This is a repository copy of *A simple Bayesian approach to tree-ring dating*.

White Rose Research Online URL for this paper:
https://eprints.whiterose.ac.uk/142496/

Version: Accepted Version

Article:

Hassan, M., Jones, E. and Buck, C. (2019) A simple Bayesian approach to tree-ring dating. Archaeometry, 61 (4). pp. 991-1010. ISSN 0003-813X

https://doi.org/10.1111/arcm.12466

This is the peer reviewed version of the following article: Hassan, M. M., Jones, E., and Buck, C. E. (2019) A simple Bayesian approach to tree-ring dating. Archaeometry, which has been published in final form at https://doi.org/10.1111/arcm.12466. This article may be used for non-commercial purposes in accordance with Wiley Terms and Conditions for Use of Self-Archived Versions.

Reuse

Items deposited in White Rose Research Online are protected by copyright, with all rights reserved unless indicated otherwise. They may be downloaded and/or printed for private study, or other acts as permitted by national copyright laws. The publisher or other rights holders may allow further reproduction and re-use of the full text version. This is indicated by the licence information on the White Rose Research Online record for the item.

Takedown

If you consider content in White Rose Research Online to be in breach of UK law, please notify us by emailing eprints@whiterose.ac.uk including the URL of the record and the reason for the withdrawal request.

eprints@whiterose.ac.uk
https://eprints.whiterose.ac.uk/

A Simple Bayesian Approach to Tree-ring Dating

Masoud M. Hassan[1], Emma Jones and Caitlin E. Buck[2]

[1] Corresponding author: Faculty of Science, University of Zakho, Kurdistan-Iraq,
Masoud.Hassan@uoz.edu.krd.
[2] School of Mathematics and Statistics, University of Sheffield, UK

Abstract

Tree-ring dating involves matching sequences of ring-widths from undated timbers to dated sequences known as 'master' chronologies. Conventionally, the undated timbers (from a building or woodland) are sequentially matched against one another, using t-tests to identify the relative offsets with the 'best' match, thus producing a 'site' chronology. A date estimate is obtained when this is matched to a local master chronology of known calendar age.

Many tree-ring sequences in the UK produce rather low t-values and are thus declared not to have a 'best' match to a master chronology. Motivated by this and the routine use of Bayesian statistical methods to provide a probabilistic approach to radiocarbon dating, this paper investigates the practicality of Bayesian dendrochronology. We explore a previously published model for the relationship between ring-widths and the underlying climatic signal, implementing it within the Bayesian framework via a simulation-based approach. Probabilities for a match at each offset are produced, removing the need to identify a single 'best' match. The Bayesian model proves successful for matching in both simulated and real examples.

Keywords: Tree-ring Dating, Statistical Models, Bayesian Statistics, Prior Information, Markov Chain Monte Carlo Simulation.

1 Introduction

Dendrochronology, or tree-ring dating, uses the patterns of tree-ring growth to date timber samples. Each year a tree grows a new extra ring, and the width of that ring depends on several factors; mainly the climate and growth trend. It is assumed that trees of the same species within the same geographical region receive the same climatic signal throughout a given year because they are exposed to similar climatic growth conditions, but this signal varies from year to year (Litton and Zainodin, 1991). Good growing seasons usually provide wide rings, whereas poor ones produce narrow rings. This pattern of ring widths is the key to both dendrochronology and dendroclimatology (using the pattern of tree-ring growth as an indicator of past ecological processes and to reconstruct past climate). For more information about dendrochronology and dendroclimatology, the reader is referred to Cook et al. (1990) and Fritts (1976). The focus of this paper, is dendrochronology.

Dendrochronologists use patterns of annual ring-widths to date timbers by matching a group of trees from the same geographical location one with another to ensure that every single ring is matched to its exact date of formation. This process is called "cross-matching" or "cross-dating" and is now usually based on statistical techniques (detailed in Section 2) which are used to measure the similarity between the cross-matched sequences. In order to use the pattern of tree-ring widths to date timbers and provide the calendar period during which a tree grew, it is essential to build a master chronology, which is a long, mean ring-width sequence that is made from large numbers of continuously overlapping timbers. Then a cross-matching process can be used to date a ring width sequence from a timber of unknown date by comparing it with the relevant master chronologies.

Site chronologies seldom comprise any trees of known age and so are initially undated. Hence the need for a regional chronology that does contain measurements from trees of known age so that, when all of the available tree-ring index sequences from that region are matched one-to-another, we obtain calendar date estimates for every tree-ring in the sequence.

Over the past decades, many efforts have been made to develop statistical models for dendrochronology. The earlier statistical models, such as those suggested by Fritts (1976) and Litton and Zainodin (1991), were typically based on extending linear, empirically-determined relationship between tree-ring indices and climate. This article explores the use of the statistical model first proposed by Litton and Zainodin (1991). This is fully probabilistic and provides a basis for the implementation of a Bayesian approach to tree-ring dating. It was not widely adopted by the dendrochronology community at the time of publication, however, as the use of Bayesian methods were not common and they were difficult to implement. The routine use and current success of Bayesian methods in radiocarbon dating, through modern radiocarbon calibration software such as OxCal (Bronk-Ramsey, 2008) and BCal (Buck et al., 1999), means that it now seems timely to explore the (Litton and Zainodin, 1991) model again. Those not familiar with the Bayesian approach to radiocarbon dating might like to consult Buck et al. (1996) (in particular Chapter 9) prior to reading the details of this paper. Our eventual goal is a fully Bayesian approach to the dating of timbers that will allow dendrochronological dates to be formally combined with those from radiocarbon dating, which is currently not practical due to the incompatibility of the inference methods used.

Section 2 of this paper provides a brief literature review of the existing statistical methods that are key to understanding the process of dendrochronology, including preprocessing of tree-ring data, cross-matching sequences, constructing chronologies and modelling tree-ring growth. Section 3 introduces our Bayesian approach to tree-ring dating which involves formalisation of the cross-matching process, and implementation alongside the model proposed by Litton and Zainodin (1991). Section 4 includes results of the Bayesian implementation using both simulated and real data to investigate the proposed model and matching process. We present several experiments, matching undated tree-ring sequences to both local and regional master chronologies. Section 5 summarises the research work and draws conclusions from it, offers recommendations for the use of the suggested model and matching process by the dendrochronologists, and suggests further work that is needed before Bayesian dendrochronology could be adopted routinely.

All of the code for the implementation of the models suggested within this paper are written in R (R Core Team, 2015).

2 Existing Statistical Methods in Dendrochronology

Dendrochronological studies and analysis depend on a series of statistical procedures. Currently these start by preprocessing data to remove any growth-trend from the data (via fitting a curve to the raw tree-ring sequences), then statistical measures such as correlation coefficient and Student's t-value are used in cross-matching ring-width sequences and hence providing a calendar date for an undated timber.

2.1 Preprocessing Data

Before using tree-ring data for cross-matching, they are preprocessed to remove any age growth effect and non-climatic factors. The process of removing trend from tree-ring width sequences is called "detrending", and the resulting preprocessed data are called ring-width "indices". One of the main non-climate factors that exists in ring-width data is age growth trend. When the tree is younger it usually grows faster, and a wider ring is formed. As the tree ages, the growth of ring-width slows down. Thus, before dating timbers in dendrochronology, this age-related trend must be identified and removed from raw ring-width measurements for physical and statistical reasons. Physically to remove the geometrical impacts of the growth trend; and statistically to obtain stationary time-series sequences which are comparable. Removing the growth trend can be achieved by filtering the data (fitting a moving average) or standardising the data (fitting a growth curve and finding the ratio of the raw ring-width divided by the expected ring-width from the curve). For detrending our data in this paper, we used the "modified negative exponential" method suggested by Fritts (1976). For more information about this method and other detrending methods, the reader is referred to Fritts (1976) and Cook et al. (1990).

2.2 Cross-dating Tree-ring Sequences

Having successfully prepared tree-ring width data by preprocessing them to remove age trend, the patterns of the obtained ring-width indices from the same geographical location can then be compared with one another in order to date them. There are several methods currently used by dendrochronologists for matching tree-ring width sequences. The following is one commonly used illustrative example; for others see (Cook et al., 1990; Fritts, 1976).

