Data Compilation and Analysis Procedures for Young Stand Monitoring in British Columbia

A Procedures Manual

Prepared for: Forest Analysis and Inventory Branch , Ministry of Forests, Lands, and Natural Resource Operations

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LIST OF ABBREVIATIONS AND ACRONYMS

AAC   Allowable Annual Cut
AU   Analysis Unit
BC   British Columbia
BGC   Biogeoclimatic Ecological Classification
CMI   Change Monitoring Inventory
DBH   Tree Diameter at Breast Height
FAIB   Forest Analysis and Inventory Branch
GY   Growth and Yield
IMU   Individual Monitoring Unit
MFLNRO   Ministry of Forests, Lands and Natural Resource Operations
MPB   Mountain Pine Beetle
MSYT   Managed Stand Yield Tables
MU   Monitoring Unit
MV   Merchantable Volume
NVAF   Net Volume Adjustment Factor
OAF   Operational Adjustment factor
PAI   Periodic Annual Increment
PSP   Permanent Sample Plot
RMU   Regional Monitoring Unit
SABC   Sensitivity Analysis on the Base Case
SAS   Statistical Analysis System
TFL   Tree Farm License
TSA   Timber Supply Area
TSR   Timber Supply Review
VRI   Vegetation Resources Inventory
WSV   Whole Stem Volume
YSM   Young Stand Monitoring

1   Introduction

1.1   Purpose of this Document

This document describes *minimum data compilation and analysis procedures* that are recommended for the young stand monitoring (YSM) initiative of the BC Ministry of Forests, Lands, and Natural Resource Operations (MFLRNO) Forest Analysis and Inventory Branch (FAIB). The objectives of the compilation and analysis are to check the accuracy of the growth and yield (GY) predictions of key attributes used in a management unit timber supply review (TSR), and to provide data to meet other YSM objectives, including describing the current status of young stands (e.g., current forest structure and health) and various special projects. The management unit could be a timber supply area (TSA) or a Tree Farm License (TFL). The key GY attributes include stand gross volume, net merchantable volume, site index, total age, site height, and species composition.

The compilation involves obtaining the plot summaries (actual values) for the key attributes from the monitoring plots, and their predicted or assumed values from GY models and used in TSR, at Time 1 and Time 2 (remeasurement). The analysis involves comparing the actual and predicted yields at Time 1 and Time 2, and the change between Time 1 and Time 2.[1] These procedures can be implemented in programs such as Microsoft Excel or Access, although some procedures may require more sophisticated statistical packages such as Statistical Analysis System (SAS) (SAS Institute Inc., Cary, NC, USA) or R (The R Foundation for Statistical Computing, Vienna, Austria). Examples of the compilation and analyses are given in the reports by Omule (2013) and FAIB (2013).

1.2   Organization of this Document

Section 2 outlines step-by-step procedures for compiling the actual and predicted values of the attributes of interest. Section 3 outlines the procedures for comparing the actual and predicted vales. Sections 4 and 5 outline the reporting of the analysis procedures and forest status reporting, respectively. The last section presents some applications of the analysis results.

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[1] These comparisons are limited to two time points: Time 1 and Time 2. They will need to be modified if there is more than one re-measurement, to enable simultaneous comparison of GY estimates at three or more time points (i.e., comparing growth curves).

2   Compilation of Actual and Predicted Values

2.1   Overview

The purpose of the compilation is to produce data for checking the accuracy of predicted values (VRI current values and TSR assumptions), and for other uses, such as state-of-the-forest reporting. The YSM ground plot attributes are considered to be "actual", "measured" or "truth" while the VRI or TSR-derived predictions are considered "estimates" or "predicted" vales. If there is a difference between the ground attributes and the VRI or TSR estimates, the VRI or TSR estimates are considered to be biased. A summary of the sources of data for various attributes and purpose are outlined in Table 1; definitions of the attributes are given in Table 2.

Table 1. Summary of desired stand attributes and data sources (definitions of attributes are given in Table 2).

Stand attribute	*Tree component*	*Source of data*	
		Ground values	*Predicted values*
Total age	Suitable trees	YSM: species-matched plots	VRI: species-matched polygons
Site height	Suitable trees	YSM: species-matched plots	VRI: species-matched polygons
Site index (SI)	Suitable trees	YSM: species matched plots	VRI or Site Productivity Layer: species-matched polygons
Leading species	All live trees	YSM: all plots	VRI: all polygons
Trees/ha	All live trees, excluding residuals*	YSM: all plots	TIPSY: all plots
Basal area/ha	All live trees, excluding residuals	YSM: all plots	TIPSY: all plots
Gross volume/ha	All live trees, excluding residuals	YSM: all plots	TIPSY: all plots

Stand attribute	Tree component	Source of data	
		Ground values	*Predicted values*
Net merchantable volume /ha	All live trees, excluding residuals	YSM: all plots	TIPSY: all plots

* Residuals are trees classified as veterans and those that exceed specified DBH, age or crown class thresholds. The thresholds are set on a project-specific basis.

