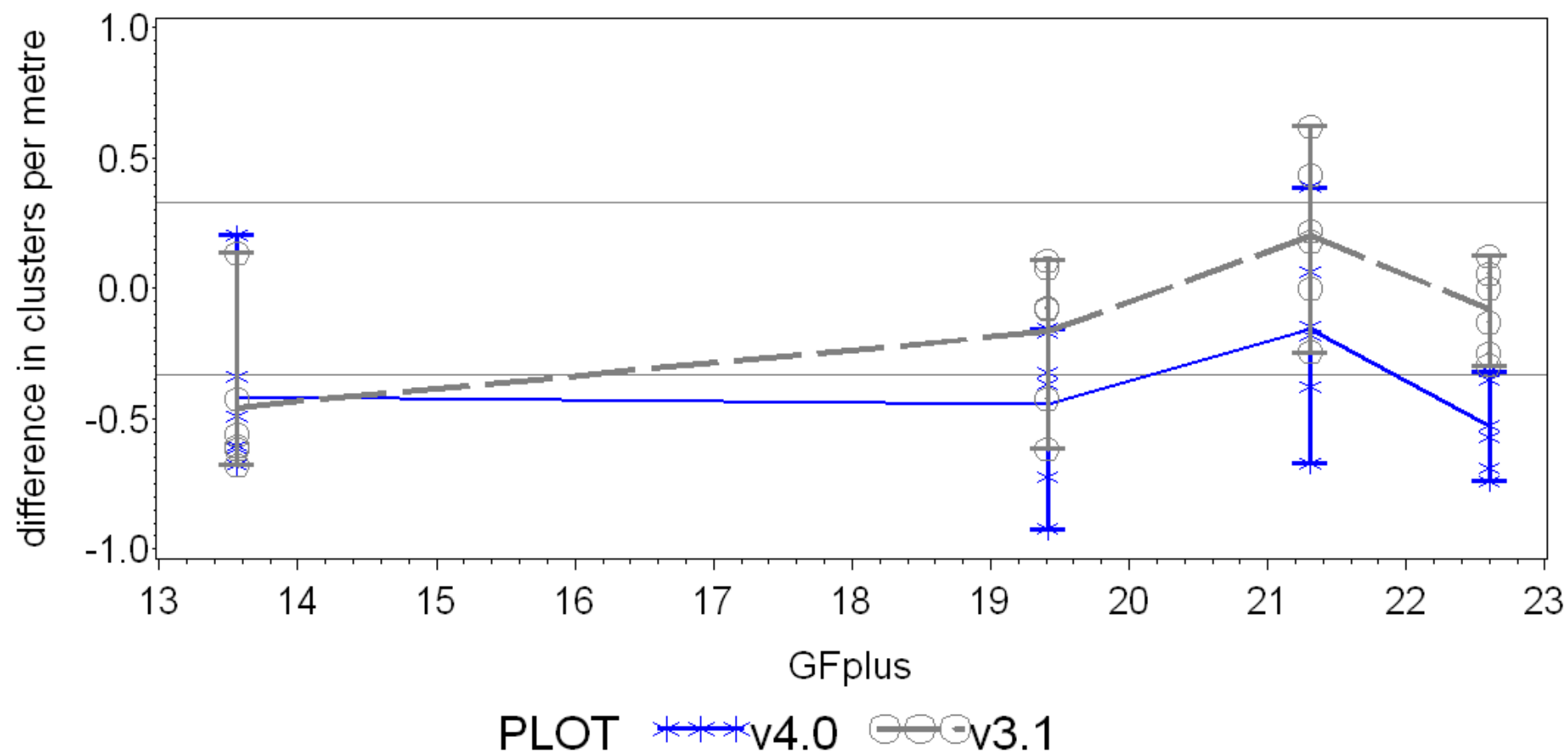


Figure 5c: Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1 for FR121/2, Kinleith