2.2.1 t-test Method

The Student's t-value, suggested by Baillie and Pilcher (1973), is now commonly and routinely used by dendrochronologists to decide how good the match is between the two ring-width sequences when cross-matching. For the t-value calculation to be a valid measure of significance, it must be assumed that the sequences of tree-ring indices are independent observations that follow a normal distribution with mean zero and constant variance.

Let there be two stationary sequences of ring-width indices, y_1 and y_2, of length l_1 and l_2 respectively. Let there also be at least q rings in common between the two sequences resulting in $l_1 + l_2 - 2q + 1$ possible offsets. Now, let $r(y_1; y_2; \Delta)$ be the Pearson correlation coefficient between the two standardised sequences, y_1 and y_2, at offset Δ. The Student's t-value for each possible offset, Δ, between the two sequences, y_1 and y_2, is calculated as follows,

$$t(y_1, y_2, \Delta) = \frac{r\sqrt{q-2}}{\sqrt{(1-r^2)}}.$$

As the value of r increases, the t-value increases, and this indicates that the two sequences are matching well at offset Δ.

Baillie and Pilcher (1973) used a threshold t-value of 3.5 to indicate an acceptable match for tree-ring dating, which gives a 0.1% significance level for overlaps greater than 100 rings. The higher the t-value, the better the match is between the two sequences. The use of an arbitrary 3.5 t-value threshold has become routine practice in dendrochronology. However, it does not suggest that any offset with t-value higher than this threshold is correct, and there might be a cases where the match with a t-value of ≤ 3.5 gives a correct offset or a t-values ≥ 3.5 gives an incorrect offset (Wigley et al., 1987). This method of matching timbers has been used by many dendrochronologists, including Baillie (1977, 1995); Brown et al. (1986); Hillam (2008); Mills (1988); Orton (1983); Pilcher (1990); Sander and Levanic (1996); Walker (2005). Here, we will use this method as a classical approach to be compared with the Bayesian approaches that we propose.

2.3 Constructing Chronologies

Having successfully matched single sequences with one another (using a t-test or one of the other methods described in (Fritts, 1976)), the next step is to build a site chronology. A "site" can be defined as the timbers from a building or from a specific (well defined) geographic region for example, a woodland. Once pairwise matching has been successful, groups of sequences are said to be matched, for any three sequences A, B and C, with:

- A and B matching at offset D(A,B),
- B and C matching at offset D(B,C),
- A and C matching at offset D(A,C),

if and only if the following condition holds:

- D(A,C)=D(A,B)+D(B,C)

If the dendrochronologist is satisfied (via such pairwise matching) that the groups of sequences have a strong enough match to be considered to have ring-widths that grew in the same year, then a site chronology can be established by averaging the ring-widths that are aligned at the same offset D. See Section 2.3.3 for details on how this is done

A master chronology is an average (arithmetic mean) ring-width sequence for a specific species, which is built by successively matching a group of long tree-ring width sequences (Laxton and Litton, 1988). If ring-width sequences are included of known date, for example from samples of living trees, then a date can be assigned to each ring-width in the entire master chronology and thus it can be used for dating other ring-width sequences of unknown age. Master chronologies can draw on data from a single site or from large geographical areas and are described as either "local" or "regional" respectively.

2.3.1 Local Master Chronology

As described above, a 'local' or 'site' master chronology is a sequence created by cross-matching a group of overlapping trees from a single location or small geographic region. The robustness of the resulting chronology is typically measured by the number of trees whose rings contribute to the chronology in each year, which may well vary over its length. Using classical statistical methods, it has been shown that a reliable site chronology can typically be created from 8–10 overlapping trees of the same species (Baillie and Pilcher, 1973). It is also common practice to create a site chronology using tree-ring index sequences in which all pairs of trees overlap by at least 40 rings (Laxton and Litton, 1988). Such practices lead to site chronologies in the standard databases of tree-ring sequences which vary from 100 to 500 years in overall length.

2.3.2 Regional Master Chronology

A "regional" master chronology is a long sequence created from cross-matching, and averaging, a group of site chronologies from a particular region, typically including at least one dated chronology. Regional master chronologies thus tend to represent a larger geographical area than site chronologies and can serve as a "reference" for cross-matching undated tree-ring width sequences.

UK regional chronologies typically vary from 200 years to more than 1000. For example, the UK East Midlands chronology (Laxton and Litton, 1988) covers 1100 years (882–1981 AD) and was built from 59 local master chronologies. Litton and Zainodin (1991) suggest that a regional master chronology should comprise at least 5 to 10 overlapping site chronologies.

2.3.3 Producing a Site Chronology

Several methods have been used by dendrochronologists to combine ring-width sequences into a site master chronology. The simplest and most widely used is to average a group of standardized ring-width indices from a particular year. As long as there is a large enough number of tree-rings from each year, this minimises the effect of outliers, and the site chronology is highly validated (Baillie, 1982).

Let y_{ti} be the ring-width index value for a particular year t from tree i, where $i = 1, \ldots, I$ and I is the number of ring sequences obtained from a specific geographic location, then the value of the site chronology at year t is:

$$C_t = \sum_{i=1}^{I} \frac{y_{ti}}{I}$$

where C_t is an estimate of the climatic signal in year t, $t = 1, 2, \ldots, l$, and l is the length of the site chronology C.

2.4 Modelling Tree-Ring Growth

2.4.1 Statistical Model

A simple statistical model which represents the relationship between climatic signal and preprocessed ring-width data (or indices) was first suggested by Fritts (1976) . This model assumes that the tree-ring index in year t is equal to the underlying climatic signal (which is common to all trees within a particular geographical area) plus some noise due to non-climatic effects. The model was then used by Litton and Zainodin (1991) who sought a formal way of using statistical models for tree-ring dating and cross-matching sequences. The model is defined as follows,

$$y_{ti} = \beta + u_t + \epsilon_{ti}, \tag{1}$$

where

- y_{ti} is the fully-processed (and thus stationary and uncorrelated) ring-width index at year t for tree i, β is the overall mean of the population of ring-width indices, u_t indicates the underlying climatic signal in year t, and ϵ_{ti} denotes the noise of tree i in year t.
- the noise component ϵ_{ti} includes all other non-climatic factors, such as soil condition, site location, presence of pest and disease, and competition among trees for sunlight.
- the signal u_t and the noise ϵ_{ti} are assumed to be independent for statistical convenience. They are both independent and identically normally distributed with mean 0 and variance σ_u^2 and σ_e^2 respectively; $u_t \sim N(0, \sigma_u^2)$ and $\epsilon_{ti} \sim N(0, \sigma_e^2)$.

- the ring-width index y_{ti} is thus independent and identically normally distributed with mean 0 and variance $\sigma_u^2 + \sigma_e^2$.
- the signal-to-noise ratio (S), which identifies the strength of similarities among groups of tree-ring index sequences, is defined as

  $$S = \frac{\sigma_u^2}{\sigma_e^2}; \quad \sigma_u^2,\ \sigma_e^2 > 0 \quad \Longrightarrow S > 0, \tag{2}$$

  where σ_u^2 and σ_e^2 are respectively the variance of the climatic signal u_t and the variance of the noise ϵ_{ti}. The larger the value of S, the more similar the trees are.

2.4.2 Using the Statistical Model for Dating

The model described in Equation (1) was successfully used by Litton and Zainodin (1991) for dating ring-width sequences using the following three approaches.

Cross-matching Two Samples

Let two trees i and i' ($i \neq i'$) from the same geographical region be compared for the purpose of dating. The correlation coefficient r between the two compared sequences for the same year t can be calculated as follows:

$$r(y_{ti}, y_{ti'}) = \frac{\sigma_u^2}{\sigma_u^2 + \sigma_e^2} = \frac{S}{S+1}.$$

The similarity between the two sequences can be evaluated via the signal-to-noise ratio, S. As the value of S increases, the correlation r between the two cross-matched ring-width sequences increases and the similarity between them increases too. The 'best' match is then at the offset with the highest value of S.