Table 2. Attribute definitions.

Attribute	Definition
Site height	Mean Height of all suitable height trees by species.
Stand age	Mean Total Age of all suitable age trees by species.
Site index	Mean Site Index of the site indices of all suitable trees by species. The site index of each suitable tree is computed using SiteTools.
Leading species	Leading Species by Basal Area: The species with the highest BA out of a species composition list of the top 5 species ranked by % of BA (from highest to lowest).
Gross volume	Whole stem volume / ha (live trees): Whole stem volume/ha of living trees by species. It includes the volume of the main stem, including stump and top as well as defective and decayed wood of the tree.
Net merchantable volume	Merchantable stem volume/ha (live trees): [Gross stem volume – cruiser-called decay volume – (volume of waste, top and stump)] x Net Volume Adjustment Factor (NVAF).
Mortality	Gross volume/ha (dead standing trees).

2.2   Ground Data Preparation

2.2.1   Data editing

Check individual tree measurements between Time t and Time t-1 (t > 2) for errors such as abnormal changes in diameter, height, status (live/dead), and species labels. This is usually done in the field using the electronic data recorder TIMVEG developed by MFRNO. The data are also screened using appropriate criteria to detect any departures from the intended YSM population.

In particular, the data are screened for large, old trees as well as any identified as residuals.[2] This screening is particularly important in the comparison of the YSM data with the TIPSY predictions, which do not include residuals. Note that for the state-of-the-forest reporting, residuals are not excluded.

2.2.2   Species matching

Species matching is used to select data pairs to be used to analyze age, height and site index. Following the matching procedures developed for VRI (FAIB, 2011), match the YSM ground data with the corresponding Phase I inventory data for the parent polygon. The objective is to find those YSM plots that match the YSM ground leading species to the VRI Phase I inventory leading or secondary species. If a match cannot be made at the Sp0 (genus) level, conifer-to-conifer (or deciduous-to-deciduous) matches are allowed. However, conifer-deciduous matches are not acceptable. Then the ground plot heights and ages from the matched plots are compared with the corresponding VRI Phase I estimates.

The five possible matching cases are as follows:

- Case 1: Phase I inventory leading Sp0 matches the YSM ground leading Sp0.
- Case 2: Phase I inventory second Sp0 matches the YSM ground leading Sp0.
- Case 3: Phase I inventory leading species and the YSM ground leading species are both coniferous or are both deciduous.
- Case 4: Phase I inventory second species and the YSM ground leading species are both coniferous or are both deciduous.
- Case 5: No match.

The species matching rules are also used for site index, but only the plots in Case 1 and Case 2 are considered satisfactory matches. Site index comparisons could be expanded to more observations since ground site tree data are collected from all species in the YSM ground plots. The site index comparison could be made based on predictions from the provincial site productivity tile (where available and permitted). This way the site index comparison can be made for almost all species where ground site tree data are collected and not just the leading species.

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[2] Residuals are trees classified in the field as veterans, or those that are found during analysis to exceed specified DBH, age or crown class thresholds. These thresholds depend on the structure of the target population, and are, therefore, set on a project-specific basis.

2.3   Ground GY current values and change

2.3.1   Live-tree stand attributes

Compile the ground growth and yield values for each plot as follows:

1. Compile the edited individual tree data for key at*tribu*te*s f*or both Ti*me t a*n*d* Time *t-1* measurements using an updated version of the VRI/CMI compiler of the MFRNO. Alternatively, obtain compiled individual tree data from FAIB for each plot at Time 1 and Time 2 from an up-to-date version of the VRI/CMI Compiler. For each plot, extract from the Compiler output the current values of gross volume, net merchantable volume, site index by species, total age, site height and leading species at Time 1 and Time 2 (Table 2). Note that the pest and disease incidence data are not available in summary form (i.e., not part of the VRI/CMI Compiler standard output). They need to be custom compiled.

2. Calculate the change in volume (gross and net merchantable, for live trees of minimum DBH limit):
   a. Net change: The plot volume at Time 2 minus the plot volume at Time 1. This is survivor growth (volume growth of trees that survived between Time 1 and Time 2), plus ingrowth (volume of trees growing into merchantable size between Time 1 and Time 2) minus mortality.
   b. Periodic annual increment (PAI): net change divided by the number of years in the period Time 1 and Time 2.

