Testing and Analysis of Internal Hardwood Log Defect Prediction Models

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ABSTRACT

The severity and location of internal defects determine the quality and value of lumber sawn from hardwood logs. Models have been developed to predict the size and position of internal defects based on external defect indicator measurements. These models were shown to predict approximately 80% of all internal knots based on external knot indicators. However, the size of the actual knot differed from the size of its prediction on average by 0.32 inch in length and 1.49 inches in width. Depending on the defect type, the mean absolute error of the prediction model varies from 0.4 to 1.8 inches in length and 0.3 to 0.8 inch in width at the defect cross-sectional size at the midpoint depth. Given the current models and their associated known prediction errors, this paper seeks to identify the effect, if any, these errors would have on the quality and value of lumber sawn from logs whose internal defects are generated using the prediction models. Twenty-six high-resolution laser-scanned logs were digitally sawn and the resulting lumber graded and analyzed to test the models.

1. INTRODUCTION

The severity and location of internal defects determine the quality and value of lumber sawn from hardwood logs. The Forest Service hardwood log grading rules (Hanks et al. 1980) are based on the established relationship between defect occurrence and lumber recovery. The ability to use internal defect information such as location, size, and shape during the sawing process has been shown to significantly improve the value of hardwood lumber sawn by as much as 21% (Steele et al. 1994, Wagner et al. 1990). Historically, two research programs have been testing the use of x-ray/CT (Computed Tomography) and MRI (Magnetic Resonance Imaging) as ways of gathering internal log defect information (Chang 1992). However, scanning a log using these methods can be costly due to equipment cost and time consuming depending on resolution and processing (Schmoldt et al. 2000). At the time of this writing, the expected cost of a x-ray/CT log scanner is in excess of US$1,000,000.

Several researchers have sought to understand the relationships between external log defects and their internal features (Schultz 1961, Hyvärinen 1976, Lemieux et al. 2001). Recently, a series of internal defect prediction models have been developed that can predict internal defect position, shape, and size based on external defect indicators (Thomas 2008, 2009). These models were developed to predict internal defect features using defect information gathered by automated defect detection using a high-resolution laser log scanner (Thomas et al. 2006). The defect detection software determines the length, width, rise, and type of the log surface defect. Using this information, the models infer an internal description of the defect. The ultimate goal of this research is to provide much of the benefits of using x-ray/CT scanning, but at the cost and speed of laser scanning. In general, laser scanning systems cost a fraction of that of x-ray/CT scanning systems. For example, the test bed laser scanning system developed for this research had a total equipment cost of less than US$30,000.

The internal log defect prediction models are based on a series of multiple linear regression analyses. Each defect type or class has a specific prediction model. The independent (input) variables for the model are: log diameter at the defect, surface defect width, length, rise, and type. The dependent (output) variables from the model are: encapsulation depth (EDEPTH) which is the depth of clear wood that has grown over the internal defect, if any; total penetration depth (TDEPTH), penetration angle (RAKE) of the internal defect; and the cross-sectional width (HWID) and length (HLEN) of the internal defect at one-half the penetration depth