FR121/13 Golden Downs - Comparing TreeBLOSSIM Version 3.1 and Version 4.0

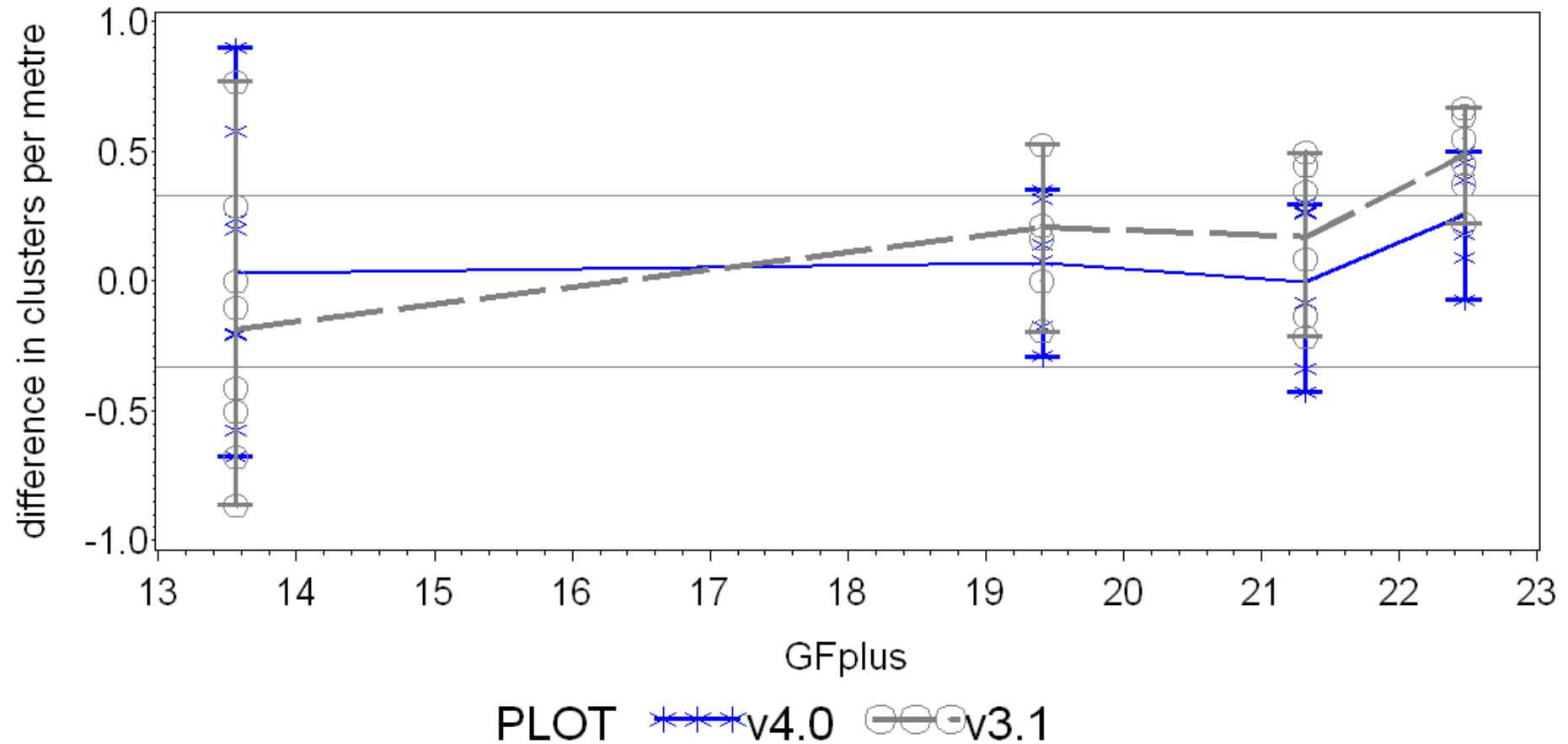


Figure 5d: Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1 for FR121/13, Golden Downs.