3. Calculate the change in height and site index between Time 1 and Time 2 for each plot.

2.3.2   Stand and stock tables

Calculate the percent distribution of the number of stems per hectare, and volume per hectare, by species.

2.3.3   Mortality

Compile the actual mortality at each plot as follows:

1. Obtain individual tree data at Time 1 and Time 2 from the data entry tool.
2. Identify the mortality trees, i.e., those trees that are of minimum DBH limit (e.g., DBH ≥ 7.5 cm) and alive at Time 1, and dead at Time 2.
3. Calculate the gross and net merchantable volume per hectare of the mortality trees at Time 2.
4. Obtain live (standing) volume from the VRI/CMI Compiler of the MFLRNO FAIB at Time 2 (Table 1).
5. Calculate the mortality gross volume per hectare as a percentage of the total gross volume (live plus mortality at Time 2).

6. Examine the amount of individual plot mortality for excessive mortality, which could indicate catastrophic mortality (see Section 3.1). Deciding on what excessive mortality is quite subjective. We could, for example, set the threshold at approximately 58% of the plot total merchantable volume (MV) lost to mortality, which is the currently projected provincial MV lost to the MPB infestation reported by Walton (2012, p.8).[3]

2.3.4   Ingrowth

Compile the actual ingrowth as follows:

1. Obtain individual tree data from the data entry tool.
2. Identify the ingrowth trees as those trees that are of below the minimum DBH limit (e.g., DBH ≥ 7.5cm) and alive at Time 1, and have attained the minimum DBH limit and alive at Time 2.
3. Calculate the gross volume and number of stems per hectare of the ingrowth trees at Time 2.

2.4   Predicted Current Values and Change

Compile the predicted GY estimates for each plot as follows:

1. Obtain Analysis Unit (AU) definitions and assumptions including species composition, site index and establishment density.
2. Use TIPSY to generate managed stand yield tables (MSYT) for each AU.
3. Assign each ground plot to an AU, and the GY predictions associated with that plot are taken from the MSYT at the appropriate ages (Time 1 and Time 2).
4. Calculate the plot predicted gross volume and net merchantable volume PAI between Time 1 and Time 2, using the predicted yield in Step 3.
5. Obtain the VRI projected inventory stand age, site height and site index from the VRI Phase I files for each plot at Time 1 and Time 2.
6. Obtain predicted site index from the site productivity layer for each plot at Time 1.
7. Calculate the plot predicted height PAI between Time 1 and Time 2, using the predicted yield in Step 5.
8. Calculate the change in VRI site index between Time 1 and Time 2 for each plot.

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[3] A. Walton. 2012. Provincial-level projections of the current mountain pine beetle outbreak: Update of the infestation projection based on the provincial aerial overview surveys of forest health conducted from 1999 through 2011 and the BCMPB model (year 9). BC Forest service, Victoria, BC. Available at: http://www.for.gov.bc.ca/ftp/hre/external/!publish/web/bcmpb/year9/BCMPB.v9.BeetleProjection.Update.pdf

2.5   Bias of Predicted GY Estimates

2.5.1   Total bias

Calculate the total bias of predicted values at each YSM plot, as the difference between actual values and predicted GY values as follows:

1. Calculate the plot differences between the actual and predicted values for gross volume, net merchantable volume, site index, stand height and stand age at Time 1 and at Time 2.
2. Calculate the plot differences between the actual and predicted PAI values for gross volume, net merchantable volume and height.
3. Calculate the plot differences in site index between Time 1 and Time 2.

These values are then used to make the comparisons in Section 3.

2.5.2   Volume bias components

Calculate the volume total bias (gross or merchantable) components as follows:

Total Bias   = VOL1 – VOL3
Model Bias   = VOL1 – VOL2
Attribute Bias   = VOL2 – VOL3

where:

VOL1: Ground-based whole stem plot volume. The data are screened and residual trees removed. VOL1 is identical to the ground-compiled volume except for the removal of residual-tree volumes. The compiled ground plot volumes must match as closely as possible the predicted volumes generated from yield curves (e.g., may include a minimum DBH limit, close utilization levels, and/or inclusion of decay, waste, and breakage factors).

VOL2: TIPSY-predicted volumes for each YSM ground sample, using ground plot inputs together with Management Plan (MP)-based analysis unit assumptions. The ground-based input attributes include site index and species composition. The predicted volume assigned to each ground sample will be at the location on the MSYT where the height of the ground-based site trees match the top height predicted from the TIPSY MSYT.

VOL3: These are the volumes the predicted volumes from Section 2.4 – usually the predicted volumes from the TSR yield curves.