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(Figure 1). Combining the input and output variables of the models creates a simplified view of the entire defect.
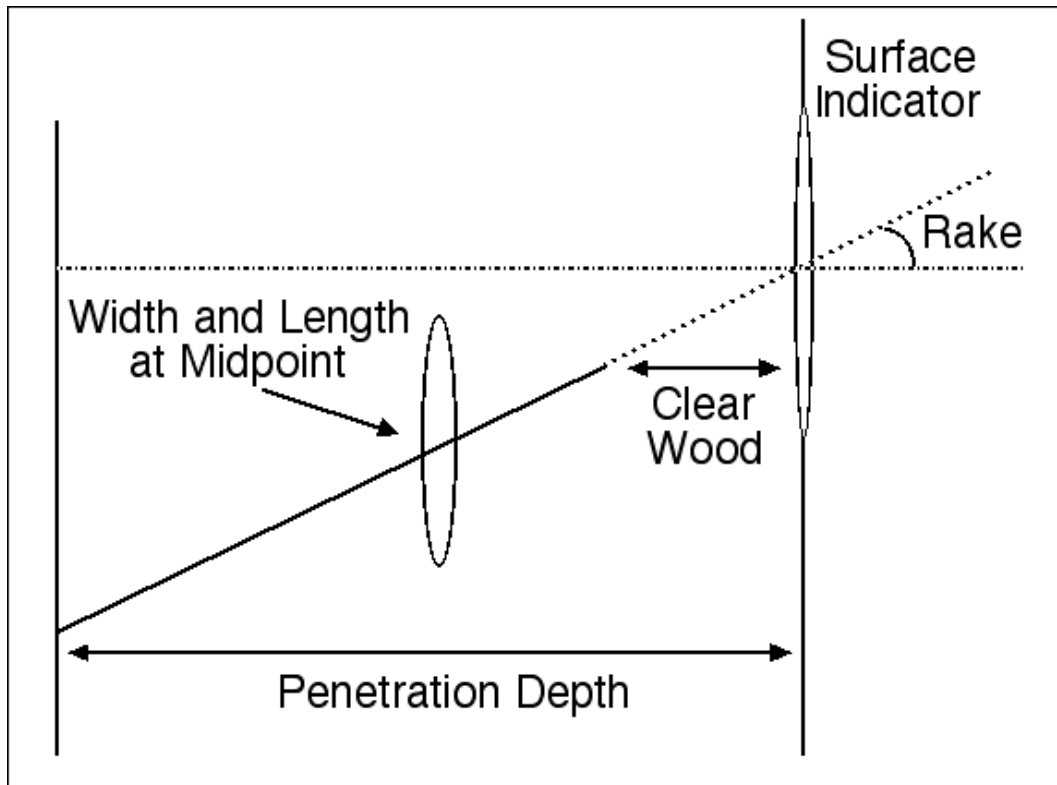

Figure 1. Illustration of internal and external defect variables.

In a recent study, the capability of the models to predict internal knot defects was tested on a sample of four red oak (*Quercus rubra L.*) logs (Thomas 2011). From the four logs, a total of 41 boards were sawn and the knots on the face nearest the outside of the log were counted for each board. This is because the inner face of one board is nearly identical to the outer face of the next board (only kerf width separates the two). A total of 83 knot defects were observed on the outer board faces. The models predicted the occurrence of 67 knots (80.7%) on the board faces and missed predicting 16, or about 19.7% of the knot defect total. In addition, the model predicted the occurrence of 49 additional knot defects on the boards' faces which did not exist.

For the 67 defects which were predicted, there were two additional types of error: positional and size. Positional error is the distance difference between the centers of the actual defect location and the predicted defect. The median of the absolute value of the lineal position errors was 0.875 inch. In 35 instances or 52.2% of those predicted, the mean positional error was 1.0 inch or less. In 49 instances, or 73.1% of those predicted, the mean positional error was 2.5 inches or less. Size error is the difference between the actual defect and predicted defect surface areas. The median of the size error was 5.6 square inches. However, in several cases the actual error was much smaller. In 22 instances (32.8%) the size error was less than 2.5 square inches. The maximum size error observed was 42.81 square inches and was due to a single overgrown knot cluster with a large surface indicator and a small internal defect that occurred on four board faces. If these occurrences are omitted from the analysis, the median absolute size error becomes 4.94 square inches. Although this error size may sound large, it corresponds to small prediction error in internal defect width and length. For example, the mean absolute error (MAE) for light distortion defect width is 0.4 inch and defect length is 1.1 inches. The complete list of the MAEs and correlation coefficients for the red oak prediction models by defect type are given in Table 1. Given a knot defect measuring 3 by 3 inches on a board face, then adding the mean absolute error to the width and length could potentially give a defect that measures 3.4 by 4.11 inches. The difference in area between the predicted and actual defects would be 4.94 square inches (13.94-9.00 square inches). Table 2 lists average and median observed and predicted defect widths and lengths. In general, the prediction models

slightly overestimate the size of internal defects, making the models a conservative estimate of internal log quality.

Table 1. Correlation and mean absolute error statistics for red oak knot-type defects.