Cross-matching a Sample to a Chronology

Under the assumptions of the model in Equation 1, a single tree-ring index sequence y_{ti} can be compared to a well replicated average sequence $\bar{y}_{t.}$ at year t, and the correlation between the two sequences would be:

$$r(y_{ti}, \bar{y}_{t.}) = \frac{\sigma_u^2}{\sqrt{(\sigma_u^2 + \frac{\sigma_e^2}{I})(\sigma_u^2 + \sigma_e^2)}} = \frac{S}{\sqrt{(S + I^{-1})(S+1)}},$$

where $\bar{y}_{t.}$ is the average sequence created from I samples of ring-width indices from the same region, with $E(\bar{y}_{t.}) = 0$ and $Var(\bar{y}_{t.}) = (\sigma_u^2 + \frac{\sigma_e^2}{I})$. Zainodin (1988) concluded that the correlation between a sample and an average sequence from the same geographical region is always greater than that between the two individual sequences; $r(y_{ti}, \bar{y}_{t.}) > r(y_{ti}, y_{ti'})$.

Cross-matching Two Chronologies

The same statistical model can also be used for cross-matching two averaged sequences. Let $\bar{y}_{t.}$ and $\bar{y}_{t.'}$ be two chronologies created from I_1 and I_2 trees respectively, with zero means and variances $Var(\bar{y}_{t.}) = \sigma_u^2 + \frac{\sigma_e^2}{I_1}$ and $Var(\bar{y}_{t.'}) = \sigma_u^2 + \frac{\sigma_e^2}{I_2}$, respectively. The correlation coefficient between the two cross-matched chronologies is:

$$r(\bar{y}_{t.}, \bar{y}_{t.'}) = \frac{\sigma_u^2}{\sqrt{(\sigma_u^2 + \frac{\sigma_e^2}{I_1})(\sigma_u^2 + \frac{\sigma_e^2}{I_2})}} = \frac{S}{\sqrt{(S + \frac{1}{I_1})(S + \frac{1}{I_2})}}.$$

Zainodin (1988) also noted that a higher correlation coefficient is obtained between two averaged chronologies than between an average and a sample or two individual samples; i.e.

$$r(\bar{y}_{t.}, \bar{y}_{t.'}) > r(y_{ti}, \bar{y}_{t.}) > r(y_{ti}, y_{ti'}),$$

thus, grouping trees from the same climatic region is preferable for all currently used and proposed tree-ring dating methods.

3 Bayesian Dendrochronology: A New Approach

In this section a Bayesian approach for tree-ring dating using the statistical model (in Equation 1) is introduced. This new probabilistic approach involves simultaneously fitting the model and sequentially matching the undated trees to the dated master chronology with a view to identifying the offset with the highest probability of a match and thus the most likely date for the undated chronology. Following is a brief summary of our proposed Bayesian implementation of tree-ring dating.

3.1 Matching Notation

Let the dated master chronology be of length l years, and comprise I trees. Let the start and end dates of the dated master chronology be Δ_s and Δ_e, respectively, so that $l = \Delta_e - \Delta_s + 1$. For tree i, $i = 1, 2, \ldots, I$, let δ_i be the start date of the tree i, l_i be its age (length of the sequence) in years, and $\delta_i + l_i - 1$ be its felling date. Similarly, let the undated site chronology be of length l^* years, and have I^* trees. Let Δ^* be the unknown start date of the undated site chronology. For tree i, $i = I + 1, \ldots, I + I^*$, let $\delta_i = \Delta^* + h_i$ be its unknown start date (where $h_i \geq 0$, is the offset of tree i relative to Δ^*), l_i^* be the length of the tree, and $\delta_i + l_i^* - 1$ be the end date of the tree.

Now, the dating process starts by consecutively matching the undated site chronology to the dated master chronology at all possible offsets from $t = \Delta_s - l^* + q$ to $t = \Delta_e + l^* - q$, where q is the minimum overlap of rings between the dated and undated sequences. Therefore, the total number of all possible offsets between the two sequences is equal to $l + l^* - 2q + 1$.

3.2 Model Outline and Implementation

The model and matching process are implemented within a Bayesian framework. As in all such implementations, we must define and compute a prior distribution and likelihood for each parameter in the model, and then multiply these together to estimate the posterior distribution for each parameter and, in particular, estimate the calendar age of each (undated) tree-ring.

3.2.1 The Likelihood

Adopting the basic statistical model in Equation 1, let $\mathbf{y}^D = (y_1, \ldots, y_I)$ and $\mathbf{y}^{UD} = (y_{I+1}, \ldots, y_{I+I^*})$ represent the tree-ring indices for all dated and undated trees, respectively, so that the indices for all trees together are $\mathbf{y} = (\mathbf{y}^D, \mathbf{y}^{UD}) = (y_1, \ldots, y_n, y_{I+1}, \ldots, y_{I+I^*})$. The likelihood of the dated and undated master chronologies can be given respectively as,

$$p(\mathbf{y}^D|\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2) \propto \prod_{i=1}^{I} \left[\prod_{t=\delta_i}^{\delta_i+l_i-1} (\frac{1}{\sigma_e^2})^{\frac{1}{2}} \exp(-\frac{1}{2\sigma_e^2}(y_{ti} - \beta - u_t)^2) \right]$$

$$p(\mathbf{y}^{UD}|\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2, \Delta^*) \propto \prod_{i=I+1}^{I+I^*} \left[\prod_{t=\Delta^*+r_i}^{\Delta^*+r_i+l_i-1} (\frac{1}{\sigma_e^2})^{\frac{1}{2}} \exp(-\frac{1}{2\sigma_e^2}(y_{ti} - \beta - u_t)^2) \right],$$

hence the likelihood of all data can be obtained by combining both the likelihood of the undated site and dated master chronologies as follows,

$$p(\mathbf{y}|\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2, \Delta^*) \propto p(\mathbf{y}^D|\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2)\ p(\mathbf{y}^{UD}|\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2, \Delta^*)$$

3.2.2 The Priors

In order to make inference about the unknown parameters $(\beta, \sigma_u^2, \sigma_e^2, \Delta^*)$, we define prior distributions for each model parameter as follows.

Prior for β

The parameter β, should have a symmetric distribution with a mean close to zero as the ring-width indices have been standardised and are distributed with zero mean and variance 1. Accordingly, an appropriate prior distribution for this parameter would be normally distributed with zero mean and variance k, where k is a constant to be determined. For the experiments in the next section, we used a non-informative prior for β, with a value of k chosen to be 1000 to give a flat prior as we consider having little knowledge about the data and hence it has the least effect on the inference process.

Prior for σ_u^2 and σ_e^2

For practical statistical reasons, it is common practice to model the precision, $\frac{1}{\sigma^2}$, rather than the variance itself due to the conjugacy properties between the normal and gamma distributions which simplifies the sampling procedure. The gamma is a fairly flexible distribution and can, when appropriate, give an uninformative flat prior when the parameters of the gamma distribution are small. We chose the prior distribution for $\frac{1}{\sigma_u^2}$ and $\frac{1}{\sigma_e^2}$ to be $\Gamma(a_u, b_u)$ and $\Gamma(a_e, b_e)$ respectively, with the shape (a_u and a_e) and rate (b_u and b_e) parameters to be determined. For the experiments in the next section, we used a small value of 0.01 for the shape and rate parameters. We chose such a prior largely because it is mathematically convenient and is flat (and thus uninformative) over most of the range zero to one. It does, however, place a large weight near zero, which could produce undesirable results in some circumstances and would certainly be worth revisiting in future work. In practice, in all the examples considered in this paper, we found that there is sufficient information about these parameters in the data that the choice of prior did not have a marked impact on the posterior.

Prior for Δ^*

Current practice in dendrochronology is to assume that *a priori* any possible date is just as likely as any other; thus it is desirable to use a non-informative prior for the unknown date; one which allows equal weight to each of the possible Δ^* available. An obvious and simple prior distribution for Δ^* is thus a discrete Uniform distribution such that $p(\Delta^*) \sim U[\Delta_s - l^* + q, \Delta_e + l^* - q]$. The prior probability of each date in $t = 1, 2, \ldots, l$ is thus $\frac{1}{l+l^*-2q+1}$.

