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ROBUST BENEFIT FUNCTION TRANSFER: A BAYESIAN MODEL AVERAGING APPROACH

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Robust Benefit Function Transfer: A Bayesian Model Averaging Approach[*]

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Abstract: A Benefit Function Transfer obtains estimates of Willingness-to-Pay (WTP) for the evaluation of a given policy at a site by combining existing information from different study sites. This has the advantage that more efficient estimates are obtained, but it relies on the assumption that the heterogeneity between sites is appropriately captured in the Benefit Transfer model. A more expensive alternative to estimate WTP is to analyse only data from the policy site in question while ignoring information from other sites. We make use of the fact that these two choices can be viewed as a model selection problem and extend the set of models to allow for the hypothesis that the benefit function is only applicable to a subset of sites. We show how Bayesian Model Averaging (BMA) techniques can be used to optimally combine information from all models.

The Bayesian algorithm searches for the set of sites that can form the basis for estimating a Benefit function and reveals whether such information can be transferred to new sites for which only a small dataset is available. We illustrate the method with a sample of 42 forests from U.K. and Ireland. We find that BMA benefit function transfer produces reliable estimates and can increase about 8 times the information content of a small sample when the forest is 'poolable'.

Keywords: Benefit Transfer, Bayesian Model Averaging, Exchangeability, Non-market Valuation, Panel Data

JEL Classification: C11, C33, C81, Q23, Q26

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1 Introduction

The technique of Benefit Function Transfer (BFT) was first proposed by Loomis (1992) as a theoretically sounder method than the transfer of unconditional mean values to obtain estimates of recreational benefits for policy sites. This technique is applicable to natural resource sites for which site-specific data is not available, too costly to obtain or too urgently needed for policy appraisal to allow for a full-blown on-site study. The method BFT obtains estimates of the visitors population's (conditional) mean and median Willingness-To-Pay (WTP) for recreational access to a site (e.g. forest) by combining information from different sites for which on-site data on WTP are available from previous surveys.

In the same issue of Water Resources Research, Smith (1992) revised the practice of benefit transfer and—after assessing the practical importance of this in policy contexts—outlined some research strategies. Smith emphasized how, up until then, legislation had relied

> "on using research as the basis for these evaluations [thereby assuming that] research on valuing non-market resources is systematically "stocking the research shelf" with models that ultimately will respond to future policy needs. In fact, this is not the way research has proceeded" (page 691)

We feel that, nearly fifteen years down the road, this statement is still quite true. The theoretical advantages of BFT as a technique in non-market valuation are well known (cost-effectiveness, increased efficiency of conditional estimates, time-saving procedure etc.), yet studies investigating its robustness have given ambiguous results. For example, negative results on reliability have been reported by a number of authors (e.g. Loomis *et al.* (1995), Downing and Ozuna (1996), Kirchhoff *et al.* (1997), and Feather and Hellerstein (1997)). The econometric techniques used in most of these studies though, require the data analyst to choose *a priori* which sites form the basis for the estimation of the benefit function. Hence, it is possible that a different selection of sites may change the outcome of the reliability test.

Another limitation of the standard approach to reliability testing is that the test will have low power when the sample size is small. As a consequence, one might too often accept the null hypothesis that the benefit transfer estimate is reliable when in fact it is not. Because of this limitation, reliability studies are usually carried out in the context of large samples. Finally, as discussed by Kristofersson and Navrud (2005), some empirical studies might well have had a misplaced emphasis in testing hypotheses.

The main contribution of this study is to broaden the existing approach so as to relax this dependency on large samples and on an arbitrarily chosen set of sites. We propose a Bayesian Model Averaging (BMA) algorithm that systematically searches for the subset of sites in which the assumptions of homogeneity are valid. In addition, in the event of an inconclusive reliability test, perhaps due to a small sample size, the Bayesian estimation averages WTP estimates over all specification hypotheses, providing credible (i.e. confidence) intervals that are robust to the hypotheses in question. Hence, our ultimate goal is not to decide which model is generating the data, but to provide efficient and reliable interval and point estimates of WTP.

We view the decision to use benefit transfer estimates as a model selection problem. The most general model that we consider has different parameters for each site. Estimation of this model is equivalent to analysing data for each site separately. The most restrictive model is the traditional BFT model. In addition, we consider intermediate cases, in which the BFT model only applies to a subset of sites, whereas each of the other sites has different parameters. Hence, our approach combines models that completely rule out any type of exchangeability with models that assume some type of homogeneity in parameters.

In order to evaluate these models we use a Bayesian Model Averaging (BMA) approach. The posterior density in the BMA approach is a weighted average of the posterior densities that arise from each model and the weight is equal to the posterior probability of each model. Therefore, the extent to which our final WTP estimates rely on assumptions of homogeneity is determined by the data, which inform the posterior probability of each specification.

Although there are previous studies that propose procedures to test the reliability of transfer estimates and also Bayesian approaches to benefit transfer (e.g. Atkinson, Crocker and Shogren, 1992, León et al. 2002, León, León and Vázquez-Polo 2007, Moeltner, Boyler and Paterson, 2006), the BMA-BFT approach has a number of advantages over previous approaches. Firstly, the BMA approach does not require the data analyst to decide *a priori* which is the the set of sites where the homogeneity or exchangeability assumptions apply. Note that it is quite likely that assumptions of homogeneity or exchangeability are applicable only to a subset of sites (the 'poolable' or exchangeable set), whereas the benefit for the remainder set of sites (the 'non-poolable' set) may well be generated by completely different processes. The BMA approach evaluates all possible subsets. Secondly, the proposed approach also provides valid credible (i.e. confidence) intervals for WTP when only a small sample is available for the site for which a benefit transfer estimate is being considered. This contrasts with the traditional frequentist approach to testing, which suffers from the problem of 'low statistical power' when the sample size is small. Since there is greater need of benefit transfer estimates when the sample size is small, this is an important advantage.