Defect type	Internal feature	R2	Mean abs. error
Light distortion	Half width (inches)	0.19	0.4
	Half length (inches)	0.34	1.1
	Rake (degrees)	0.03	14.7
	Depth (inches)	0.09	1.2
	Encapsulation (inches)	0.08	1.0
Medium distortion	Half width (inches)	0.13	0.3
	Half length (inches)	0.23	1.8
	Rake (degrees)	0.10	9.9
	Depth (inches)	0.16	0.8
	Encapsulation (inches)	0.10	1.1
Heavy distortion	Half width (inches)	0.55	0.3
	Half length (inches)	0.47	0.4
	Rake (degrees)	0.40	8.5
	Depth (inches)	0.27	0.7
	Encapsulation (inches)	0.08	0.6
Overgrown, sound, and unsound knots	Half width (inches)	0.54	0.4
	Half length (inches)	0.60	0.9
	Rake (degrees)	0.39	12.7
	Depth (inches)	0.46	1.0
Overgrown, sound, and unsound knot clusters	Half width	0.65	0.8
	Half length	0.63	1.4
	Rake (degrees)	0.09	10.9
	Depth (inches)	0.40	1.1

Table 2. Average and median observed and predicted defect widths and lengths.

Defect statistic	Observed		Predicted		Difference		
	Length	Width	Length	Width	Length	Width	Area
	- - - - - inches - - - - -						- sq. inches -
Average size	1.92	1.45	2.24	2.94	0.32	1.49	3.81
Median size	1.63	1.25	2.00	2.75	0.37	1.25	3.46
Standard error	1.36	1.11	1.39	1.84	–	–	–

However, it is unknown if the positional and size errors have a significant impact on the value and quality of the lumber sawn using the scanned external log data and predicted internal log defects. The goal of this project is to determine the effect, if any, these prediction errors have on the resulting lumber value and quality.

2. METHODS

Twenty-five red oak logs were scanned and used for this study. The logs ranged in quality from no defects to logs with numerous defects of several types. Eleven logs are from one sample site, the remaining 14 are from another site approximately 130miles distant. However, most logs had less than six total combined knot and knot cluster defects. Table 3 lists the measurements, scale, and defect characteristics of the study logs. The logs were manually diagrammed with the location, size, and type of all surface defects recorded. Manual defect identification was used rather than the automated detection system to remove the effect of any detection errors on defect prediction results. This information was used by the internal defect prediction models to estimate internal defect features; thus creating a 3D data set for each log that includes log shape (diameter all along length, taper, sweep, crook, and ovality) as well as external and internal defect sizes, shapes, position, and type.

Table 3. Summary of log characteristics.

Original log ID	Position in tree	Large end diameter	Small end diameter	Length	Defects counts by category			
					Distortions	Knot and bumps	Knot clusters	Adventitious knots/clusters
		- - - - - inches - - - - -			- - - - - # - - - - -			
10D	4	11	10	126	2	1	3	2
17B	*2*	*17*	*17*	*127*	*3*	*2*	*0*	*3*
15B	2	14	13	105	7	2	0	1
14B	2	19	17	131	0	2	2	1
30D	4	16	14	126	4	2	3	3
17C	*3*	*17*	*16*	*126*	*3*	*2*	*6*	*6*
28B	2	14	13	126	1	3	1	4
30E	5	15	12	146	1	3	1	0
31B	*2*	*17*	*16*	*125*	*3*	*3*	*1*	*1*
33C	*3*	*17*	*16*	*157*	*1*	*3*	*7*	*0*
30C	3	15	14	126	1	4	0	0
26C	3	14	12	110	3	4	1	1
11D	4	12	11	125	1	5	1	0
8B	2	19	18	123	0	6	0	0
11C	*3*	*14*	*13*	*158*	*1*	*6*	*2*	*1*
5B	2	13	13	123	0	6	3	2
28C	*3*	*14*	*12*	*123*	*0*	*6*	*4*	*4*
20Y	2	12	11	134	1	7	0	4
22C	*3*	*15*	*14*	*126*	*1*	*8*	*1*	*0*
25D	*4*	*16*	*14*	*148*	*2*	*8*	*2*	*0*
8C	3	18	17	131	0	9	0	1
32D	*4*	*15*	*14*	*100*	*2*	*9*	*5*	*3*
31C	*3*	*17*	*15*	*129*	*5*	*10*	*1*	*0*
32C	*3*	*17*	*16*	*159*	*1*	*10*	*3*	*4*
5C	3	13	11	101	0	14	2	2
Average		15.2	14.0	128.4	1.7	5.4	2.0	1.7
Standard error		2.2	2.2	15.8	1.7	3.3	1.9	1.7

For each log diameter class, a sawing pattern was created to match the diameter only and did not consider any other log features. The sawing pattern for each log was used five times with different starting rotation angles: 0, 22.5, 45, 90, and 150 degrees. Approximately two to four boards were sawn from each log face depending on log diameter. For each sawing pattern and log combination, a series of 33 sawing simulations were performed with different variations of the internal prediction models, these were:

a) One model with the normal predicted values. Results from this model are labeled NORM.
b) One model with the MAE for each feature added to the NORM values. This resulted in a maximum sized defect with a maximum location deviation. Results from this model are labeled MAX.
c) One model with the MAE for each feature subtracted from the NORM values. This resulted in a minimum sized defect with a minimum location deviation. Results from this model are labeled MIN.

