Summary of PhD thesis

The aims of this thesis were (1) to investigate the effects of sequence length, sensitivity and provenance on cross-matching, (2) to extend the chronologies for Exeter, and (3) to investigate the role of dendrochronology in the study of seasoning/stockpiling intervals and architectural history.

Dendrochronological analysis in Exeter Cathedral produced two dated chronologies; XMEAN52 (AD1137-1332) derived from original roof timbers and XMEAN60 (AD1662-1783) derived from undocumented replacements. Whereas many post-medieval timbers retained waney edge, most medieval timbers lacked sapwood leading to a lack of precise felling dates. Consequently, provenance and stockpiling/seasoning intervals could not be identified by comparison of felling dates with documentary evidence of construction. Analysis of the documented medieval timber supply showed two local woodlands were used frequently. Other sources were used during a period of exceptional demand in AD1323-5. The earliest possible construction dates for different parts of the medieval roof were identified.

The chronology EXMED11 (AD1367-1616) included timbers from the Cathedral, and from the Quay, Guildhall and 41/42 High Street. Identification of two felling phases allowed precise dating of some Quay developments. A Guildhall timber was felled in AD1592 in nearby Duryard Wood, and was used green.

Previous studies in Exeter have indicated that short sequences and complacency have hindered cross-matching. This study has shown that while sensitivity is not important, sequence length may be very influential in determining the success of cross-matching. Test sequences created from longer sequences of known date were used to assess the performance of three statistical techniques in dating short sequences. CROS-TWENTY and RESAMPLE (Okasha 1987) performed better than CROS (Baillie and Pilcher 1973) in differentiating the correct date from “strongly-indicated” incorrect dates. It is shown that if all three programs are used together, indication of the same date in all methods’ results suggests reliable dating for sequences as short as 50 years.

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