3.2.3 The Posterior

Under the Bayesian framework, combining the likelihood (detailed in Section 3.2.1) and prior distributions (detailed in Section 3.2.2), the joint posterior distribution of the model parameters and matching process is given by

$$p(\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2, \Delta^* | \mathbf{y}) \propto p(\mathbf{y} | \beta, \mathbf{u}, \sigma_u^2, \sigma_e^2, \Delta^*)\ p(\beta)\ p(\sigma_u^2)\ p(\sigma_e^2)\ p(\Delta^*).$$

It is not practical to evaluate this distribution algebraically. So, instead, we used a Markov Chain Monte Carlo (MCMC) simulation method which allows sampling from the posterior distribution. The reader is referred to Gilks et al. (1996) for an introduction to general MCMC methods and implementation, and to Goldstein (2011) for an introduction to MCMC sampling for multilevel statistical models.

3.2.4 Implementing the Bayesian Model

A standard Gibbs sampler is used to estimate the marginal distributions, by sampling from the full conditional distribution for each parameter, as outlined in Appendix A.

3.3 Simulating Data for Model Implementation

In order to test our MCMC implementation of the Bayesian statistical model, and associated matching process, we simulated tree ring-width indices using the model given in Equation 1 (pseudo-code for each step of our simulation is given in Appendix B). In specifying the features of our simulated data, we explored the International Tree-Ring Data Bank (`http://www.ncdc.noaa.gov/paleo/treering.html`), which is the world's largest archive of tree ring data, using our findings to characterise a range of common data properties as follows.

1. **Signal-to-noise ratio**
   The signal-to-noise ratio (S), detailed in Equation 2, measures how similar a group of tree-ring width sequences are within a chronology. When σ_u^2 is large (relative to σ_e^2), the signal-to-noise ratio is large; and vice-versa. For simulating data to test the Bayesian implementation of the model, we used a range of S values (given in Table 1) to mimic a plausible range of data types. Since raw tree-ring data are typically detrended, prewhitened and then normalised as detailed in Section 2, the data we simulated are normally distributed with mean 0 and variance 1. This implies that the sum of the climatic signal variance, σ_u^2, and the model noise variance, σ_e^2, is 1.

   This change requires a slight amendment to our model so that, in equation 1, $u_t \sim N(0, \sigma_u^2)$, where $\sigma_u^2 < 1$, and $\epsilon_{ti} \sim N(0, 1 - \sigma_u^2)$. Implementing this requires an amendment to the Gibbs sampler algorithm outlined in Appendix A, whereby step 5 simply becomes "Set $p(\sigma_e^{2(1)}|\mathbf{y}, \beta^{(1)}, \mathbf{u}^{(1)}, \sigma_u^{2(1)}, \Delta^{*(0)}) = 1 - \sigma_u^{2(1)}$". We make this change now, rather than modelling in this way originally, since the original model is more general. If our approach is adopted more widely, we hope that users will find that they can use the model and implementation described in section 2.4 and 3.2.4, without the need for detrending, prewhitening and normalising, since modelling data directly is always more satisfactory than transforming. For the moment, however, we adopt standard practice.

2. **The dated master chronology**
   A dated site master chronology is required for the cross-matching process. Dated sequences were simulated by adding normally-distributed noise, $N(0, \sigma_e^2)$, to the simulated climatic signals u_t. A dated master chronology was then obtained by grouping of simulated trees, with the following parameters.

   - **The length of the dated master chronology (l)**
     The length of dated site master chronologies varies from one site to another; between 50 and 500 years. Regional chronologies often cover many more years than site chronologies, as they contain many more samples. To test the Bayesian implementation of the model and matching process, we simulated chronologies of length 200 years to represent a local site master chronology, and chronologies of length 1000 years to represents a regional master chronology.
   - **Number of samples (I) in the dated master chronology**
     The number of trees in the dated master chronologies also varies from one site

S	σ_u^2	σ_e^2	S	σ_u^2	σ_e^2
0.1	0.1001	0.8999	1.1	0.5238	0.4762
0.2	0.1667	0.8333	1.2	0.5455	0.4545
0.3	0.2308	0.7692	1.3	0.5652	0.4348
0.4	0.2857	0.7143	1.4	0.5833	0.4167
0.5	0.3333	0.6667	1.5	0.6000	0.4000
0.6	0.3750	0.6250	1.6	0.6154	0.3846
0.7	0.4118	0.5882	1.7	0.6296	0.3704
0.8	0.4444	0.5556	1.8	0.6429	0.3571
0.9	0.4737	0.5263	1.9	0.6552	0.3448
1.0	0.5000	0.5000	2.0	0.6667	0.3226

Table 1: Different signal-to-noise ratios (S) with corresponding model variance components, used for simulating data for exploring our Bayesian implementation of the model in Equation 1.

   to another. For the experiments that follow, we simulated site chronologies with 10, 5, 2, and 1 sequence(s), and regional chronologies with 100 sequences.

   - **The length of individual trees (l_i) in the dated master chronology**
     We randomly simulated trees of length ($75 \leq l_i \leq 150$) to mimic real trees of the dated site chronologies.

3. **Minimum overlap between dated and undated site chronologies**
   Standard practice in dendrochronology (as first suggested by Laxton and Litton, 1988) tends to require between 40–50 rings of overlap between dated and undated chronologies. Here, a minimum of 50 rings of overlap will be used for simulating data.

4. **The undated site chronology**
   An undated site chronology was obtained by grouping simulated trees, with the following parameters:

   - **The length of the undated site chronology (l^*).**
     The length of the undated site chronology should be shorter than the length of the dated master chronology, $l^* \leq l$, to ensure the matching process. Thus, for the data simulation we considered undated site chronologies of length 200, 100 and 50 years.
   - **Number of samples (I^*) in the undated site chronology**
     The number of individual trees in the undated site chronologies should also be less than or equal to the number of individual trees in the dated site chronologies, $I^* \leq I$. Therefore, chronologies with $10, 5$ and 1 samples were simulated.
   - **The length of the individual trees (l_i^*) in the undated site chronology.**
     For our Bayesian model implementation, we simulated undated trees of length ($50 \leq l_i \leq 100$) to mimic real undated trees in the International Tree-Ring Data Bank

5. **The true offset of the undated site master chronology**
   The true date offset of the undated site master chronology to the dated site master chronology is fixed at index 100 throughout the experiments. This is in order to compare the results of the experiments as the other parameters are changing.

3.4 Further Implementation Considerations

For each experiment in Section 4, an initial run of 10,000 iterations of the Gibbs sampler was simulated, using start values that were known not to be close to the true posterior values. Although not reproduced here, iteration-by-iteration plots of the output from the MCMC simulation for each parameter (known as trace plots) were used to informally approximate the length of burn-in required for convergence of the MC for each continuous parameter. The Raftery and Lewis diagnostic test (Raftery and Lewis, 1992) was also used to check the length of burn-in and to establish whether or not thinning of the MC was desirable (to obtain uncorrelated samples) and how many iterations the chain should be run after burn-in (to obtain a representative sample from the posterior).

As Δ^* is a discrete variable, it was difficult to ascertain a diagnostic test to ensure that the chain had converged. Instead a check on the reproducibility of the results was conducted by using three MCMC runs each with a different random number generator seeds. The posterior probabilities for Δ^* for each of the three runs were then compared. This determined how many iterations were needed to produce results for Δ^* that were reproducible to two decimal places. The number required varied between experiments.

4 Results of Bayesian Cross-matching Experiments

4.1 Local Site Chronology Examples

In this section we report results from a selection of experiments on test data derived as outlined in Section 3.3. We compare the Bayesian results directly with those from conventional tree-ring dating methods and highlight the key advantages of using probabilities rather than t-values to convey the strength of match between sequences.

4.1.1 Matching an undated sample to a dated site master, with a match

Consider first the situation where we have simulated data for a master chronology and an undated sample using the same underlying model; thus ensuring that there is a match between the two. Table 2 shows results for such experiments which match a single undated tree-ring index sequence, of length 100 years, to a dated site master chronology containing 10 samples which covers a period of 200 years. When the signal-to-noise ratio, S, is greater than or equal to 0.3, the posterior probability of a match at the true offset is 1. For all of such experiments, the true offset has a t-value that is very large in comparison to t-values at any other date offset and the Bayesian implementation provides the highest posterior probability of a match at the true offset for any $S \geq 0.2$.