Thirty models with a random amount of error ranging from -MAE to +MAE added to the NORM predicted defect feature values.

The logs were sawn with RAYSAW (Thomas 2010), a ray-tracing based sawing simulator. Ray-tracing is a computerized method of simulating objects and their interaction with light to produce photo-realistic images. Ray-tracing works by tracing the light rays from a light source and recording where the light ray hits and reflects off of different objects. In RAYSAW the light rays are replaced with a saw that does not reflect but penetrates the log and defect surfaces. RAYSAW records where the blade intersects the log and any defects. Board faces are then generated from the intersection points. RAYSAW functionally simulates a carriage incrementally moving a log into a saw. RAYSAW processed the log surface and external and internal defect data to produce virtual boards for this study. The boards were edged where needed to improve grade and graded to NHLA rules (NHLA 1998) using the UGRS computer program (Moody et al. 1998). Values were assigned to the graded lumber using average green 4/4 Appalachian red oak lumber values (Table 4) from Hardwood Market Report (HMR 2010). The RAYSAW sawing model was validated as part of a log

processing study where virtual boards from RAYSAW were compared to actual sawn boards from the same sawing position (Thomas 2011).

Table 4. Red oak lumber prices by NHLA grade (HMR 2010).

Lumber grade	Price per thousand board feet
	- - - $ - - -
FAS	1015
F1F	1005
Selects	700
1 Common	640
2A Common	515
3A Common	440
Below Grade	50

There are five groups of data for each log corresponding to the five sawing rotation starting points. Different rotational starting points were analyzed as each starting point generates different internal defect positioning. This allows for a more thorough examination of internal defect model positioning error. Each group of data is composed of 33 sets of lumber, one for each defect model variation used. Thus, for each log a total of 165 different sawing and defect model variations are examined. The distribution of lumber grades were compared within each rotational starting point and log grouping using Friedman's test (Sheskin 2003) with log and cutting position being fixed effects. Numeric codes 0 through 6 were assigned to the boards for "Below Grade" through FAS grades, respectively. Grades were compared because the difference between each grade was uniform, as opposed to value, where the differences between grades were not uniform. This non-uniformity could mask slight differences between results and prevent a thorough analysis.

Friedman's test identified the sets of boards within each log and rotation grouping whose grades were significantly different. Friedman's test is a non-parametric, randomized block analysis of variance used to detect differences in treatments across multiple test attempts. Friedman's test is sometimes referred to as a two-way analysis on ranks. In addition, a Friedman post-hoc test (Galil 2010) was performed to identify the boards which were significantly different among the 33 sets of lumber sawn within each rotation and log grouping. All of these tests were performed using the R statistical analysis computer program (R Development Core Team 2009) at a significance level of 0.05.

3. RESULTS

Table 5 lists the number of significant differences within the sets of boards sawn from each log and starting rotation combination. Table 5 also lists the number of boards sawn from each log. The logs are listed in order of quality, from highest to lowest. There are two groups of results: the first includes all random defect size variations and the MIN, NORM, and MAX size variations; the second group contains only the random size variations. Instances where all or most significant differences were with a single defect size variation are indicated in the legend of Table 5.

3.1. RANDOM VARIATIONS ONLY

Overall, there were few instances of significant differences among all random defect variation size sets. In five instances, the differences were all between a single variation and all other variations. In some cases, these differences were minor. For example, with log 26C and the 90° starting position, the only difference was with 1 of 10 total boards where one variation produced a F1F board while all others produced a FAS board. Similarly, log 11C and the 22.5° starting position, one defect variation produced three boards that were one grade higher than the other defect size variations (2A, 1C, and 1C vs. 3A, 2A, and 2A, respectively). Log 28C had significant differences with both 22.5° and 45°rotations. However, both instances were due to one board in one variation grading as a 1C board, while all other defect variations produced a 2A Common board. With log 31B all significant differences were between two variations and the remaining variations. In most instances the differences are the production of four F1F boards rather than one 1 Common and three FAS boards. In all other log and rotation angle combinations the number of differences were fewer and more minor.