SD682, Dean - Comparing TreeBLOSSIM Version 3.1 and Version 4.0

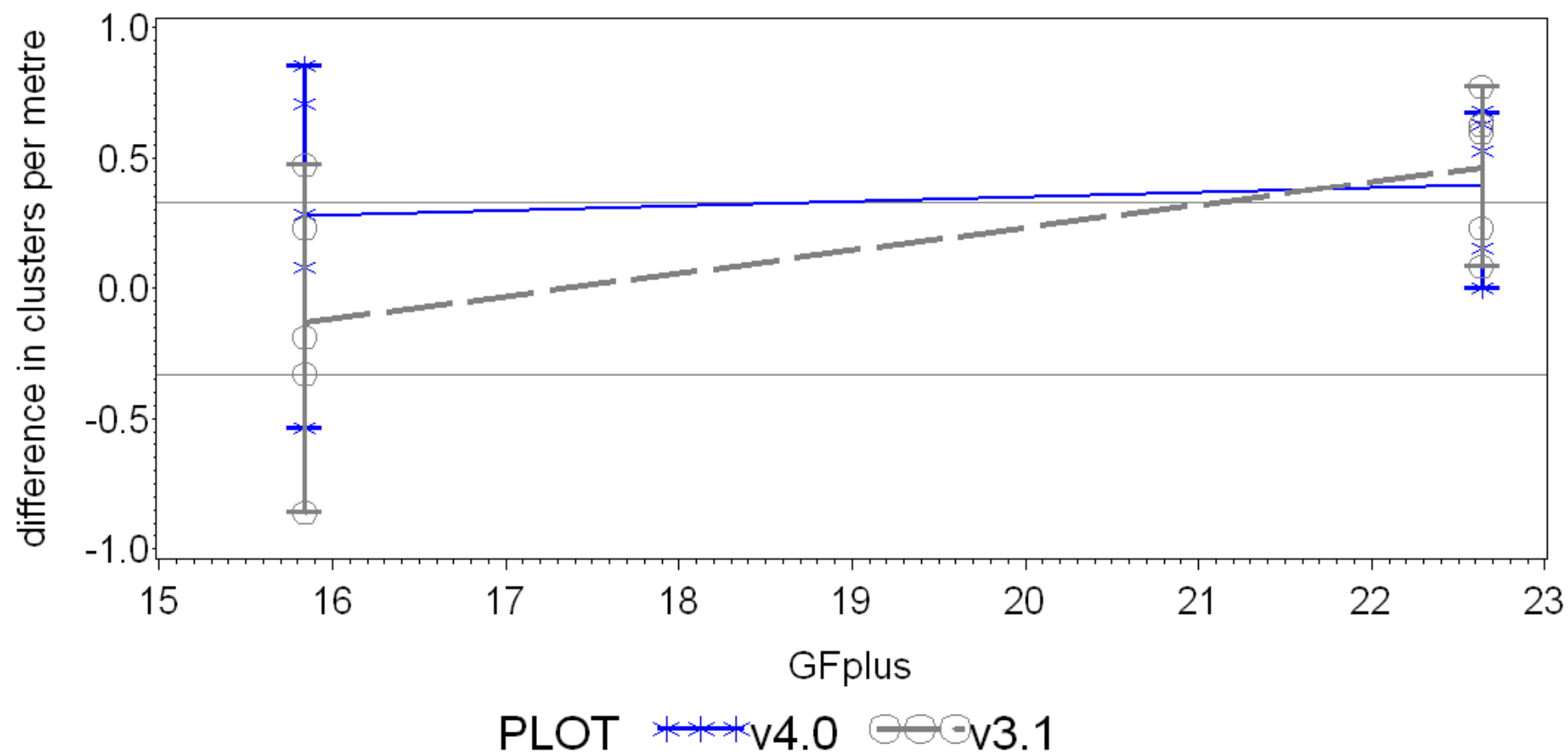


Figure 5e: Performance of TreeBLOSSIM Version 4.0 versus TreeBLOSSIM Version 3.1 for SD682, Dean.

APPENDIX 2 – Preliminary comparison of mean branch diameter for seedlots with similar GFPlus stem diameter ratings but very different GFPlus branch habit scores.

The mean branch diameter between 5 m and 8 m was calculated from TreeD images for two seedlots with similar GFPlus ratings for stem diameter growth:

- GF14 (GFPlus rating for stem diameter=18.0; GFPlus branch habit score=0.1432)
- GF13 /LI 25 (GFPlus rating for stem diameter=18.6; GFPlus branch habit score =-2.114)

The TreeD images came from four sites:

- FR121/1 (Tungrove)^[8]
- FR121/2 (Kinleith)^[9]
- FR121/3 (Gwavas)^[8]
- FR121/13 (Golden Downs)^[8]

Apart from one site, the mean branch diameters for the GF13/LI25 seedlot (Table A2) were bigger but within 1 cm of the values for the GF14 seedlot. Given that the mean branch diameters are within 1 cm on each site, and the GFPlus ratings for stem diameter growth are similar, this suggests that it would be reasonable to use the GFPlus rating for stem diameter growth to predict the influence of tree breeding on branch diameter growth

Table A2: Mean branch diameter (mm) between 5 m and 8 m calculated from TreeD image data

Site	Seedlot: GF14	Seedlot GF13/LI25
FR121/1 - Tungrove	57	47
FR121/2 - Kinleith	63	71
FR121/3 -Gwavas	62	69
FR121/13 – Golden Downs	43	49