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Dating Wooden Samples Through Cross-Matching Tree-Ring Patterns

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Abstract: Weather conditions vary from month to month and these contribute to the variation in the annual ring width. The varying ring width patterns allow local timbers to be dated. The ring width gives a complete record of the patterns. The pattern in the size of ring widths should be similar for all trees of the same species growing in an area under the same local conditions. This paper will demonstrate the process of dating of sample using a newly developed similarity measure.

Keywords: Ring Width Patterns, Cross Matching, Dating

Introduction

Timbers from buildings, waterfront structures, bridges, ships etc. can be dated based on the variation in the annual ring width of the timbers involved that is caused by the variation of weather conditions that vary from time to time. This dating procedure is done using a well-established technique called dendrochronology. Trees that grow in the same climatic region will have a similar pattern in the size of ring widths. Thus, using appropriate technique they will be grouped in the same respective group based on some similarity measure.

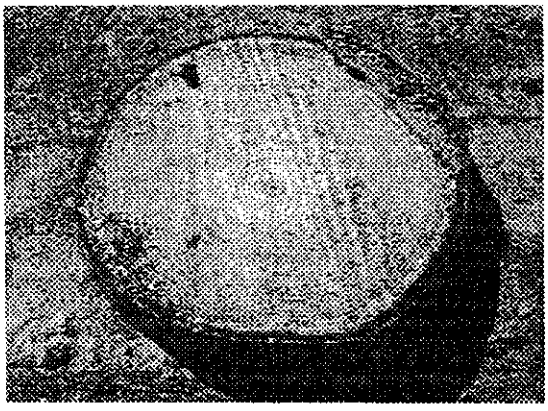

Fig. 1: Cross-section of a timber

In this work, a similarity measure is used and some results are shown to demonstrate the effectiveness of the clustering procedure. Two contemporary tree-ring width sequences from the same climatic zone should be similar. This is possible because the variation in tree ring width will not be exactly the same.

Extreme Value Determination: Before cross-matching procedure can be carried out, all the raw ring-width is filtered using the filter suggested in Laxton, Zainodin and Greig (1996). This is so in order to produce a stationary time-series. Thus, the raw ring widths are transformed to sequences of indices.

The resulting sequences are then cross-matched with each other using the following similarity measure, which is defined as

$$z = \frac{1}{2}\sqrt{n-3}\,\ln\left(\frac{1+r}{1-r}\right) \qquad (1)$$

These resulting sequences of indices with wide and narrow indices are compared among the available sequences. The best relative position is obtained when the similarity measure used give the maximum values. For the sake of further explanation we define these values as extreme values.

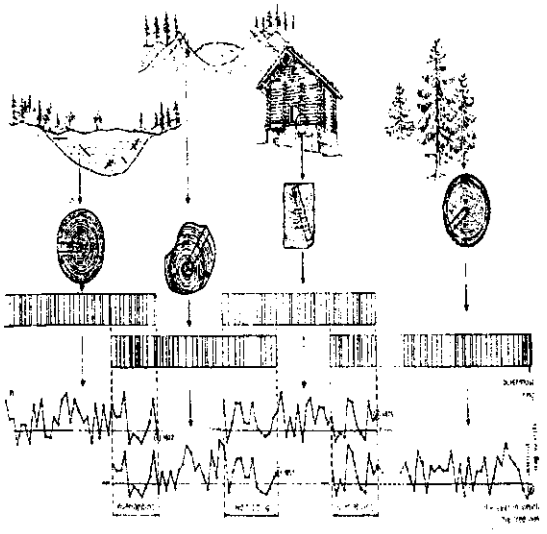

Fig. 2: Cross matching of tree-ring patterns from various time periods

Table 1: Values of similarity measure (lower triangle) with the corresponding offsets (upper triangle) for each pair of sequences

Samples	1	2	3	4	5	6	7	8	9
1 THO-A01B	###	9	12	-9	10	-6	32	95	21
2 THO-A02A	5.16	###	3	1	1	3	15	16	13
3 THO-A03A	3.37	9.61	###	-2	-2	0	12	13	10
4 THO-B01A	3.19	3.04	4.13	###	0	2	14	15	11
5 THO-B02B	3.40	3.71	3.88	5.00	###	12	14	15	12
6 THO-B03B	3.88	3.17	3.62	4.53	4.50	###	12	13	10
7 THO-B04A	3.84	5.22	5.13	4.35	6.85	5.16	###	1	-2
8 THO-B05A	3.12	4.11	5.04	4.77	4.48	3.50	5.84	###	-52
9 THO-O01C	3.71	4.10	4.05	2.67	3.18	3.55	4.31	2.57	###

Fig.3:Histogram of similarity measure indicating the extreme value from a pair of sequences

THO-B04A THO-B05A

	1	2	3	4	5	6
Tval	5.8354	2.8949	2.6074	2.5192	2.5017	2.2425
Tdiff	2.9405	0.2875	0.0883	0.0175	0.2592	0.0407
OFFSET	1	43	-47	29	-32	-8