Table 5. Summary of significant differences among sawing results where variation
columns show number of significant differences within each specific sawing group.

Log ID	Board count each set	All random and MIN/MAX/NORM MAE defect variations					All random defect variations				
	- - - # - - -	- - - - - Starting rotation angle - - - - -									
		0°	22.5°	45°	90°	150°	0°	22.5°	45°	90°	150°
10D	8	32[3]	0	0	0	0	0	0	0	0	0
17B	*20*	*2*	*28[4]*	*18[4]*	*4[4]*	*21[4]*	*3*	*1*	*7*	*0*	*5*
15B	12	0	0	0	31[1]	6[4]	0	0	0	0	0
14B	22	1	0	32[1]	7[3]	1[1]	0	0	6	0	0
30D	*14*	*1[1,3]*	*7[2]*	*7[2]*	*1[1,3]*	*32[1]*	*0*	*0*	*0*	*0*	*0*
17C	*18*	*22[2]*	*62[5]*	*18[1]*	*25[1]*	*35[4]*	*0*	*1*	*0*	*0*	*4*
28B	12	0	0	15[3]	0	3[3]	0	0	0	0	0
30E	12	0	0	0	0	0	0	0	0	0	0
31B	*20*	*4[3]*	*9[5]*	*23[4]*	*2[3]*	*49[2]*	*0*	*0*	*5*	*0*	*22*
33C	*18*	*12[1]*	*38[4]*	*12[1]*	*4[1]*	*33[2]*	*9*	*0*	*0*	*0*	*1*
30C	14	0	0	14[5]	1[1,3]	0	0	0	0	0	0
26C	10	0	0	12[3]	32[6]	3[1]	0	0	0	29[6]	0
11D	8	9[4]	0	4	1	0	4	0	0	3	0
8B	22	0	0	15[2]	16	0	0	0	3	8	0
11C	*12*	*0*	*58[1]*	*32[1]*	*1*	*29[4]*	*0*	*25[6]*	*2*	*0*	*3*
5B	12	9[1]	3[1]	3[1]	22[3]	1[1]	0	0	0	0	2
28C	*10*	*3*	*32[3]*	*32[1]*	*32[1]*	*2[1]*	*0*	*29[6]*	*29[6]*	*0*	*0*
20Y	8	0	23[3]	1	0	0	0	0	29[6]	0	0
22C	*14*	*32[3]*	*2[3]*	*32[2]*	*11[3]*	*1[3]*	*0*	*0*	*0*	*0*	*0*
25D	*14*	*7*	*41[5]*	*12[5]*	*25[1]*	*10[3]*	*16*	*1*	*1*	*0*	*1*
8C	20	3[3]	24[3]	13	13[1]	0	0	0	0	4	0
32D	*16*	*30[5]*	*39[5]*	*32[2]*	*4[1]*	*38[5]*	*0*	*0*	*0*	*0*	*3*
31C	*18*	*33[5]*	*32[2]*	*32[2]*	*35[5]*	*32[2]*	*1*	*0*	*0*	*0*	*0*
32C	*18*	*33[2]*	*11[1]*	*1*	*0*	*0*	*2*	*0*	*0*	*0*	*0*
5C	8	22[4]	8	4	2[3]	21	0	4	3	0	1

[1]   All significant differences are with MAX MAE results
[2]   Most significant differences are with MAX MAE results
[3]   All significant differences are with MIN MAE results
[4]   Most significant differences are with MIN MAE results
[5]   Equal numbers of significant differences with MAX and MIN MAE results
[6]   All significant differences within a single defect variation group (other than MAX or MIN results)

3.2. ALL VARIATIONS

There were a greater number of significant differences for the all defect size model variations than with the only random variations defect data. These differences were all due to significant differences with the MIN and MAX sized defect variations. Table 5 summarizes the significant differences among the MIN, MAX, and NORM defect size variations. The fewest number of significant differences were between the MIN and NORM size variations (Table 5). The MIN and NORM size variations produced boards that had significant grade differences in only 18 of 130 comparisons. The MAX and NORM size variations had significant differences in 33 of 130 comparisons (Table 5). However, in most instances the differences in board grades sawn from the MAX and MIN size variations were significantly different in 80 of 130 comparisons.