S	σ_u^2	σ_e^2	Posterior		$\hat{\sigma}_u^2$	$\hat{\sigma}_e^2$	$\hat{S}$	Traditional Results	
			Offset	Probability				ρ	t-value
0.3	0.2308	0.7692	100	1.00	0.23	0.77	0.3	0.451	5.004
			118	0.00				0.310	2.912
0.2	0.1667	0.8333	100	0.79	0.16	0.84	0.2	0.372	3.969
			118	0.10				0.278	2.649
			101	0.05				0.284	2.850
			-48	0.01				0.243	1.768
			14	0.01				0.191	1.921
0.1	0.1001	0.8999	101	0.17	0.09	0.91	0.1	0.271	2.778
			100	0.14				0.277	2.851
			118	0.10				0.233	2.215
			14	0.08				0.203	1.999
			7	0.05				0.240	2.282

Table 2: Results of experiments when matching one undated tree-ring index sequence of length 100 years to a dated master chronology containing 10 samples which covers a period of 200 years. The matches with the highest posterior probabilities are reported; they do not always sum to 1 as there were offsets with very small posterior probabilities. The true offset of the undated site chronology is 100. The signal-to-noise ratio varies from S=0.3 to S=0.1; as the signal-to-noise ratio decreases, the posterior probability of a match at the true offset decreases. To obtain these results, the Gibbs sampler was run for a total of 100,000 iterations and thinned every 10, leading to a final sample of 10,000

Focussing now on the results in Table 2 (and Figure 1) relating to the experiments when S=0.2, we begin to see the real power of the Bayesian approach. Figure 1 provides reliable estimates for the parameters of the model and a summary of the posterior probabilities of a match at all possible offsets. The posterior probability of a match at the true offset (ring 100) is 0.79 which is more than 7 times higher than that of the match with the next highest probability (ring 118). By contrast the respective t-values are 3.969 and 2.649 (see Table 2) which are both close to the 3.5 threshold commonly used in conventional tree-ring dating to indicate a candidate match, and on an arbitrary scale, so would be difficult to interpret reliably were this a real dating problem. When S=0.1, the posterior probability of a date match at the true offset is small, 0.12, and is not the offset with the highest posterior probability of a match (offset 101 provides the highest posterior probability of a match of 0.16). Nonetheless, the Bayesian approach provides posterior probabilities for each offset which are highly interpretable and could offer valuable prior dating evidence for future dating efforts. By contrast, when S=0.1, the traditional methodology provides t-values which are all below the 3.5 threshold, and are very similar in size, resulting in an

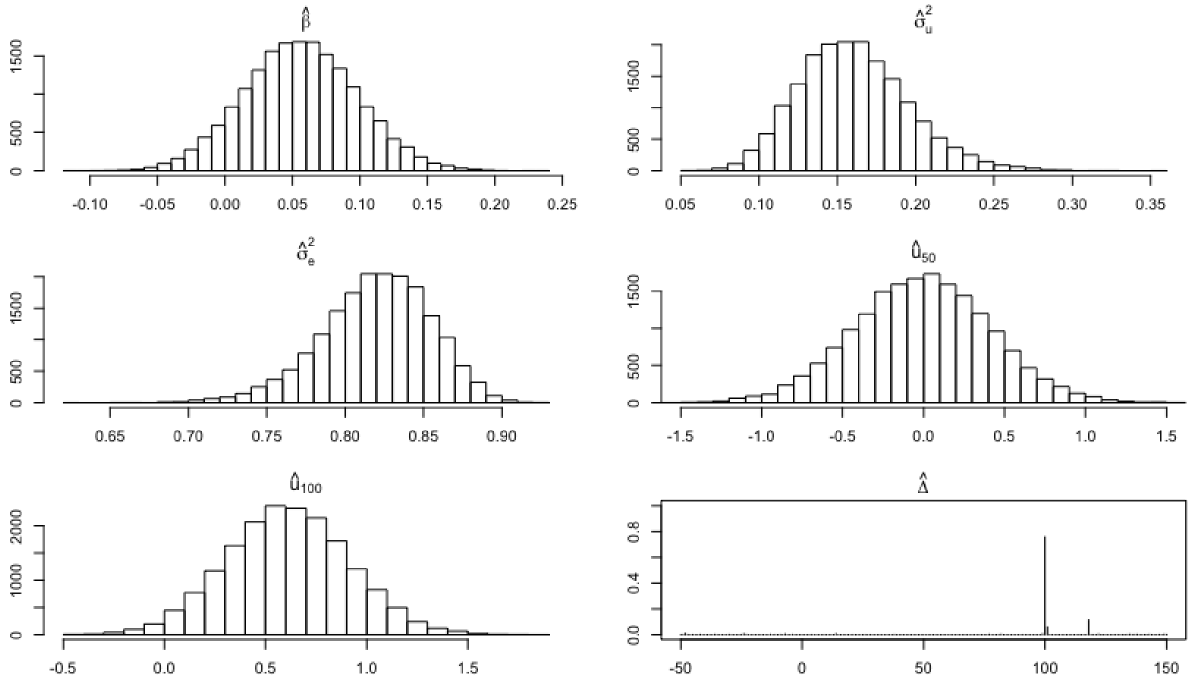

Figure 1: Plots of the posterior distributions of $\hat{\beta}$, $\hat{\sigma}_u^2$, $\hat{\sigma}_e^2$, $\hat{u}_{50}$, $\hat{u}_{100}$ and $\hat{\Delta}^*$ for the experiment which matched one undated tree-ring index sequence of 100 years to a dated master chronology with 10 samples, covering 200 years, when the signal-to-noise ratio was S=0.2. The estimates for each parameter are very close to the values used to simulate the data. Note, in particular, however that the true off-set (100) has a posterior probability of 0.79 and all other offsets have very small, but non-zero, posterior probabilities.

inconclusive date estimate of little value in future work.

Expanding on these observations a little, Figure 2 provides a summary of the relationship between t-value and posterior probability from a selection of the experiments on simulated data obtained during the course of preparing this paper. Observe that a range of t-values can be associated with a single posterior probability, which means that the two scales are not monotonically related. We see the same in Table 2 where we note that the rank order of offsets differs between the posterior probabilities and the t-values, meaning that there is not a one-to-one relationship between the two scales. Figure 2 also gives some idea of why the t=3.5 threshold has worked so well for many years: there is a plateau of t-values just below this threshold which are associated with samples that lead to quite a wide range of posterior probabilities (around 0.75). Samples with t-values above the 3.5 threshold, however, all give rise to posterior probabilities of around 0.8 and above.

Given these observations, were practitioners to seek a posterior probability threshold with which to replace the current t-value one, a probability of 0.80 would be a good candidate.

This observation could lead readers to conclude that, in practical terms, there is little difference between the two approaches. This is far from the case, however, since we did not develop this approach simply with a view to replacing the classical acceptance/rejection approach to the matching of tree-ring samples with a Bayesian one. Rather our goal was to offer a more subtle and powerful way to work with poorly matching timbers. The Bayesian approach provides a) the ability to quantify the relative plausibility of multiple possible matches using probability (rather than t-values), and b) the possibility to integrate coherently dendrochronology with other dating methods. For example, by combining our approach with a Bayesian approach to radiocarbon wiggle-matching, one might rule out many of the possible matches in a case like the third one in Table 2. The key point here is that all dendrochronological matches are uncertain to a degree because they are obtained by a statistical matching process, but the Bayesian matching process allows us to get useful results in situations of lower certainty than current approaches do.