3   Analysis of Actual and Predicted Values

3.1   Catastrophic mortality

Examine the magnitude of the plot ingrowth and mortality (see Section 2.1). Separate endemic mortality plots from catastrophic mortality plots, since these two types of mortality are generally treated differently in timber supply review. Endemic mortality is incorporated into timber supply yield curves while catastrophic mortality, such as the Mountain Pine Beetle (MPB) attack, is adjusted separately. A catastrophic mortality threshold should be set, depending on the MU and stand conditions and history.

Summarize the statistics for the catastrophic mortality plots. Use the endemic mortality plots for further analysis (graphical and statistical comparisons) as in the following sections.

3.2   Volume

A. Conduct graphical comparisons of actual and predicted gross volume and net merchantable volume growth (PAI) and yield (Time 1 and Time 2) TIPSY-generated estimates as follows:[4]

1.   Plot the actual plot volume (gross or net) versus actual age, and overlay an analysis unit yield curve (Figure 1). Examine the scatter of the data, which could suggest a need for post-stratification (e.g., by leading species).
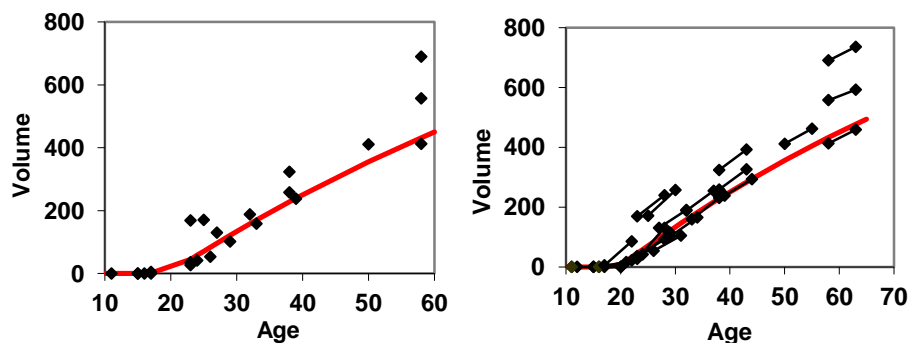
Figure 1. Example graphs of actual volume (gross or net; m³/ha) versus age (yr) at Time 1 (left), and Time 2 re-measurement. The plotted curve (in red) is an analysis unit yield curve used in TSR (assume all plots are in the same analysis unit).

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[4] Adapted from the report: *Graphical & Statistical Analysis for Monitoring Estimates of Change at the Management-Unit Level (Version 2.0).* Contract report prepared by J.S. Thrower & Associates Ltd. for the Resources Inventory Branch, BC Ministry of Forests, Victoria, BC.

2. Plot the actual volume versus the predicted volume at Time 1 and Time 2, and 5-year volume PAI (Figure 2; only Time 1 volume shown). If predicted values are accurate, then most points should fall along the 1:1 line of correspondence for the unit the plots represent.   Outliers can be flagged and examined to determine if any potential problems in prediction are indicated.
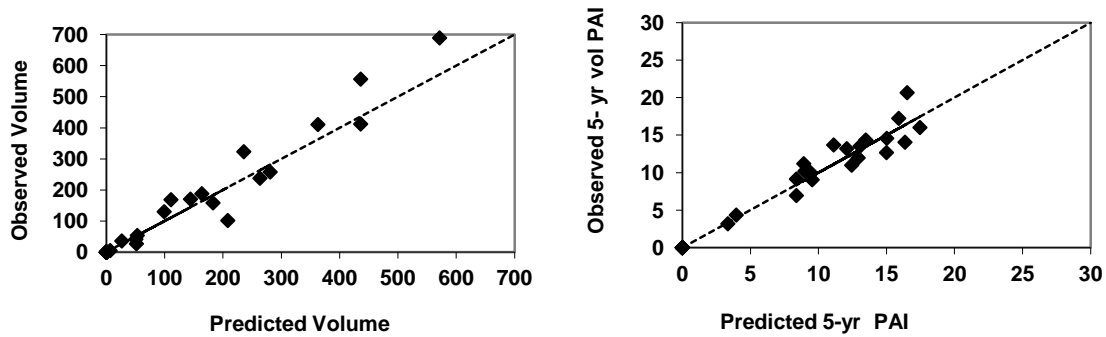
Figure 2. Example graphs of actual volume versus predicted volume at Time 1 (m^3/ha) (left), and 5-year volume PAI (m^3/ha).

3. Plot the differences between the actual and predicted volume and volume PAI versus age (Figure 3; only PAI example is shown). This may indicate trends of over- or under-prediction for different age ranges. The same absolute differences at younger and older ages have different implications. Thus, expressing   differences as a percent of the actual value can provide a better view of the differences over time and age (Figure 3).