This approach is of particular interest in contexts in which an agency managing outdoor recreation sites is in the process of 'stocking the research shelf' for future use. We note that the estimation of nonmarket values is periodically carried out by many public land management agencies. For example, the UK Forestry Commission recently assessed nonmarket values (Willis *et al.*, 2003) and the study indicates that they vastly exceed the market value of timber and other tradeable goods. In contexts such as these, once the agency has collected moderately large sample sizes for a number of sites, WTP in other sites could be reliably estimated with smaller sample sizes. As we show in the empirical application, a small sample size of 50 observations might yield as much information as 450 if information from previous studies is taken into account. Thus, in practice our approach is likely to reduce substantially the costs of reliably estimating WTP at new sites.

We illustrate the BMA methodology with dichotomous-choice contingent valuation data collected with the same survey instrument in spring-summer 1992 at 42 natural parks from U.K and Ireland. The rest of the paper is organized as follows. In the following section we describe the method. Section 3 illustrates the method with both real and artificial data. The last section concludes.

2 Econometric Methodology

2.1 Models for different degrees of transferability

2.1.1 Complete Transferability

Let us assume that there are $j = 1, 2, \dots, J$ sites, each site j contributing with N_j respondents to the total sample. Our Benefit Transfer setup allows N_j to be small for one or several sites. It is chiefly for these sites that the BT exercise is carried out, thereby using information from other sites and possibly improving the accuracy of WTP estimates. However, in our setup it is not necessary to provide different notation for sites with small samples, and therefore all sites enter in the model with the same notation, regardless of their sample size. Each site j is also described on the basis of a site-specific vector $\mathbf{q}_j$ of site attributes relevant for recreational purposes, and hence expected to explain the variation of benefits from forest access by visitors. Information from other sites is most useful when all the relevant differences among the sites are adequately captured in the vector of site characteristics $\mathbf{q}_j$. In our setup, the assumption that information from other sites is transferable simply means that we can use the following benefit function (Scarpa *et al.* 2007):

$$\ln(WTP_{ij}) = \alpha + \mathbf{q}_j\beta + \mathbf{s}_{ij}\gamma + \lambda^{-1}\varepsilon_{ij} \qquad i = 1, ..., N_j \qquad j = 1, ..., J \quad (1)$$

where $\varepsilon_{ij} \sim \mathcal{N}(0, 1)$, i denotes respondents and j denotes sites, $\mathbf{q}_j$ is a horizontal vector of site attributes describing the j^{th} site, $\mathbf{s}_{ij}$ is a horizontal vector of socioeconomic characteristics of the i-th respondent interviewed in site j, α is an unknown intercept and γ, β are vectors of unknown parameters. Parameter λ controls the variance of $\ln(WTP)$ and also influences the expected value of WTP, but not its median or any quantile. Our analysis assumes dichotomous choice data (single or double-bounded) or open-ended data.[1]

Equation (1) is the most restrictive specification that we consider. However, it has the advantage

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[1] Single-bounded dichotomous data means that each respondent i answers to a dichotomous choice question as to whether or not she would be willing to pay a proposed bid t_{ij}. Data is double-bounded when each respondent is presented with a second bid. Data is open-ended when the exact value of $\ln(WTP_{ij})$ is observed.

that if the underlying assumptions are correct, it results in the most accurate estimates of mean WTP.

2.1.2 No transferability.

There are always plausible explanations as to why any particular assumption of exchangeability could be wrong. In our setup it is possible that the *WTP* for each site depends on site attributes missing from the vector of descriptors $\mathbf{q}_j$ available to the researchers. In addition, the parameters in γ associated with respondents' characteristics might be different for each site. Under these two assumptions, the BFT model (1) is incorrectly specified and might lead to seriously biased *WTP* estimates. These considerations lead us to consider this alternative model:

$$\ln(WTP_{ij}) = \alpha_j + \mathbf{s}_{ij}\gamma_j + \lambda_j^{-1}\varepsilon_{ij} \qquad i = 1, ..., N_j \qquad j = 1, ..., J \tag{2}$$

Note that all parameters are site-specific and therefore equation (2) is the least restrictive case that we consider. It results in a total lack of transferability or in other words, it rules out any assumption of exchangeability. [2] More precisely, information on sites $(1, ..., h-1, h+1, ..., J)$ is irrelevant to learn about WTP in site h, for every h. However, this model results in less precise estimates of mean *WTP* for each site.

2.1.3 Partial Transferability

Equation (1) assumed that the BT function was applicable to all sites, whereas equation (2) assumed that it was applicable to none. We now consider the intermediate and most likely case in which the BT function (1) is applicable only to a subset of sites. Thus, benefit transfer is possible for a subset of sites but not for others. The BT function selected by the analyst might be not applicable to a given site j if *WTP* to access this site depends on site characteristics that are not contained in $\mathbf{q}_j$, or if the response of the log-WTP function to the individual characteristics (the

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[2] For definitions of different types of exchangeability see Bernardo and Smith, 1994, pp. 167-171

value of γ_j) is in that site different from that in the BTF. Thus, to estimate mean WTP in such a site one cannot rely on a transfer, but needs to use only data collected at that site (equation (2)).

For convenience we define the following two groups of sites. Group NP (where NP stands for 'not pooling' information) consists of sites for which information from other sites is not transferable. That is, the benefit function (1) is not applicable to sites in NP. Let the group with the rest of sites be denoted by P (where P stands for 'pooling' information) and assume that the benefit function (1) is valid for all sites in P. Therefore, in contrast with NP sites, the WTP for each site in P can be validly estimated by the specification chosen by the researcher and described in (1) using the data for the sites in P and ignoring those in the NP set. Hence, this partial transferability (PT) model can be described with the following two equations:

$$\begin{aligned} \ln(WTP_{ij}) &= \alpha + \mathbf{q}_j\beta + \mathbf{s}_{ij}\gamma + \lambda^{-1}\varepsilon_{ij} \qquad j \in P \\ \ln(WTP_{ij}) &= \alpha_j + \mathbf{s}_{ij}\gamma_j + \lambda_j^{-1}\varepsilon_{ij} \qquad j \in NP \end{aligned} \tag{3}$$

We would argue that for each WTP data collection across recreational sites this mixture of specifications represents the most likely reality faced by analysts. By explicitly allowing for such mixture our proposed approach is improving the state of practice.

2.2 Benefit Transfer, Bayesian Model Averaging and Random Effects Models

Note that while each of the equations (1) and (2) corresponds to just one model, many models are represented by equation (3), since there are many possible partitions (P, NP). In this paper we consider only partitions in which the regression matrix has full rank. Note that this requires the number of sites in P to be greater than the number of attributes in $\mathbf{q}$.