Total Positions= 186

1	6.5000	7.0000	0	
2	6.0000	6.5000	0	
3	5.5000	6.0000	1	* <
4	5.0000	5.5000	0	
5	4.5000	5.0000	0	
6	4.0000	4.5000	0	
7	3.5000	4.0000	0	
8	3.0000	3.5000	0	
9	2.5000	3.0000	4	****
10	2.0000	2.5000	5	*****
11	1.5000	2.0000	9	*********
12	1.0000	1.5000	15	***************
13	0.5000	1.0000	24	************************
14	0.0000	0.5000	35	***********************************
15	-0.5000	0.0000	30	******************************
16	-1.0000	-0.5000	27	***************************
17	-1.5000	-1.0000	17	*****************
18	-2.0000	-1.5000	10	**********
19	-2.5000	-2.0000	4	****
20	-3.0000	-2.5000	4	****
21	-3.5000	-3.0000	1	*
22	-4.0000	-3.5000	0	
23	-4.5000	-4.0000	0	

THO-B04A	THO-B05A	1	-3.0218	5.8354	
7	8	1	5.8354	8.8572	
Range	Skew	std-skew	***	Kurt	std-kurt ***
8.8572	1.296	0.809	*	5.818	0.738 ***

Result of Distinct Values

The extreme value obtained by sliding two sequences in a systematic manner for possible combinations. Details of the results are shown in Table 1 where the upper triangle is the corresponding offset.

Most of the extreme values obtained indicate the correct date of the targeted sample. This is done by checking the coherent property of the 3 related sequences i.e. p(i, j) = p(i, k) + p(k, j) where i, j and k are the sequences involved.

Figs. 3, 4 and 5 illustrate all the z values obtained in sliding two sequences at all possible relative positions.

Fig. 4 shows the extreme value obtained is not very distinct. The value is lumped with the second highest. This indicates the corresponding date suggested is not the correct date. This is clearly indicated by checking the *coherent criteria* that is, p(THO-A01B, THO-B04A) = 32 and p(THO-A01B, THO-B05A) - p(THO-B04A, THO-B05A) = 94. The two relative positions are not the same thus they are not recommending correct date.

Though sequence verses sequence failed to indicate correct date but through clustering algorithm sequences can be dated correctly. The work has been mentioned in Litton & Zainodin (1987). Thus, here the cluster (group) formed using this similarity measure produce a better group of samples and converged at the early stage (step). More work need to be carried out on other samples especially from different time period and from distinct locations before a very conclusive statement can be made regarding the used of this similarity measure.

Fig.4;Histogram of similarity measure indicating the extreme value overlapped from a pair of samples

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          THO-A01B  THO-B05A
                1         2         3         4         5         6
Tval       3.1190    3.0402    2.8161    2.7529    2.7337    2.5144
Tdiff      0.0787    0.2241    0.0631    0.0193    0.2193    0.4130
OFFSET         95       -20       -23       -92       -51       -59
          Total Positions=   209
    1     4.5000    5.0000         0
    2     4.0000    4.5000         0
    3     3.5000    4.0000         0
    4     3.0000    3.5000         2 **     <
    5     2.5000    3.0000         4 ****
    6     2.0000    2.5000         1 *
    7     1.5000    2.0000        14 **************
    8     1.0000    1.5000        17 *****************
    9     0.5000    1.0000        34 ***********************************
   10     0.0000    0.5000        34 ***********************************
   11    -0.5000    0.0000        33 **********************************
   12    -1.0000   -0.5000        28 ****************************
   13    -1.5000   -1.0000        24 ************************
   14    -2.0000   -1.5000        11 ***********
   15    -2.5000   -2.0000         4 ****
   16    -3.0000   -2.5000         1 *
   17    -3.5000   -3.0000         2 **
   18    -4.0000   -3.5000         0
   19    -4.5000   -4.0000         0
THO-A01B  THO-B05A   95   -3.0460    3.1190
        1         8   95    3.1190    6.1649
    Range     Skew  std-skew  ***     Kurt  std-kurt  ***
   6.1649    0.915     0.229  ***    3.699     0.948  ok
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Fig. 5: Histogram of similarity measure indicating the extreme value close together from a pair of sequences

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          THO-B05A  THO-O01C
                1         2         3         4         5         6
Tval       2.5738    2.5619    2.4195    2.2858    2.1977    2.1977
Tdiff      0.0119    0.1424    0.1337    0.0881    0.0000    0.0218
OFFSET         -52        -4        80       -38        66       -74
Total Positions=          187
    1     3.5000    4.0000         0
    2     3.0000    3.5000         0
    3     2.5000    3.0000         2 **  <
    4     2.0000    2.5000         8 ********
    5     1.5000    2.0000        10 **********
    6     1.0000    1.5000         8 ********
    7     0.5000    1.0000        26 **************************
    8     0.0000    0.5000        39 ***************************************
    9    -0.5000    0.0000        38 **************************************
   10    -1.0000   -0.5000        26 **************************
   11    -1.5000   -1.0000        14 **************
   12    -2.0000   -1.5000         8 ********
   13    -2.5000   -2.0000         5 *****
   14    -3.0000   -2.5000         3 ***
   15    -3.5000   -3.0000         0
THO-B05A  THO-O01C  -52   -2.7383    2.5738
        8         9   -52    2.5738    5.3121
    Range     Skew  std-skew  ***     Kurt  std-kurt  ***
   5.3121    0.898     0.000  ***    3.823     1.982  ok
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Conclusion

The above result shows dating for any sample done successfully. Cross matching from sample to sample indicates the correct relative position enables one to group samples into the respective groups. Group representation formed is then cross-matched with the master chronology to determine the date. The results shown in the previous section indicate the correct date. The overall result shows the capability of the similarity measure. The work suggests that the similarity measure can be applied to any sample of the same species to the dated correctly. Before a global claim can be made, further work along this line need to be done especially using samples from other sites or from other time periods.

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