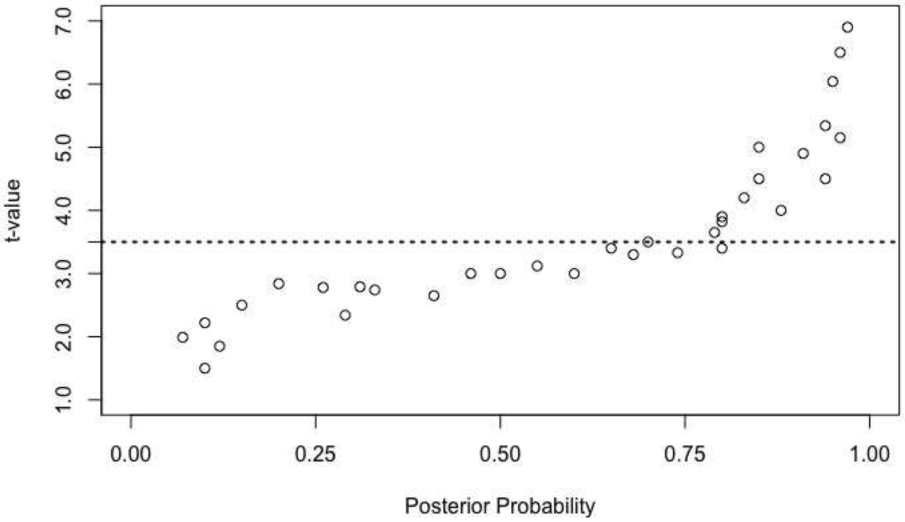

Figure 2: The relationship between t-value and posterior probability obtained from several experiments of matching undated sequences to dated master chronologies. Each point on the graph shows the highest posterior match probability and corresponding t-value for experiments on simulated data of the sort outlined in Section 4.1. The dotted line highlights the t-value threshold commonly used in conventional tree-ring dating to indicate a candidate match.

4.1.2 Matching an undated sample to a dated site master, with no match

Until now we have focussed on situations where a true match exists between the undated sample and the relevant dated master chronology. In practice, however, it is fairly commonn for no reliable match to be found. Using a signal-to-noise ratio of S=0.2, we first simulated a master chronology and then, quite independently, simulated an undated site sample. Cross-matching the two, results in posterior probabilities at all possible off-sets summarised in Figure 3. We see clearly that although some off-sets have higher posterior probabilities than others, all are very low. Indeed, the highest posterior probability is 0.034 making it clear that this sample cannot be reliably dated.

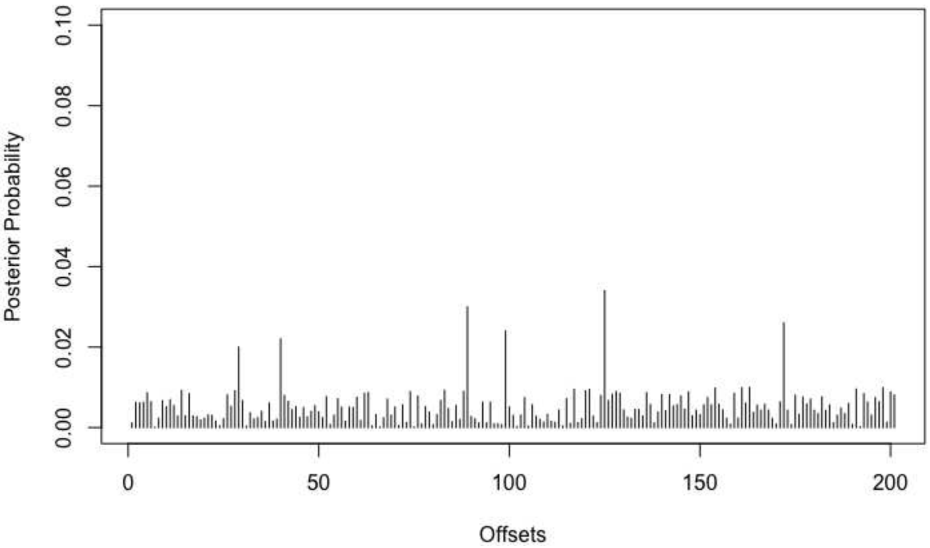

Figure 3: The posterior distribution of the unknown date for the experiment of matching an undated site chronology, covering 100 years, to a dated master chronology, covering 200 years, when there is no true offset between the two chronologies, and when the signal-to-noise ratio is S=0.2. All posterior probabilities are very low.

4.1.3 Matching an undated site chronology to a regional master

Returning once again to experiments for which we know there is a true match in the master chronology, Table 3 shows results from the experiment of matching a 100 year undated site chronology (comprising 5 tree-ring index sequences) to a 200 year dated master chronology containing 10 samples from a subregion with a signal-to-noise ratio of 0.2, using both the traditional approach to tree-ring dating and the Bayesian approach that we propose.

Focusing on the Bayesian results, it can be seen that the two chronologies are matched at the true offset with a posterior probability of 1. Posterior probabilities of 1 were also produced for similar experiments but with signal-to-noise ratios greater than 0.2, and are not reported here. Such conclusive results are not a surprise since as the numbers of samples in the site and master chronologies increase and/or the signal-to-noise ratio becomes larger, the climatic signal is stronger, and so matching to the true off-set becomes

S	σ_u^2	σ_e^2	Posterior		$\hat{\sigma}_u^2$	$\hat{\sigma}_e^2$	$\hat{S}$	Traditional Results	
			Offset	Probability				ρ	t-value
0.2	0.1667	0.8333	**100**	1.00	0.18	0.82	0.2	0.527	6.146
			80	0.00				0.303	2.647

Table 3: The results when an undated site chronology comprising 5 tree-ring index sequences, covering 100 years, is matched to a dated master chronology constructed from 10 tree-ring index sequences, covering 200 years, when the signal-to-noise ratio is S=0.2. The true offset at which the undated sequence matches the master chronology is 100 with a correlation of 0.527 and t-value of 6.146. Offset 80 has the second highest t-value; the Bayesian implementation of the statistical model and the matching process have a posterior probability of 0 at this offset. To obtain these results, the Gibbs sampler was run for a total of 50,000 iterations and thinned every 5, leading to a final sample of 10,000.

more likely.

4.2 Regional Master Chronology Examples

In this section we consider experiments with matching simulated, undated site master chronologies to a simulated dated regional master chronology following the experimental approach suggested in Section 3.3. As a reminder, the dated regional master chronology covers a period of 1000 years and is well replicated, comprising 100 tree-ring index sequences. The undated site master chronology covers a period of 200 years and contains 10 sequences. As the number of sequences in the dated regional master chronology increases, the sampler speed decreases, thus to ensure good replication of indices within each year of the dated regional master chronology, each simulated tree-ring index sequence will be of length 200 years. Three different experiments are conducted for each signal-to-noise ratio; each experiment has a different true date offset. The three experiments allow exploration of different correlations between the undated site master chronology and the dated regional master chronology.

Three separate undated site chronologies were simulated at three arbitrarily chosen offsets and so each undated site chronology matches to the dated regional chronology with a different correlation. The results reported in this section required fewer iterations to provide converged posterior estimates than those in Section 4.1; the MCMC sampler was run for 30,000 iterations after a small burn-in period and thinned every 3 iterations, giving reproducible results for 3 chains each with different random number generator seeds. We found that the posterior estimates for $\hat{\sigma}_u^2$ and $\hat{\sigma}_e^2$ were very close to the true values in all three cases.