The extent to which information is transferable boils down to deciding which of the equations, (1), (2) or (3) is more appropriate given the data. Therefore, deciding whether information between sites is transferable can be expressed as a problem of uncertainty over model specifications for which Bayesian techniques offer a compelling treatment. For example, BMA point estimates are optimal in the sense that they minimise the expected value of a loss function, when the expectation is taken with respect to the prior. In particular, the posterior mean minimises the expected square error, while the posterior median minimises expected absolute error. In addition, credible intervals have appropriate Bayesian coverage.[3] For a review of the statistical properties of BMA see Raftery and Zheng (2003), who also show, in the context of a linear model, that BMA is quite robust to mis-specification of the prior.

Let θ_h be the parameter of interest, which in our context is usually mean or median *WTP* for a site h. For instance, median *WTP* for site h evaluated at $\mathrm{s}_{ih} = \mathrm{s}^*$ is given by:

$$\begin{aligned} \widehat{W}_{h,\mathbf{s}_*} &= \exp\left(\alpha + \mathbf{q}_h\beta + \mathbf{s}^*\gamma\right) && \text{if } h \in P \\ \widehat{W}_{h,\mathbf{s}_*} &= \exp\left(\alpha_h + \mathbf{s}^*\gamma_h\right) && \text{if } h \in NP \end{aligned} \tag{4}$$

and similar expressions exist for mean *WTP*. Let each model be represented by m_j, $j = 1, ..., M$, and let y denote the observed data. The posterior density of θ_h is a mixture of the posterior densities under each specification:

$$\pi(\theta_h \mid y) = \sum_{j=1}^{M} \pi(m_j \mid y)\pi(\theta_h \mid y, m_j) \tag{5}$$

where $\pi\left(\theta_h \mid y, m_j\right)$ is the posterior density of θ_h conditional on model m_j and $\pi\left(m_j \mid y\right)$ is the posterior probability of model m_j (Koop 2003, p.p. 23-26).

In our context, given a particular site h, it is illustrative to divide the set of models into two groups: M_h^P are those models in which $h \in P$ and M_h^{NP} are those in which $h \in NP$. Note that models in M_h^{NP} analyse data for site h separately from all the other sites. In other words,

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[3] A credible interval is the Bayesian analogue to the classical confidence interval (Koop 2003, p. 44). Bayesian coverage, as in the frequentist case, can be defined in terms of repeated sampling (e.g. Raftery and Zheng, 2003). The difference is that in the frequentist case all samples come from the same population (i.e. all samples are generated using the same fixed value for the parameters), whereas in the Bayesian case each sample comes from a different population (i.e. the vector of parameter values for each sample is a random draw from the prior). When only one model is considered, there are many cases in which Bayesian and classical intervals are identical (e.g. in the linear regression model with a flat prior).

these are models that yield the same estimates for θ_h that would be obtained by analysing only the data for site h while ignoring data for all the other sites. In this sense, therefore, these are models in which no benefit transfer takes place for site h. Note that all the models in M_h^{NP} yield the same posterior for θ_h. In contrast, models in M_h^P assume that the WTP function in site h has parameters in common with other sites. Given this division, we can see the posterior density of θ_h as a mixture between the posterior density that arises when $m_h \in M_h^{NP}$ and the posterior densities corresponding to $m_h \in M_h^P$. Thus, equation (5) can be rewritten as:

$$\pi\left(\theta_h \mid y\right) = \pi\left(h \in P \mid y\right) \pi\left(\theta_h \mid y, h \in P\right) + \left(1 - \pi\left(h \in P \mid y\right)\right) \pi\left(\theta_h \mid y, h \in NP\right) \tag{6}$$

where:

$$\pi\left(h \in P \mid y\right) = \sum_{j \mid m_j \in M_h^P} \pi\left(m_j \mid y\right) \tag{7}$$

$$\pi\left(\theta_h \mid y, h \in P\right) = \frac{1}{\pi\left(h \in P \mid y\right)} \sum_{j \mid m_j \in M_h^P} \pi\left(m_j \mid y\right) \pi\left(\theta_h \mid y, m_j\right) \tag{8}$$

and $\pi\left(\theta_h \mid y, h \in NP\right)$ is the posterior of θ_h that arises when information for site h is analysed independently of other sites. Note that the probability $\pi\left(h \in P \mid y\right)$ determines the extent to which models in M_h^P affect the posterior of θ_h. In other words, it determines the extent to which WTP estimates for site h will rely on benefit transfer functions, as opposed to relying only on site-specific data. As mentioned above, this probability has good statistical properties: it guarantees that point estimates are optimal and that credible (i.e. confidence) intervals have appropriate coverage (e.g. Raftery and Zheng, 2003).

An analogy arises with the random effects model, which has been proposed for benefit transfer in previous literature (e.g. Atkinson *et al.* 1992 and Moeltner *et al.* 2006). As noted by Atkinson *et al.* (1992), the posterior mean for θ_h in the random effects model is a weighted average between the estimate that uses only data for site h (the NT estimate) and the pooled estimate that results from assuming that all sites share a common WTP function (the BT estimate). However, a random effects (RE) model is much more restrictive than BMA, since it assumes that departures from the common WTP function follow a parametric distribution, usually normal. Furthermore, a RE model, unlike the BMA approach, assumes that all sites are exchangeable. To illustrate this, recall that in a RE model the weight given to the BT estimate is $\sigma_{\epsilon}^2/(\sigma_{\epsilon}^2 + N_h\sigma_{\alpha}^2)$, where σ_{α}^2 is the variance of the random effects, σ_{ϵ}^2 the variance of the other error term and N_h is the sample size in site h. Note that the weight of the BT estimate is the same for each site (except for the sample size effect), because all sites are assumed to be exchangeable. In contrast, the weight of BT estimates in the BMA approach ($\pi\left(h \in P \mid y\right)$) is site specific. This greater flexibility results from explicitly allowing for the possibility that each site belongs to NP and is thus not 'poolable'. That is, our analysis does not rule out that information for sites $(1, ..., h-1, h+1, .., J)$ could be irrelevant to learn about WTP at site h.