Figure 3. Example graphs of differences of 5-year volume PAI: Absolute difference (m^3/ha/yr) versus age (yr) (left), and percent difference (% actual) versus age.

B. Post-stratify the data by source of predicted values (VDYP7 or TIPSY), as well as possibly other variables. Conduct a statistical comparison of the actual and predicted values by post-strata for the variables: volume at Time 1, volume at Time 2, and volume PAI. For each variable comparison, proceed as follows:

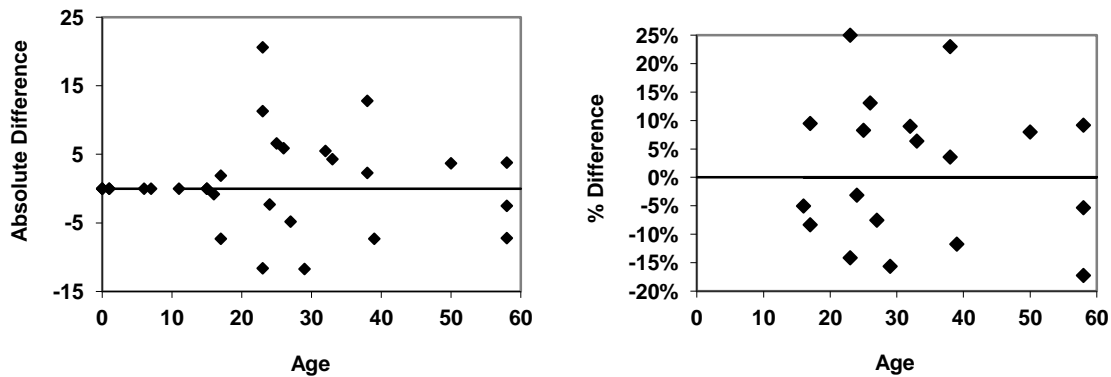1. Treat the actual and predicted values as if they were a paired sample and calculate the plot differences between actual and predicted values.

2. Calculate the descriptive statistics of the differences between actual and predicted values: mean difference ($\bar{d}$) and standard deviation of the differences   ($\hat{\sigma}$).

3. Calculate the paired sample t-test statistic: $t = \dfrac{\bar{d}}{\hat{\sigma}/\sqrt{n}}$, where *n* is the number of plots.

4. Compare the calculated *t*-value (Step 3) with a tabulated t-value ($t_{\alpha/2}$), with n-1 degrees of freedom and α probability level of a Type I error (usually 0.05). If the calculated *t*-value is greater than the tabulated *t*-value then the actual differences are statistically significant.[5]

5. Calculate the power of the *t*-test using a statistical package such as SAS (e.g., PROC POWER procedure).

Example of volume PAI comparison:
An example of the PAI comparisons is shown in Table 3.

Table 3. Example of the volume PAI paired *t*-test comparison (*n* = 10).

Plot No.	Actual volume PAI (m^3/ha)	Predicted Volume PAI (m^3/ha)	Difference (m^3/ha)
1	32.3	39.1	6.8
2	17.1	25.6	8.5
3	41.2	45.8	4.6
4	3.5	9.8	6.3
5	0.5	1	0.5
6	23.7	29.2	5.5
7	15.8	23	7.2
8	12	18.9	6.9
9	0.5	1	0.5
10	4.1	11.4	7.3

[5] Note that the above t-test statistical comparisons are conditional on the actual sample, which should be representative, and the plot selections are not based on any criteria that are being compared. The grid-based (systematic) sample selection, which is recommended for YSM, meets these criteria. For calculating the standard deviation we assume that the systematic sample is a simple random sample. Another option would be to use a non-parametric test based on the bootstrap or randomization (see, e.g., B.F.J. Manly (2006). Randomization, Bootstrap and Monte Carlo Methods in Biology. Third Edition, Chapman & Hall, London).