Table 4 shows that for signal-to-noise ratios of 0.2 and above, regardless of the correlation between the dated regional chronology and the undated site master chronology, the posterior probability of a match at the true offset is 1. When the signal-to-noise ratio decreases to S=0.1, the t-values at the true offset are close or very close to the 3.5 threshold. The associated posterior probabilities at each date offset reflect this uncertainty, but

S	σ_u^2	σ_e^2	Posterior		$\hat{\sigma}_u^2$	$\hat{\sigma}_e^2$	$\hat{S}$	Traditional Results	
			Offset	Probability				ρ	t-value
0.3	0.2308	0.7692	552	1.00	0.23	0.77	0.3	0.545	9.147
			115	0.00				0.241	3.491
			346	1.00	0.23	0.77	0.3	0.562	9.570
			509	0.00				0.283	3.159
			632	1.00	0.23	0.77	0.3	0.598	10.501
			486	0.00				0.367	3.694
0.2	0.1667	0.8333	552	1.00	0.16	0.84	0.2	0.429	6.684
			115	0.00				0.242	3.517
			346	1.00	0.16	0.84	0.2	0.456	7.205
			509	0.00				0.293	3.147
			632	1.00	0.16	0.84	0.2	0.495	8.007
			486	0.00				0.363	3.617
0.1	0.1001	0.8999	552	0.90	0.10	0.90	0.1	0.262	3.823
			115	0.03				0.249	3.399
			346	0.98	0.10	0.90	0.1	0.306	4.442
			509	0.00				0.174	3.003
			632	0.96	0.10	0.90	0.1	0.349	5.148
			486	0.00				0.344	3.473

Table 4: Results of experiments which match three separate undated site chronologies each comprising 10 trees (which cover a period of 200 years) to a single dated regional master chronology (comprising 100 trees which cover a period of 1000 years). The signal-to-noise ratios vary from S=0.1 to 0.3 and the true offsets of the undated site sequences are 552, 346 and 632, respectively. Two matches with the highest posterior probabilities are reported; they do not always sum to 1 as there were offsets with posterior probabilities less than 0.005. The two most probable matches are the two with the highest t-values in all cases. To obtain these results, the Gibbs sampler was run for a total of 100,000 iterations and thinned every 10, leading to a final sample of 10,000

nonetheless offer very high probabilities at the true offset and would thus provide reliable date estimates suitable for immediate interpretation or use as a prior for future dating work. These results correspond closely with those from Section 4.1.

4.3 A Real Example from the South West of England

It is notoriously difficult to match, and thus date, timbers from the South West of England and the success rate, at 30-40%, in this area is well below the national average. Given this, we chose data from this region to test our methods. Data of known age for five subregions from South West of England were obtained from English Heritage and investigated here. The South West regional chronology were constructed from these data consisted of just 4 subregions (Horner Wood, Abbeyford Wood, Clovelly and Bocconoc) because the remaining subregion (River Dart) matched to the others with low t-values.

Posterior		$\hat{\sigma}_u^2$	$\hat{\sigma}_e^2$	$\hat{S}$	Traditional Results	
Offset	Probability				ρ	t-value
1879	0.98	0.14	0.86	0.16	0.363	4.066
1892	0.01				0.166	1.720
1777	0.00				0.291	3.18

Table 5: The results of an experiment which matched an undated site chronology from the River Dart to a dated regional master chronology from the South West of England. The true offset at which the undated chronology matches the regional master chronology is 1879. The three matches with the highest posterior probabilities are reported, they do not sum to 1 as there were offsets with posterior probabilities less than 0.005. To obtain these results, the Gibbs sampler was run for a total of 50,000 iterations and thinned every 5, leading to a final sample of 10,000

This approach mimicked the traditional methodology implemented by most dendrochronologists and resulted in a regional master chronology comprising 45 timbers, spanning AD 1879-1993.

In order to test the Bayesian modelling approach and matching process, the 8 timbers from River Dart were then treated as undated and combined together to form a site chronology which was then matched to the dated regional master chronology previously constructed.

Table 5 shows that the Bayesian implementation of the statistical model and the matching process successfully located the true date offset of the undated sequence with posterior probability of 0.98. This posterior probability is much higher than any of the posterior probabilities at alternative date offsets. The traditional methodology provided a t-value of 4.066 at this offset; which is greater than the current 3.5 threshold, but most dendrochronologists would prefer a much higher t-value in order to feel confident in the date match before reporting the result.

Results in this section show that the Bayesian implementation of the statistical model and matching process successfully located the true date offset of the undated sequence with high posterior probability. The advantage of the Bayesian approach, however, is that we now have directly interpretable posterior probabilities which are potentially useful priors for future work.

5 Conclusions and Further Work

The implementation of dendrochronology using Bayesian techniques has successfully been achieved. A series of experiments were conducted to investigate Markov-chain Monte-Carlo-based implementations of the statistical model and associated index matching processes. These implementations proved successful under the traditional assumptions that both chronologies to be matched are correctly built, the chronologies are contemporary to one another and that all the tress within both chronologies have grown under the same climatic conditions.

The proposed implementation enables dendrochronologists to provide posterior date estimates for timbers in the form of probabilities rather than the commonly used t-value. This change in presentation of date estimates enables their results to be more widely understood especially by those without any formal statistical training and, perhaps more importantly, has the potential eventually to allow dating evidence from dendrochronology and radiocarbon dating to be interpreted within the same inferential framework. Alternatively, the posterior date estimates from tree-ring dating could simply be used to provide informative prior distributions for radiocarbon dating.

As we have seen for Bayesian tree-ring dating, the specification of prior distributions for the model parameters and date offsets is necessary. Informative prior distributions for real dating projects could be derived from the wealth of knowledge held by ancient-building experts and dendrochronologists, and from studies of known age timbers. At present, such prior knowledge can only be used informally in tree-ring dating. With the Bayesian framework, such prior information can formally be incorporated within the inference process.

Dendroclimatologists now use mechanistic forward models for representing the relationship between climate and ring-width. The earlier statistical models, such as those suggested by Fritts (1976) and Litton and Zainodin (1991), were typically based on extending linear, empirically-determined relationship between tree-ring indices and climate. However, linear empirical-statistical analyses alone cannot reveal a physical or biological mechanism for variability of tree growth. Hence, underlying physiological processes that modulate the details of tree growth are needed for dendroclimatology models, both in order to accurately reconstruct palaeoclimate and also to help better interpret the process of growth. With this motivation in mind, dendroclimatologists (Evans et al., 2006; Touchan et al., 2012; Vaganov et al., 2006) suggested a deterministic, process-based model of the relationships between tree-ring growth and their limiting climate factors known as the VS (Vaganov-Shashkin) model. Recently, a significantly simplified version of the full VS model was proposed by Tolwinski-Ward et al. (2013, 2011) called VSLite.

Such mechanistic models aim to capture the mechanisms of key features of the complex system which links climate to tree-ring growth. By directly modelling the way in which raw ring-widths arise, the need for preprocessing is removed. The success of the use of mechanistic models within the dendroclimatology community suggests that their application to dendrochronology could also have merit. Although the resulting model to describe the relationship between the raw ring-widths, the climate and growth processes may be more complex, the eventual process of tree-ring dating would be simpler as it would not be necessary to pre-process the data. Therefore, our next step will be to investigate the use of a mechanistic forward model, such as the VSLite, for tree-ring dating.

We will then need to compare results from the approach proposed in this paper with those from a mechanistic model-based approach and make firm recommendations to the user community about which Bayesian approach to use. In approaching this work, the following issues will need be considered. First, we will need to ensure acceptable efficiency and runtime of code, because our experimental code is written in R (R Core Team, 2015) and is not fast enough to be used for daily practice in dendrochronology laboratories. We might, for example, recode some functions in a lower-level programming language (such as C or C++) in order to speed up the program and make it of greater practical use. Furthermore, it is likely that the MCMC sampling could be improved. For example if the model in Equation 1 is fitted using raw (as opposed to standardised) data then, although they will not sum to one, σ_u^2 and σ_e^2 are likely to be strongly anti-correlated in the posteriors. Given this, a joint proposal, rather than the independent ones suggested in Appendix A, is likely to improve mixing. Second, we will need to develop a fully functional software package in R (or some other suitable environment). A similar package to that introduced by Bunn (2008) for classical dendrochronology could be developed fairly easily from our current R code. We choose not to do this now, however, since it will be most efficient to do so only after we establish whether this or a forward model-based approach is most effective.

Acknowledgements

We are grateful to all those who supported us in completing this work. Particularly Bob Laxton who inspired our early work and Cliff Litton who was a co-supervisor on Jones' PhD on which parts of this paper are based. We would like to give a special thank you to the Ministry of Higher Education and Scientific Research, Kurdistan Regional Government-Iraq and the University of Sheffield (who funded Hassan's contribution to this work) and to the UK Engineering and Physical Sciences Research Council and English Heritage (who funded Jones' contribution to this work via a Doctoral Training Partnership award and a collaborative partnership respectively).