2.3 Prior Density

2.3.1 Prior for each model

In order to determine the prior probability of each model, let us define δ_j as the prior probability that site j belongs to P. Note that each model is associated with a partition (P, NP): the BFT model (1) arises when NP is an empty set, while the NT model (2) arises when P is an empty set. Let I_j be an indicator function that takes value 1 if $j \in P$ and zero otherwise. The prior probability of a model M_h associated with $(I_1, ..., I_J)$ is:

$$p(M_h) = \prod_{j=1}^{J} \left(\delta_j\right)^{I_j} \left(1-\delta_j\right)^{1-I_j} \tag{9}$$

2.3.2 Prior for Parameters

In order to reduce the number of parameters that need to be elicited *a priori*, we specify a g-prior (Zellner, 1983). Let us reparameterize the model as:

$$\begin{aligned} \ln(WTP_{ij}) &= \underline{\alpha}_P + (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)\gamma + (\mathbf{q}_j - \bar{\mathbf{q}}_P)\beta + \lambda^{-1}\varepsilon_{ij} \quad \text{if} j \in P & (10) \\ \ln(WTP_{ij}) &= \underline{\alpha}_j + (\mathbf{s}_{ij} - \bar{\mathbf{s}}_j)\gamma_j + \lambda_j^{-1}\varepsilon_{ij} \quad \text{if} j \in NP & (11) \end{aligned}$$

where $\bar{\mathbf{q}}_P$ and $\bar{\mathbf{s}}_P$ are the sample means of $\mathbf{q}_{ij}$ and $\mathbf{s}_{ij}$ in sites that belong to P, and $\bar{\mathbf{s}}_j$ is the sample mean of $\mathbf{s}_{ij}$ in site j. We assume that, for $j \in NP$, the vector $(\underline{\alpha}_j, \gamma_j, \lambda_j)$ is independent of $(\underline{\alpha}_P, \gamma, \beta, \lambda)$. This implies that information for sites in P is analysed independently of information for sites in NP. Similarly, for $(j, l) \in NP$, the prior assumes that the vector $(\underline{\alpha}_j, \gamma_j, \lambda_j)$ is independent of $(\underline{\alpha}_l, \gamma_l, \lambda_l)$. The prior for $(\underline{\alpha}_j, \gamma_j)$ conditional on λ_j is a normal with mean $(\bar{t}_j, \mathbf{0})$. A zero mean for γ_j implies that γ_j has the same probability of being positive as being negative. The variance-covariance matrix is specified as in a g-prior:

$$g_j\lambda_j^{-2}\begin{pmatrix} N_j & 0 \\ 0 & \sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_j)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_j) \end{pmatrix}^{-1}$$

Note that this is proportional to the inverse of the cross-products of the matrix of regressors. The prior for λ_j is $N(0, K_j g_j)$, which implies that the prior for λ_j^{-2} is an inverted Gamma-2 distribution with one degree of freedom (Bauwens, Lubrano and Richard (1999), Appendix A).

Similarly, the prior for $(\underline{\alpha}_P, \gamma, \beta)$ conditional on λ is a normal with mean $(\bar{t}_P, 0, 0)$ and variance-covariance matrix:

$$g_P\lambda^{-2}\begin{pmatrix} \sum_{j\in P} N_j & 0 & 0 \\ 0 & \sum_{j\in P}\sum_i(\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{q}_j - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i(\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \\ 0 & \sum_{j\in P}\sum_i(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{q}_{ij} - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \end{pmatrix}^{-1}$$

and the prior for λ is $N(0, K_P g_P)$.

2.3.3 Prior Elicitation

With this prior specification the parameters that have to be elicited *a priori* are: $(\bar{t}_j, g_j, K_j)$ for $j \in NP$, and $(\bar{t}_P, g_P, K_P)$. In our empirical application we choose the value of these parameters to approximate the prior information that the bid design reveals. For this purpose note that $\underline{\alpha}_j$ is the log of median *WTP* for site j evaluated at $\mathrm{s}_{ij} = \bar{\mathrm{s}}_j$. We choose its prior mean $(\bar{t}_j)$ to be the mid-point between the lowest and the highest log-bid in site j. The value of $\bar{t}_P$ is chosen in the same way, but considering the minimum and the maximum of the log bids offered in all the sites in P.

In order to choose a value for K_j, we note that this parameter determines the prior probability that median *WTP* for site j is between the smallest and the largest bid. To see why, note that *a priori* $(\underline{\alpha}_j - \bar{t}_j)(g_j/N_j)^{-1/2}|\lambda \sim N(0, \lambda^{-2})$, and recall that $\lambda_j \sim N(0, K_j g_j)$. Thus, if we marginalize over λ_j we obtain that $(\underline{\alpha}_j - \bar{t}_j)(K_j N_j)^{1/2}$ follows a t_1 (i.e. Student t distribution with one degree of freedom). This result can be used to select a value of K_j such that median *WTP* (i.e. $\exp(\underline{\alpha}_j)$) lies in a given interval with high probability.

For example, if we choose K_j so that $Pr(t_j^l \leq \underline{\alpha}_j \leq t_j^h) = p$, where t_j^l is the log of the lowest bid and t_j^h is the log of the highest bid, then the value of K_j is given by the following expression:

$$K_j = \frac{c_p^2}{N_j(t_j^h - \bar{t}_j)^2} \tag{12}$$

where c_p is a value from the table of the Student t distribution verifying that $Pr(-c_p \leq t_1 \leq c_p) = p$ and where we have used that $\bar{t}_j = (t_j^h - t_j^l)/2$. Note that (12) does not depend on the value of g_j. Finally recall that a student t with one degree of freedom has very fat tails. Thus, we still allow, although with a small prior probability, for $\exp(\underline{\alpha}_j)$ to take values that are far outside the interval (t_j^l, t_j^h).