Because of the number of significant differences within the lumber sets for the all variations data, the discussion is limited to the 10 logs with the greatest number of significant differences: (31C, 17C, 32D, 11C, 28C, 25D, 33C, 31B, 17B, 22C), and the 10 logs with the most significant Friedman test statistics: (17C, 32D, 32C, 25D, 31C, 17B, 33C, 28C, 31B, 22C). It is interesting to note that nine logs appear in both groups. The logs in these groups are highlighted in italics in Tables, 3, 5, and 6. In only a few instances was the NORM variation significantly different from any of the random variations. Because of this the NORM variation is used as a point of comparison, illustrating the significant differences among the MAX, MIN, and random size variations.

Table 6. Results showing presence of significant board grade differences among the MIN, NORM, and MAX defect variation data by log and rotation angle.

Log ID	Norm Min	Norm Min	Min Max	Norm Min	Norm Max	Min Max	Norm Min	Norm Max	Min Max	Norm Min	Norm Max	Min Max	Norm Min	Norm Max	Min Max
	- - - 0° - - -			- - - 22.5° - - -			- - - 45° - - -			- - - 90° - - -			- - - 150° - - -		
10B	X		X												
17B				*X*		*X*	*X*		*X*				*X*		*X*
15B											X	X			X
14B			X					X	X			X			X
30D			X			X			X			X			X
17C			*X*	*X*	*X*	*X*			*X*			*X*	*X*	*X*	*X*
28B									X						
30E															
31B			*X*			*X*	*X*		*X*			*X*		*X*	*X*
33C		*X*	*X*		*X*	*X*			*X*			*X*		*X*	*X*
30C									X			X			
26C															
11D	X		X									X			
8B				X	X							X			
11C							*X*		*X*			*X*	*X*	*X*	
5B			X			X			X	X		X			X
28C			*X*		*X*	*X*	*X*		*X*		*X*	*X*			*X*
20Y				X	X				X						
22C	*X*	*X*				*X*	*X*		*X*			*X*			*X*
25D				*X*	*X*	*X*	*X*		*X*		*X*	*X*		*X*	*X*
8C			X	X		X			X		X	X			
32D	*X*		*X*	*X*	*X*	*X*	*X*		*X*			*X*	*X*	*X*	*X*
31C		*X*	*X*		*X*	*X*	*X*		*X*		*X*	*X*		*X*	*X*
32C		*X*	*X*			*X*			*X*						
5C	X		X			X			X		X	X	X		X

For the logs with significant differences identified above, the MAX defect size variation resulted in an average difference of approximately five boards per set grading 1 to 2 grades lower than the boards obtained from the NORM-sized defects with an average value difference of $5.40 (Table 7).

The greatest differences occurred when FAS boards obtained using the NORM data group were downgraded to 1 Common when sawn from the MAX-sized defect data. In many instances, boards from the MAX size variation were significantly different from all or most other defect size variations. There was a total of 33 size variations; in 7 of these cases the MAX variation was significantly different from all other variations. In 13 additional cases the MAX variation was significantly different for more than half (17 or more) of all other variations with an average of 18.6. This information is shown in the "Number of significant differences" in Table 7.

The MIN defect size variation resulted in an average difference of five boards per set grading 1 to 2 grades higher than the boards obtained from the NORM-sized defects with an average value difference of $8.50 (Table 8).

The number of significant differences is lower between the MIN and NORM lumber data with an average of 12.7 than with the MAX and NORM data. In only two instances was the MIN size variation in grade significantly different from all other size variations. In addition, the MIN size variation was significantly different to more than half of all other size variations in only nine cases. Thus, it appears that on the whole the smaller sized defects of the MIN size variation are more similar to the random and NORM variations than those of the MAX variation. This also is indicated in Table 6 which shows fewer instances where the MIN variation is significantly different from the NORM variation.

Table 7. Summary of significant differences between MAX and NORM board sets by log and rotation angle.