Mean difference $\bar{d}$	5.4
Standard deviation $\hat{\sigma}$	0.9
Calculated *t*-value	6.128
Tabulated *t*-value	2.262
Statistical power	0.05

The difference between actual and predicted volume PAI is statistically significant at the α = 0.05 significance level (two-tail *t*-test). The power of the test is approximately 0.05 (or 5%), which is quite weak, probably because the sample size in this example is only 10 plots. The suggested minimum power is 0.6 (or 60%) (FAIB 2012).[4]

3.3   Site Index

A.   Conduct graphical comparisons of actual site index and estimated site index by leading species as follows:
   1. Plot the actual site index versus estimated site index at Time 1 and Time 2 (Figure 4).
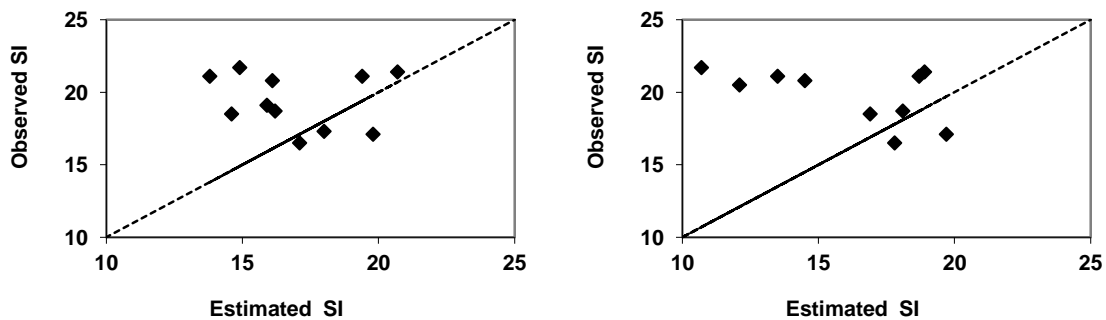
Figure 4. Example graphs of actual (observed) versus estimated site index at Time 2 (left) and Time 1, and 1:1 line of correspondence, for a given species.

If predicted values are accurate, then most points should fall along the 1:1 line of correspondence for the unit the plots represent. Outliers can be flagged and examined to determine if any potential problems in prediction are indicated.

2. Plot the differences between SI at Time 1 and Time 2 (Figure 5). Expressing   differences as a percent of the predicted value can provide a better view of the differences.

Figure 5. Example graphs of difference between SI at Time 2 and Time 1 versus age at Time 2 absolute (left), and percent difference (% of actual), for a given species.

B. Post-stratify the data by leading species. Conduct a statistical comparison of the actual and predicted values of the following attributes, by leading species: site index at Time 1, site index at Time 2, and difference in site index between Time 1 and Time 2. For each attribute comparison, proceed as described in Section 3.2B, where, here, *d* is defined as the difference between actual and predicted site index.

3.4   Stand Age and Site height

The procedures for analyzing stand age and site height are similar. Therefore, only the stand age procedures are given. The analysis should be done for both variables. The results of the comparisons of these variables, which are related to site index, should help interpret the results of the site index comparisons.

A. Plot the actual age versus the VRI age (predicted age) at Time 1 (Figure 6) by leading species. If predicted values are accurate, then most points should fall along the 1:1 line of correspondence for the unit the plots represent. Outliers can be flagged and examined to determine if any potential problems in prediction are indicated.
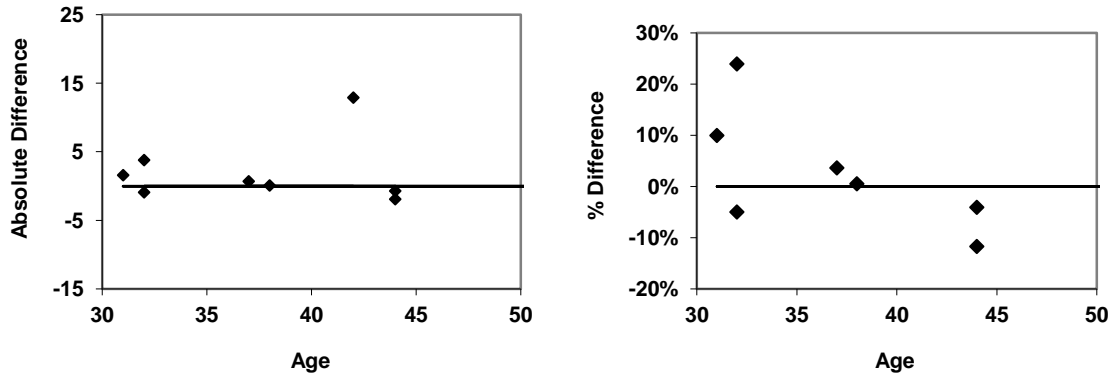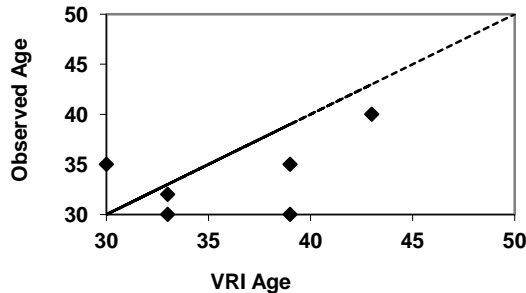

Figure 6. Example graphs of actual age versus predicted VRI age at Time 1 (yr), and 1:1 line of correspondence, for a given species. The scatter of the Time 2 data would be similar.