Similarly, we choose the value of K_P to ensure that the prior probability that $\exp(\underline{\alpha}_P)$ lies between the lowest and the highest bid is high. In order to choose a value for g_j, note that g_j controls the prior variance for all parameters. While it might be tempting to choose a large value for g_j, as noted in Dasgupta *et al.* (2006), in the context of dichotomous choice data a sufficiently large prior variance results in a very informative prior density. To see this, let us define $\overline{\pi}$ as the probability that a respondent with average characteristics ($\mathbf{s}_{ij} = \bar{\mathbf{s}}_j$) accepts to pay the amount $\exp(\bar{t}_j)$. This probability is given by $\overline{\pi} = \Phi\left(z\right)$, where Φ is the cdf of a standard normal, and z is defined as:

$$z = \frac{(\underline{\alpha}_j - \bar{t}_j)}{|\lambda_j^{-1}|}$$

Note that our prior implies that $z \sim N(0, g_j N_j^{-1})$. It is easy to see that a sufficiently large value of g_j implies a very informative prior for $\overline{\pi}$. In particular, it implies that *a priori* $\overline{\pi}$ can only be one or zero (almost certainly). Dasgupta *et al.* (2006) note that choosing $g_j = N_j$ implies that the prior for $\overline{\pi}$ is a uniform in the interval (0,1). In addition, they show that choosing $g_j = 2.46N_j$ results in a prior density for $\overline{\pi}$ that approximates well a $Beta(0.5, 0.5)$, which is a density that has been recommended in the context of estimating a probability with a binomial likelihood (e.g. Bernardo and Smith, 1994, p. 315). Therefore, in a sensitivity analysis it seems reasonable to try values for g_j that are not too far from N_j or $(2.46N_j)$. For instance, one could try values that lie in the interval $[N_j, 5N_j]$. In our empirical application we choose $g_j = N_j$ and following a similar reasoning, we fix $g_P = \sum_{j \in P} N_j$. This choice of g was also recommended by Fernández, Ley and Steel (2004) in the context of a linear model.

2.4 Computation

In order to analyze the characteristics of the posterior distribution we use the algorithm of Holmes and Held (2006). The algorithm provides an approximate random sample from the posterior distribution of (M,ψ_M), where M represents a model and ψ_M represents the parameters of model M. For example, if M is the BFT model (1), then $\psi_M = (\underline{\alpha}_P, \gamma, \beta, \lambda)$, whereas if M is the NT model (2) then $\psi_M = (\underline{\alpha}_1, \gamma_1, ..., \underline{\alpha}_J, \gamma_J)$. At each iteration the Markov Chain generates a value for M and a value for ψ_M. The Markov Chain is started at an arbitrary value and it is run for a large number of iterations. After discarding the initial iterations, the remaining values can be considered as a sample from the posterior distribution of (M, ψ_M). The posterior probability of a model m_j can be calculated as the proportion of times that the chain visited model m_j. The median (i.e. point estimate) and percentiles (i.e. credible interval) of the posterior distribution of parameters (or transformation of parameters) can also be approximated with their sample analogues. The main parameters of interest are median WTP (as defined in (4)) and mean WTP for each site. Note that by transforming ψ_M each iteration provides a value for these two parameters, and these transformed values can be used to approximate point estimates and credible intervals. The details of the algorithm are described in appendix A.

3 Robust Benefit Transfer in Irish and Scottish Parks

We illustrate the BMA methodology using data from discrete-choice contingent valuation surveys collected for a group of 42 forest parks: 14 from Northern Ireland (U.K.), 13 from Ireland, and 15 from Scotland (U.K.) (Ni Dhubhain *et al.* 1994). Reliability of benefit function transfers across the 28 Irish forest parks was first analysed in Scarpa (1999), and extended in Scarpa *et al.* (2007) within a classic BT framework. The surveys were all conducted face-to-face, had the same format and were collected within a time interval of 3-4 months in spring-summer 1992, thereby avoiding previously suggested causes for observed non-transferability results, such as temporal instability of preferences (Downing and Ozuna 1996), or diversity of survey formats.

Preliminary trials suggested that the use of 64,000 iterations after discarding the initial 1000 iterations would be adequate for our purposes. To ease comparison with previous work we include just a measure of household income in s_{ij}, and 7 variables for park attributes $\mathbf{q}_j$. These are the same variables used in Scarpa *et al.* (2007) and definitions can be found in Table 1. Table 2 shows the names and some characteristics of the 42 forests. We employ single-bounded data, although, as explained in appendix A, the same approach can be adapted to deal with double-bounded data. We use the prior described in Section 2.3.3 with p =0.90. Recall that p is the prior probability that median *WTP* evaluated at the sample mean is between the lowest and the highest log-bid. With respect to the prior for models, we choose δ_j =0.5, for $j = 1, ..., J$. As a first exploratory analysis, we obtain the BMA posterior density of median *WTP* using full sample sizes from data of the 42 forests. Median *WTP* is evaluated at the median income of each forest. We describe the posterior density with the 2.5%, 50% and 97.5% percentiles. The 2.5% and 97.5% percentiles are the bounds of a 95% credible interval (i.e. the Bayesian counterpart of the 95% confidence interval). The 50% percentile is the posterior median and plays the role of a point estimate. We also report the posterior probability that a forest belongs to NP and we label it $\Pr$. We compare the BMA estimates with the estimates from the NT model (eq. 2) and the standard BFT model (1). Table 3 shows the result for 4 selected forests (Table (8) in on-line appendix B shows the results for all the forests). These 4 are the forests with largest sample sizes for which $\Pr$ is close to one or zero. For forests 30 and 33 $\Pr$ equals one, which implies that BMA estimates are identical to NT estimates (any difference is due to simulation error). For forests 2 and 13 $\Pr$ is close to zero, and we observe that in this case BMA credible intervals still overlap with NT credible intervals, but are narrower. Thus, BMA benefit transfer can bring efficiency gains even for samples of moderate and large sizes. Note that BFT credible intervals are the narrowest. They overlap with NT intervals in forests 2 and 13, but are very different in forests 30 and 33. Given the large sample sizes (413 and 454 observations for forests 30 and 33) this difference casts doubts on the BFT estimates. The next two subsections provide examples in which sample sizes for some forests are small. Section 3.1 uses simulated data, in which case the exact true value of *WTP* is known, and Section 3.2 uses actual data.