Appendices

A Gibbs Sampling Algorithm

The Gibbs sampling procedure for the Bayesian implementation and matching process used in this paper is as follows:

1. Choose starting values $\beta^{(0)}$, $\mathbf{u}^{(0)}$, $\sigma_u^{2(0)}$, $\sigma_e^{2(0)}$ and $\Delta^{*(0)}$.
2. Sample a value from $p(\beta|\mathbf{y}, \mathbf{u}^{(0)}, \sigma_u^{2(0)}, \sigma_e^{2(0)}, \Delta^{*(0)})$ generating $\beta^{(1)}$.
3. Sample a value from $p(u_t|\mathbf{y}, \beta^{(1)}, \sigma_u^{2(0)}, \sigma_e^{2(0)}, \Delta^{*(0)})$ generating $u_t^{(1)}$.
4. Sample a value from $p(\sigma_u^2|\mathbf{y}, \beta^{(1)}, \mathbf{u}^{(1)}, \sigma_e^{2(0)}, \Delta^{*(0)})$ generating $\sigma_u^{2(1)}$.
5. Sample a value from $p(\sigma_e^2|\mathbf{y}, \beta^{(1)}, \mathbf{u}^{(1)}, \sigma_u^{2(1)}, \Delta^{*(0)})$ generating $\sigma_e^{2(1)}$.

6. Sample a value from $p(\Delta^*|\mathbf{y}, \beta^{(1)}, \mathbf{u}^{(1)}, \sigma_u^{2(1)}, \sigma_e^{2(1)})$ generating $\Delta^{*(1)}$.
7. The starting values are replaced by the generated values and the steps are repeated until the Markov Chain reaches convergence (see main test for a summary of how we established this).

B Pseudo-code for Data Simulation

In order to simulate tree-ring width indices for use in testing our approach for Bayesian matching, the following algorithm was used,

1. Specify l, I, Δ_s and Δ_e for the dated site master chronology.
2. Identify l^* and I^* for the undated site master chronology.
3. Determine a signal-to-noise ratio S and hence σ_u^2 and σ_e^2 for data.
4. Identify q, the minimum overlap between the two sequences.
5. Calculate $l + l^* - 2q$, the length of the climatic signal vector required.
6. Simulate a climatic signal vector from $u_t \sim N(0, \sigma_u^2)$.
7. Simulate a dated site master chronology:
   - Create an $(l \times I)$ matrix, by taking a subset of length (l) from the climatic signal u_t and replicate it (I) times.
   - Simulate an $(l \times I)$ noise matrix from $\epsilon_{ti} \sim N(0, \sigma_e^2)$
   - Sum the climatic signal matrix and noise to give a matrix of ring-width indices $\mathbf{y^D}$, with indices for every sample in every year.
8. Simulate an undated site chronology:
   - Calculate all possible offsets, $l + l^* - 2q + 1$.
   - Choose an offset Δ^* from $t = \Delta_s - l^* + q$ to $\Delta_e - l^* - q$.
   - Create an $(l^* \times I^*)$ matrix, by taking a subset of length (l^*) from $t = \Delta^*, \ldots, \Delta^* + l^* - 1$, and replicate it (I^*) times.
   - Simulate an $(l^* \times I^*)$ noise matrix from $\epsilon_{ti} \sim N(0, \sigma_e^2)$.
   - Sum the climatic signal matrix and noise to give a matrix of undated ring-width indices $\mathbf{y^{UD}}$.
9. Use dated and undated data for the model implementation in matching process.

References

Baillie, M. G. L. (1977). An oak chronology for south central scotland. *Tree-ring Bulletin*, 37:33–44.

Baillie, M. G. L. (1982). *Tree-Ring Dating and Archaeology.* Croom Helm. London.

Baillie, M. G. L. (1995). *A Slice Through Time.* BT. Batsford Ltd, London.

Baillie, M. G. L. and Pilcher, J. R. (1973). A simple crossdating program for tree-ring research. *Tree-ring Bulletin*, 33:7–14.

Bronk-Ramsey, C. (2008). Deposition Models for Chronological Records. *Quaternary Science Reviews*, 27:42–60.

Brown, D. M., Munro, M. A. R., Baillie, M. G. L., and Pilcher, J. R. (1986). Dendrochronology- the absolute irish standard. *Radiocarbon*, 28:279–283.

Buck, C. E., Cavanagh, W. G., and Litton, C. D. (1996). *The Bayesian Approach to Interpreting Archaeological Data.* Wiley, Chichester.

Buck, C. E., Christen, J. A., and James, G. N. (1999). BCal: an on-line Bayesian radiocarbon calibration tool. *Internet Archaeology*, 7.

Bunn, A. G. (2008). A dendrochronology program library in R (dplR). *Dendrochronologia*, 26(2):115 – 124.

Cook, E., Briffa, K., Shiyatov, S., and Mazepa, V. (1990). Tree-ring standardization and growth-trend estimation. In Cook, E. R. and Kairiukstis, L. A., editors, *Methods of Dendrochronology: Applications in the Environmental Sciences*, pages 104–123. Kluwer Academic Publishers, The Netherlands.

Evans, M., Reichert, B. K., Kaplan, A., Anchukaitis, K., Vaganov, E. A., Hughes, M. K., and Cane, M. A. (2006). A forward modeling approach to paleoclimatic interpretation of tree-ring data. *Geophysical Research*, 111:G03008.

Fritts, H. C. (1976). *Tree Rings and Climate.* Academic Press Inc. London Ltd.

Gilks, W. R., Richardson, S., and Spiegelhalter, D. J. (1996). *Markov Chain Monte Carlo in Practice.* Chapman & Hall, London.

Goldstein, H. (2011). *Multilevel Statistical Models.* Wiley, Chichester.

Hillam, J. (2008). Dendrochronology: Guidelines on producing and interpreting dendrochronological dates. English Heritage, London.

Laxton, R. R. and Litton, C. D. (1988). *An East Midlands master tree-ring chronology and its use for dating vernacular buildings.* University of Nottingham.

Litton, C. D. and Zainodin, H. J. (1991). Statistical models of dendrochronology. *Journal of Archaeological Science*, 18:429–440.

Mills, C. (1988). Dendrochronology: the long and the short of it. In Slater, E. A. and Tate, J., editors, *Science and Archaeology*, pages 549–565. BAR Brit. Ser. 196, Oxford.

Orton, C. R. (1983). The use of student's t-test for matching treering patterns. *Bulletin University London Institute of Archaeology*, 20:101–105.

Pilcher, J. R. (1990). Sample preparation, cross-dating, and measurement. In Cook, E. R. and Kairiukstis, L. A., editors, *Methods of Dendrochronology: Applications in the Environmental Sciences*, pages 40–50. Kluwer Academic Publishers, The Netherlands.

R Core Team (2015). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Raftery, A. E. and Lewis, S. L. (1992). How many iterations in the Gibbs sampler? In Berger, J. O., Bernado, J. M., Dawid, A. P., and Smith, A. F. M., editors, *Bayesian Statistics*, pages 763–773. Oxford University Press, New York.

Sander, C. and Levanic, T. (1996). Comparison of t-values calculated in different dendrochronological programmes. *Dendrochronologia*, 14:269–272.

Tolwinski-Ward, S. E., Anchukaitis, K., and Evans, M. (2013). Bayesian parameter estimation and interpretation for an intermediate model of tree-ring width. *Climate of the Past Discussions*, 9:615–645.

Tolwinski-Ward, S. E., Evans, M. N., Hughes, M. K., and Anchukaitis, K. J. (2011). An efficient forward model of the climate controls on interannual variation in tree-ring width. *Climate Dynamics*, 36:2419–2439.

Touchan, R., Shishov, V. V., Meko, D. M., and Grachev, A. (2012). Process-based model sheds light on climate sensitivity of Mediterranean tree-ring width. *Biogeosciences*, 9:965–972.

Vaganov, E. A., Hughes, M. K., Shashkin, A. V., and Grachev, A. (2006). *Growth Dynamics of Conifer Tree Rings, Image of Past and Future Environments*. Springer-Verlag Berlin Heidelberg.

Walker, M. (2005). *Quaternary Dating Methods*. John Wiley and Sons.

Wigley, T. M. L., Jones, P. D., and Briffa, K. R. (1987). Cross-dating methods in dendrochronology. *Journal of Archaeological Science*, 14:51–64.

Zainodin, H. J. (1988). *Statistical models and techniques for dendrochronology*. PhD thesis, University of Nottingham, UK.