B. Post-stratify the data by leading species, and conduct a statistical comparison of the actual and predicted values of stand age at Time 1 and at Time 2, by leading species. For each comparison, proceed as described in Section 3.2B, where, here, *d* is defined as the difference between actual and predicted stand age.

3.5   Leading Tree Species

Two leading-species comparisons of interest are: compare changes in ground leading species over time, and compare differences between the ground and inventory leading species. Construct a change matrix for leading species between Time 1 and Time 2 for each plot. Construct an error matrix for ground leading species and inventory leading species, at Time 1 and Time 2. Then use the Kappa statistic tests the null hypothesis that the leading species is not changing over time or that there is good agreement between the ground and inventory leading species.

Proceed as follows to compare changes in leading species (and similarly to compare ground and VRI leading):

1. Set up a leading-species change matrix, with the Time 2 tree species codes being the rows of the matrix and Time 1 codes the columns. This matrix must be square. Add "dummy" rows or columns, in case the original matrix is not square.

2. Populate the matrix with plot frequencies. For example (Figure 7), if the code in a plot changed from a code FD in Time 1 to a code PL in Time 2, then that plot would go into the cell defined by row FD and column PL. If there is no code change in any of the plots, then all the frequencies would line along the diagonal of the matrix.

3. Calculate the Kappa statistic (K) (Cohen, 1960)[6]using software such as SAS (PROC FREQ procedure). The K statistic is measure of agreement in leading species at Time 1 and Time 2. A statistically significant K statistic implies a high degree of agreement between leading species at Time 1 and Time 2. That is, the differences in leading species between Time 1 and Time 2 are not statistically significant.

4. In the example dataset shown in Figure 7 (n = 80), and using the SAS PROC FREQ procedure, K = 0.93 (with asymptotic standard error = 0.03), the Z value = 13.671, and the probability of the one-sided test (H_o: K = 0) is < 0.0001. In this example, the K statistic is significantly greater than 0. This means that there were no significant changes in leading species between Time 1 and Time 2. Note that a one-sided test is used

[6] Cohen, J. 1960. A coefficient of agreement for nominal scales. Educ. Psychol. Meas. 20:37-46.

because negative values of K do not normally have a meaningful interpretation (Sim and Wright, 2005, p. 265).[7] Details of this example analysis are given in Appendix B.

		Time 2 Leading Species				
		At	Bl	Fd	Pl	Se
Time 1 Leading Species	At	1				
	Bl		7			
	Fd			27	1	
	Pl			2	22	1
	Se					19

Figure 7. Example change matrix for leading species at Time 1 and Time 2 (n = 80). The cell entries are plot frequencies. If there were no differences in leading species, then all plots would lie along the matrix diagonal (shaded).

Note that we can also compare the actual and predicted leading species at Time 2, where the predicted leading species at Time 2 is the actual leading species at Time 1. This is true for those models such as VDYP7 that assume no species change over time. The value of the estimated K statistic would be identical to the earlier case; only the interpretation of the K statistic would differ. In this example, the interpretation in this case would be that there were no significant differences between the actual and predicted leading species at Time 2.

The conclusions from the leading species analysis that compares YSM ground plot and VRI polygon species compositions should be interpreted with caution since the YSM plot is typically a very small portion of the parent VRI polygon, and the comparison is not very precise since only one plot is established per sampled polygon. In addition, for young stands with small diameters, the leading species is sensitive to the utilization level. Note also that currently this analysis does not rank the importance of differences in ground plot and VRI polygon leading species between Time t and t-1; e.g., some changes in leading species may not be an issue.

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[7] Sim, J. and C.C. Wright. 2005. The Kappa statistic in reliability studies: interpretation, and sample size requirements. Phys. Ther. 85 (3):257-268.

3.6   Pest and Disease Incidence

Pool the individual tree data from all the plots in a management unit. Summarize the actual pest and disease incidence (absolute and relative frequency of occurrence, i.e., number and % trees attacked) by pest or disease for the management unit. Display the plot frequency pest and disease incidence at Time 1 and Time 2, by tree species, in a matrix as illustrated in Figure 8. Note that more than one pest or disease may occur on one tree.

Compare changes in pest and incidence over time. Construct a change matrix for pest and disease between Time 1 and Time 2 for each plot. Then use the Kappa statistic tests the null hypothesis that the leading species is not changing over time or that there is good agreement between the ground and inventory leading species.