3.1 Simulated Data

We simulate data for the 42 forests. We used the actual value of the regressors and simulated values for the dependent variable. With the exception of forests 2, 13, 30 and 33, the sample size for each forest is the same as shown in Table 2. We simulate 25 observations for each of the forests 2, 13, 30 and 33 (5 observations for each of the 5 bids). We set $NP = (16, 22, 30, 33)$. The true value of the parameters was obtained randomly as one draw from the prior. Table 6 shows the estimation results and the true value of median *WTP* for the selected 4 forests (Table 11 in on-line appendix B shows results for all forests). Table 6 shows that none of the BFT credible intervals contain the true value of median *WTP* and that they are specially misleading for forests 30 and 33. Note that the BFT model (1) makes the wrong assumption that all forests belong to P. This causes a substantial bias in the estimates of all forests, even of those that actually belong to P. In contrast, BMA credible intervals do contain the true value of median *WTP* in all forests, even for those that actually belong to NP. For forests 2 and 13 BMA credible intervals are tight, even though there are only 25 observations. The widths of credible intervals are 5 and 12 pence, respectively. Table 11 in the on-line appendix shows that NT estimates often do not achieve this level of accuracy even with full-blown on-site samples. Intervals for forests 2 and 13 are narrow because $\Pr$ takes values 0.01 and 0.06, respectively, and therefore benefit transfer takes place. In contrast, $\Pr$ takes values 0.54 and 0.21 for forests 30 and 33, which do actually belong to NP. Because of the small sample sizes, these probabilities are not conclusive. However, they are sufficiently big to give NT estimates enough weight so as to make credible intervals contain the true value of *WTP*. Figure 3 shows that the posterior density of median *WTP* for forests 30 is bimodal. One mode corresponds to the NT estimate and the other one corresponds to a benefit transfer estimate (Figure 4 in the on-line appendix B shows the same for forest 33). Table 7 shows what happens if we increase the sample size from 25 to 50. The pattern is similar, except that now $\Pr$ takes higher values for forests 30 and 33 (0.97 and 0.42, respectively), as one would expect with a larger sample size.

3.2 Real Data

From the real data we randomly select 25 observations for forests 2, 13, 30 and 33 (5 for each of the 5 bids). We use all available observations for the other forests. In this case we do not know the true value of median *WTP*. However, we expect the true value to be within the bounds of the NT 95% credible intervals based on full-samples and shown in Table 3. Table 4 shows that BFT estimates for forests 2 and 13 are consistent with the NT estimates in Table 3 and therefore seem to be reliable. However, BFT estimates for forests 30 and 33 are clearly misleading, since they are very different from the NT estimates in Table 3. In contrast, BMA estimates are consistent with the estimated true values in all cases, since credible intervals substantially overlap with the NT estimates in Table 3. There are efficiency gains in forests 2 and 13: for the same number of observations credible intervals are narrower than their NT counterparts. However, unlike in the simulated data case, 25 observations are not enough to get the same information as in a full-blown on-site study. The probabilities that forests 30 and 33 belong to NP are high: 93% and 86%. As in the simulated data case, figures 2 (in on-line appendix B) and 1 show that the posterior densities for these two forests are bimodal.

Let us examine what happens if we had samples of 50 observations in forests 2, 13, 30 and 33 (10 for each of the 5 bids). We randomly select another 25 observations from the real data and put them together with the previous 25. Table 5 shows the results for forests 2, 13, 30 and 33 (Table 10 in the on-line appendix B shows the results for all forests). With respect to BFT estimates, they continue to appear reliable for forests 2 and 13, but they are clearly very misleading for forests 30 and 33. In contrast, BMA estimates seem to be reliable since credible intervals overlap substantially with the full-sample-NT credible intervals shown in Table 3. Note that $\Pr$ takes now more conclusive values: almost zero for forests 2 and 13 and almost one for forests 30 and 33. Therefore, BMA estimates for forests 30 and 33 are virtually undistinguishable from NT estimates that use the same observations. Hence, there is no benefit transfer and no efficiency gains for forests 30 and 33. In contrast, BMA credible intervals for forests 2 and 13 are much narrower than their NT counterparts. The widths of the BMA credible intervals for forests 30 and 33 are 33 and 31 pence, respectively. We note that these are not much different from those obtained when all observations are used (413 and 454): 29 and 33 pence, respectively (Table 3). Thus, with BMA a sample of 50 observations can have a similar information content as a sample of 413 (or 454) observations.

4 Conclusions

Our empirical and simulated results illustrate that a traditional BFT approach can result in seriously misleading inferences when the homogeneity assumptions are wrong. In contrast, the BMA BFT approach increased the information content of a sample in a reliable manner. Our case study with Scottish and Irish data showed that a sample of 50 observations can yield a similar information content as a sample of 454 observations.

The main reason for the greater reliability of this method is that it relaxes the assumption of homogeneity (i.e. exchangeability) that have underlied previous benefit transfer analyses. More precisely, the BMA approach does not rule out that information on sites $(1, ..., h-1, h+1, ..., J)$ might be irrelevant to learn about site h, for every h. This is important because there are always plausible explanations as to why any assumption of exchangeability could be wrong and thus lead to very misleading estimates. The Bayesian algorithm effectively searches for the subset of sites that can form the basis of a benefit function regression. The BMA approach detects which sites are amenable for benefit transfer and which ones are not, even if the sample sizes for these sites are small. If the sample size for a particular site is small and the probability of the site belonging to the set of transferable sites is not conclusive, the BMA approach combines a benefit transfer estimate with the site specific estimate to provide reliable credible intervals. The BMA approach not only informs the analyst about the value of *WTP* from the data, but it also provides information on whether a site can be pooled with others in a single assumed specification of the benefit function.

The decision of whether or not to use information on other sites can be viewed as a model selection problem, for which Bayesian techniques offer a compelling treatment. The traditional BFT approach relies on assumptions that might be unverified for all available sites. By simultaneously considering models in which these assumptions are relaxed, one introduces prior uncertainty with regard to crucial specification assumptions. Using a BMA approach, one will then get estimates of *WTP* and credible intervals that are robust because they allow for the possibility that the homogeneity assumptions are incorrect.

To illustrate how this approach might be used in practice, consider an agency that has already collected moderate or large sample sizes for J sites, and is considering evaluating WTP at a new site $(J+1)$, for which it has no data. The agency would first collect a small sample at the new site, of say 50 observations, and carry out the BMA BFT analysis. As suggested by our empirical results, it is possible that such small sample will be sufficient to estimate WTP accurately, thereby allowing savings on further data collection. If instead the posterior credible interval turns out to be too wide, which is likely to happen if the forest is 'non poolable', then the agency would be advised to collect a larger sample at site $(J+1)$.