Log	Starting rotation angle	Number of significant differences	Number of boards graded lower	Value difference
	- - - degree - - -	- - - - - # - - - - -		- - - $ - - -
17C	0.0	17	6	6.51
17C	22.5	32	6	4.81
17C	45.0	18	5	4.77
17C	90.0	25	6	5.13
17C	150.0	4	4	3.40
31C	0.0	26	5	3.64
31C	22.5	28	4	3.36
31C	45.0	25	7	4.59
31C	90.0	32	7	4.39
31C	150.0	26	6	5.07
32D	0.0	8	4	3.96
32D	22.5	18	7	4.52
32D	45.0	24	7	5.47
32D	90.0	4	4	1.35
32D	150.0	16	10	8.14
25D	0.0	1	2	1.87
25D	22.5	29	9	9.32
25D	45.0	10	5	5.40
25D	90.0	25	4	5.72
25D	150.0	2	6	13.81
28C	45.0	32	2	1.62
28C	90.0	32	3	2.24
11C	22.5	32	2	0.62
11C	45.0	32	6	2.90
32C	0.0	32	6	4.57
32C	22.5	9	12	9.62
31B	22.5	5	5	13.89
31B	45.0	6	5	9.80
31B	150.0	25	4	5.65
33C	0.0	12	6	4.63
33C	22.5	10	4	5.18
33C	45.0	12	5	5.88
33C	90.0	4	3	4.25
33C	150.0	31	6	7.41
17B	0.0	1	6	3.29
22C	45.0	24	5	7.89
Average		18.6	5.4	5.4
Median		18.0	5.0	4.8
Standard error		11.0	2.1	3.0

4. SUMMARY

The greatest cross-sectional area error size for the prediction models is with knot clusters (Table 2). It could be expected that logs with more knot clusters might have greater variability in sawn lumber quality due to the larger range of variability permitted by the prediction models for these defect types. Examining the eight logs having more than the average number of knot clusters (three or more) shows that five are among the logs with the most significant differences: 32C, 32D, 28C, 33C, and 17C. The weakest correlations and second highest cross-sectional area error size are with the distortion defects. A similar examination of the seven logs having more than the average number of distortions (three or more) shows four are among the logs with the most significant differences among the boards due to defect size variations: 31C, 31B, 17C, and 17B. It should be

Table 8. Summary of significant differences between MIN and NORM board sets by log and rotation angle.

Log	Starting rotation angle	Number of significant differences	Number of boards graded lower	Value difference
	- - - degree - - -	- - - - - # - - - - -		- - - $ - - -
17C	0.0	4	8	8.57
17C	22.5	30	6	14.14
17C	150.0	31	8	14.14
31C	0.0	5	5	7.20
31C	22.5	4	3	4.05
31C	45.0	7	5	8.37
31C	90.0	3	5	9.57
31C	150.0	6	3	4.45
32C	0.0	1	3	4.00
32C	22.5	9	3	2.87
11C	150.0	29	4	4.49
28C	0.0	3	2	1.99
28C	22.5	32	3	3.03
25D	22.5	22	7	15.11
25D	45.0	2	4	4.60
25D	150.0	6	4	3.83
32D	0.0	22	9	8.20
32D	22.5	21	6	4.62
32D	45.0	8	7	5.37
32D	150.0	20	9	7.33
31B	0.0	4	3	12.04
31B	22.5	4	4	9.21
31B	45.0	14	7	12.86
31B	90.0	2	4	7.11
33C	22.5	28	4	11.84
33C	150.0	1	1	2.18
17B	0.0	1	3	11.15
17B	22.5	28	9	20.53
17B	45.0	12	9	19.00
17B	90.0	4	5	6.53
17B	150.0	30	7	17.49
22C	0.0	32	5	8.77
22C	22.5	2	3	9.00
22C	45.0	8	4	6.50
22C	90.0	11	4	7.89
Average		12.7	5.0	8.5
Median		8.0	4.0	7.9
Standard Error		11.2	2.2	4.8

noted that the most significant Friedman test statistic occurred on log 17C, which has an above average number of both knot clusters and distortion defects. This indicates that the red oak distortion and knot cluster prediction models need refinement and further testing.

Overall, the results are promising. There were few significant differences among the random only sawn lumber sets. The random variations data is likely to be more true to reality than the all random variations data that includes the "best" and "worst" case scenarios. For the combined random and MAX/MIN/NORM dataset there were many more significant differences between the MAX-sized variations and all other defect size variations (Tables 5 and 6). For almost all logs in the sample, there were significant differences between the MIN and MAX defect size variations (Table 6). In addition, many logs showed significant differences between the MIN and NORM and MAX and NORM size variations.

The collection of additional log defect data would likely improve the accuracy of the internal defect models. White oak (*Quercus alba L.*) log defect data collection is ongoing. One possibility is that white oak and red oak log defects are similar enough to permit data for both species to be pooled. This has the potential to improve

the distortion and knot cluster models. In addition, another sawing study is planned to compare predicted defect sizes to defects on actual board faces.

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