		Pest				
		Aphids	Weevil	Animal	Abiotic	other
Tree species	Fd			1		
	Bl		18	11		9
	Pl	10		2		
	Lw		21	24	11	4
	Cw		2	10		3

Figure 8. Example two-way table of pest incidence, by species, at Time 1. The cell entries are the frequency or number of stems (of minimum DBH limit) with pest occurrence.

4   Reporting Analysis Results

The analysis report should provide complete documentation of the compilation and analysis procedures, and the results of the GY comparisons. Information should be provided to allow the replication of the process, if required. All assumptions and non-standard procedures must be carefully noted. A list of the sample locations and sample weights should also be provided as an Appendix.

The monitoring analysis should provide a tabulation of the monitoring unit average absolute and relative differences between the actual and predicted values for the key variables used in TSR.

The intent is that the timber supply analysts can then use this information in a management unit TSR Sensitivity Analysis of the Base Case (SABC).

A suggested report outline is as follows:
1. Monitoring Objective
2. Sample Plan
     a. Target Population
     b. Sample Size
     c. Sample Selection
     d. Plot Design & Data Collection
3. Data Compilation & Analysis
4. Results & Discussion
5. Conclusions
6. Appendix: List of sample plot locations and weights.

Examples of an YSM analysis report is provided in Omule (2013)[8] and FAIB (2013).[9]

5   Forest Status Reporting

Data from the YSM plots are used to describe current stand structure of young stands in a monitoring unit. This ground information can be used, possibly along with other existing information (e.g., VRI Phase I), to report on the current status of young stands in a monitoring unit.

Calculate the following overall monitoring unit YSM descriptive statistics:
- Attributes: basal area/ha, stems/ha, gross volume/ha, net merchantable volume/ha and dead volume/ha.
- Diameter distribution: The diameter distribution of number of stems and volume per hectare.
- Forest health: Damage agents and severity on individual trees, to get an assessment of forest health. Damage agent types include abiotic, disease, insects, treatment injuries, and animal damage.

These descriptive statistics should also be included in the YSM analysis reports (Section 4).

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[8] Omule, A.Y. 2013. Young stand monitoring in the Kootenay Lake TSA: Plot establishment report.
[9] FAIB. 2013. Young stand monitoring in the Morice TSA: Plot establishment report. Victoria, BC.

6   TSR Applications

Currently, the intended application of the results of monitoring data analysis is to raise 'red flags' on the accuracy of GY predictions used in TSR, which is a stewardship responsibility of the MFLNRO. The GY comparisons may show agreement or no agreement between the actual and predicted GY values. The disagreement should, for example, be included in the Chief Forester's TSR rationale statements as impetus for further investigation, if the disagreement has a significant impact on timber supply or management decisions. This impact can be studied through an SABC using the monitoring results to set the sensitivity analysis thresholds. This is similar to the use of the inventory audit results in TSR in the 1990's. However, the YSM data should not be used to adjust the inventory. The monitoring data differences should also be included as a factor at AAC determination meetings.

Appendix A – Glossary of Statistical Terms

Change is the difference in the level of the resource (e.g., stand volume) between two time points, Time *t* and Time *t-1*.

Kappa (K) statistic is measure of agreement in, say, leading species at Time 1 and Time 2. A statistically significant K statistic implies a high degree of agreement between leading species at Time 1 and Time 2.

Monitoring is the process of observing the growth and yield (GY) in a forest and comparing this with the predicted GY of that forest.

Post-Stratification involves the division of the monitoring unit into mutually exclusive sub-populations (strata) *after* ground sampling has been completed. Samples that fall in each post-stratum are analyzed separately and the results are applied to the corresponding population post-strata to improve the precision of the inventory's overall averages and totals.

Pre-Stratification involves the division of a monitoring unit into mutually exclusive sub-populations (strata) *before* ground sampling to provide estimates for specific areas, or to increase the confidence in the overall estimates by considering the special characteristics of each stratum.

Sample Size for monitoring is the number of sample plots to be established in a management unit to meet specified goals (such as statistical power and differences to be detected).

Standard deviation is a measure of the variation (or spread) of the actual data from their average (or expected value). A low standard deviation indicates that the data points tend to be very close to the mean, and a high standard deviation indicates that the data points are widely spread out over a large range of values from the mean.

Standard error (of the mean) is the standard deviation of the observations divided by the square root of sample size.

Statistical power is the chance of correctly rejecting the null hypothesis using a statistical test (such a paired *t*-test); its value ranges from 0 to 100%.

Paired *t*-test is a *t*-test that typically consists of comparing a sample of matched pairs of similar units.

Target Population is the population from which the monitoring samples are chosen and the sample-based estimates and conclusions apply**.**