For simplicity we have assumed *WTP* to be log-normally distributed. This not necessary and future research could use existing flexible Bayesian approaches (e.g. Fernández et al 2004, Araña and León, 2005). While our analysis assumes dichotomous choice (single or double-bounded) or open-ended contingent valuation data, future research could generalize this to the case in which contingent valuation data is available for some sites and travel cost data for others. Another interesting, although challenging, avenue for future work is to study the implications of BMA BFT on the optimal sample size (e.g. Berger, 1985, Section 7.2).

TOTAR	Total Area, hundred of hectares
CONIFS	Conifers as a proportion of total number of trees
BDLEAF	Broadleaves as a proportion of total number of trees
LARCH	Larch as a proportion of total number of trees
PRE1940	Trees before 1940, as a proportion of the total
NAT	Dummy variable: 1 if it is a natural reserve
CONGESTION	Estimated number of visits divided by 100 over the number of cars that can be fitted in the car-park of the forest site.
INC	Indicator of household income bracket, from 1 to 8. 1 = under £3,999; 2 = £4000−£7,999; 3 = £8,000−£11,999; 4 = £12,000−15,999; 5 =16,000−19,999; 6= 20,000−29,999; 7 = £30,000−£39,999; 8 = higher than £40,000

Table 1: Definition of individual and site attributes

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Forest	Sample Size	TOTAR	CONIFS	BDLEAF	LARCH	NATR
1 Tollymore	392	629.2	57	5	21	0
2 Castlewellan	443	641.2	44	7	17	0
3 Hillsborough	355	198.8	57	12	17	0
4 Belvoir	310	95	24	6	27	1
5 Gosford	399	251.2	40	21	0	0
6 Drum Manor	265	94.2	20	9	0	0
7 Gortin glen	303	1459.8	70	2	3	0
8 Glenariff	424	1181.8	67	1	7	1
9 Ballypatrick	80	1461.2	81	0	3	0
10 Somerset	116	138	59	14	6	0
11 Florencecourt	105	1393	32	5	0	1
12 Lough Navar	217	2608.8	68	1	1	1
13 Castlearchdale	407	499.4	54	3	4	1
14 Crawfordsburn	346	80	5	40	1	0
15 Loch Trool	200	9399	37	1	8	0
16 Culzean	379	234	12	35	0	1
17 Calderglen	136	180	10	20	1	0
18 Vogrie	323	105	12	40	1	0
19 Almondell	181	35.6	23	41	9	1
20 Beecraigs	221	882.2	62	2	8	0
21 Kinnoul Hill	101	250	46	20	4	0
22 Tentsmuir	381	1480	93	3	1	1
23 Hermitage	77	14	66	17	5	0
24 Glenmore	224	2677	61	0	1	1
25 Strathyre	165	2772	53	3	6	0
26 Queen Eliz/David Marshall	280	20000	69	6	4	0
27 Rowardeenan	317	925	57	18	16	1
28 Aden	396	110	20	26	1	0
29 Killiecrankie	165	22	0	93	0	0
30 Lough Key	413	340	22	78	0	0
31 Hazelwood	274	70	7	93	0	0
32 Dun a Dee	171	240	51	48	1	0
33 John F Kennedy	454	252	35	60	5	0
34 Dun a Ree	183	229	64	36	0	0
35 Currachase	405	200	20	68	12	0
36 Cratloe	109	65	56	3	41	0
37 Douneraile	244	160	4	96	0	0
38 Farran	373	75	83	7	10	0
39 Guaghan Barra	98	140	46	12	42	0
40 Avondale	281	286	30	10	4	1
41 Killykeen	169	240	90	8	2	0
42 Glendalough	343	326	42	7	27	1

Table 2: Name and some characteristics of forests. The sample size is after eliminating missings and protests.

	BMA BFT					NT				BFT			
Forest	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
2	1.46	1.59	1.70	0.24	0.03	1.51	1.65	1.80	0.29	1.56	1.63	1.69	0.13
13	1.54	1.68	1.81	0.27	0.02	1.58	1.73	1.90	0.33	1.64	1.71	1.78	0.13
30	1.80	1.94	2.08	0.28	1.00	1.81	1.94	2.08	0.28	1.56	1.65	1.75	0.20
33	2.26	2.46	2.70	0.44	1.00	2.26	2.46	2.70	0.44	1.77	1.86	1.95	0.18

Table 3: Real Data with full samples. ”Est. Int.” gives the 2.5%, 50%, and 97.5% percentiles of the posterior distribution of median WTP. ”R” is the difference between the 97.5% and the 2.5% percentile. ”Pr” is the posterior probability that the forest belongs to NP

	BMA BFT					NT				BFT			
Forest	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
2	1.21	1.55	1.69	0.48	0.10	0.98	1.33	1.75	0.77	1.53	1.60	1.68	0.15
13	1.35	1.49	1.77	0.40	0.02	0.95	1.35	1.82	0.86	1.65	1.72	1.80	0.15
30	1.29	1.81	2.36	1.10	0.93	1.43	1.84	2.36	0.92	1.39	1.50	1.61	0.22
33	1.56	2.11	2.76	1.20	0.86	1.72	2.14	2.75	1.03	1.58	1.68	1.77	0.19

Table 4: Real Data with 25 observations for forests 2, 13, 30 and 33. Full samples were used for other forests. Labels are defined as in Table 3

	BMA BFT					NT				BFT			
Forest	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
2	1.30	1.47	1.63	0.33	0.02	1.19	1.50	1.90	0.70	1.53	1.60	1.68	0.15
13	1.57	1.72	1.88	0.31	0.00	1.36	1.75	2.30	0.94	1.65	1.73	1.81	0.15
30	1.61	1.94	2.31	0.69	0.96	1.61	1.93	2.30	0.69	1.39	1.50	1.61	0.22
33	1.95	2.26	2.66	0.71	1.00	1.94	2.25	2.66	0.71	1.60	1.69	1.78	0.19

Table 5: Real Data with 50 observations for forests 2, 13, 30 and 33. Full samples were used for other forests. Labels are defined as in Table 3

			BMA BFT				NT			BFT		
Forest	True	What if	Est. Int.			Pr	Est. Int.			Est. Int.		
2	0.79		0.76	0.79	0.81	0.01	0.52	0.83	1.12	0.66	0.69	0.72
13	1.06		1.02	1.06	1.24	0.06	0.97	1.23	1.54	0.94	0.97	1.00
30	1.79	2.50	1.47	2.19	2.59	0.54	1.42	1.81	2.39	2.77	2.94	3.13
33	1.18	0.88	0.85	0.89	1.25	0.21	0.90	1.13	1.33	0.73	0.77	0.81

Table 6: Simulated data with 25 observations for forests 2, 13, 30 and 33. Full samples were used for other forests. ”True” is the true value of median WTP. For a forest that belongs to NP, ”What if” is the value of median WTP if the forest belonged to P. ”Est. Int.” gives the 2.5%, 50%, and 97.5% percentiles of the posterior distribution of median WTP. ”Pr” is the posterior probability that the forest belongs to NP

			BMA BFT				NT			BFT		
Forest	True	What if	Est. Int.			Pr	Est. Int.			Est. Int.		
2	0.79		0.76	0.79	0.81	0.05	0.55	0.75	0.92	0.66	0.69	0.72
13	1.06		1.02	1.06	1.09	0.07	0.93	1.12	1.32	0.94	0.97	1.00
30	1.79	2.50	1.61	1.92	2.58	0.97	1.60	1.86	2.22	2.75	2.93	3.11
33	1.18	0.88	0.86	1.05	1.28	0.42	1.00	1.15	1.31	0.74	0.77	0.81

Table 7: Simulated data with 50 observations for forests 2, 13, 30 and 33. Full samples were used for other forests. Labels are defined in Table 6

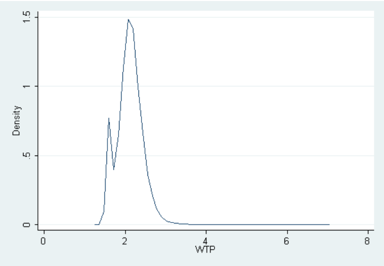

Figure 1: BMA Posterior density of median WTP for forest 33: 25 real observations

Appendix A: Algorithm

Let y_j^* be a vector containing the log WTP values for site j: $y_j^*= (\ln(WTP_{1j}), ..., \ln(WTP_{N_j j}))'$, where N_j is the number of respondents at site j, and let $y^* = (y_1^{*\prime}, ..., y_J^{*\prime})'$. The algorithm will deliver a sample from the posterior distribution of (M, y^*, ψ_M). Let us define M as a $J \times 1$ vector of ones and zeros. The i^{th} element of M is one if site $i \in P$, and it is zero otherwise.

Let (M^n, y^{*n}, ψ_M^n) be the value of (M, y^*, ψ_M) at iteration n. The algorithm to generate the value of (M, y^*, ψ_M) at iteration $(n + 1)$ can be summarised as follows:

1. Propose a candidate model M^* from a distribution over the set of models $\pi(M|M^n)$.
2. Fix $M^{n+1} = M^*$ with probability ρ and fix $M^{n+1} = M^n$ with probability $(1 - \rho)$, (ρ is defined in (13) below).
3. Sample ψ_M^{n+1} from its posterior conditional distribution given $y^* = y^{*n}$ and $M = M^{n+1}$.
4. Sample $y^{*(n+1)}$ from its posterior conditional distribution given $\psi_M = \psi_M^{n+1}$ and $M = M^{n+1}$.

In the following we describe in more detail each of these steps.

Defining $\pi(M|M^n)$

Let Q_P be the matrix which has each row equal to $(1\ q_j)$, for $j \in P$. Recall that the set of possible models is defined by all the possible partitions (P, NP) subject to the restriction that Q_P has rank equal to $(k_q + 1)$, where k_q is the number of attributes in q. In order to define the algorithm, instead of restricting the set of models, it appears more convenient to put this restriction in the prior. That is, the set of possible models include the NT model (2) plus all partitions (P, NP) with at least $(k_q + 1)$ sites in P, but partitions that result in Q_P having rank smaller than $(k_q + 1)$ have zero prior probability.

If the number of ones in M^n is greater than $(k_q + 1)$, then $\pi(M|M^n)$ is a uniform over the following set of models:

- Models that result from changing one element in M^n from zero to one.
- Models that result from changing one element in M^n from one to zero.

Note that $\pi(M|M^n)$ is a uniform over J models, and thus in this case $\pi(M|M^n) = 1/J$.

If the number of ones in M^n is exactly equal to $(k_q + 1)$, then $\pi(M|M^n)$ is a uniform over the following set of models:

- Models that result from changing one element in M^n from zero to one.
- The NT model defined by (2), where P is the empy set.

Hence, in this case $\pi(M|M^n) = 1/(J - (k_q + 1) + 1)$.

If M^n is the NT model defined by (2), then $\pi(M|M^n)$ is a uniform over the following set of models:

- Models with just $(k_q + 1)$ sites in P.

Thus, in this case $\pi(M|M^n) = \frac{1}{(\frac{J!}{(k_q+1)!(J-(k_q+1))!})}$, where $(\frac{J!}{(k_q+1)!(J-(k_q+1))!})$ is the number of models with exactly $(k_q + 1)$ elements in P.

The Acceptance Probability ρ

Formally, the algorithm generates a draw for (ψ_M, M) conditional on y^* (Holmes and Held, 2006), with ψ_M being generated from its conditional posterior distribution. The general expression for the acceptance probability for a move from (ψ_M^n, M^n) to (ψ_M^{n+1}, M^*) can be found for example at Waagepetersen and Sorensen (2001) and it is equal to:

$$\rho = \min\left\{1, \frac{\pi(M^n|M^*)}{\pi(M^*|M^n)} \frac{f_{M^*}(y^*, \psi_M^{n+1})}{f_{M^n}(y^*, \psi_M^n)} \frac{g_{M^n}(\psi_M^n)}{g_{M^*}(\psi_M^{n+1})} \frac{\pi(M^*)}{\pi(M^n)}\right\}$$

where $f_{M^*}(y^*, \psi_M)$ is product of the augmented likelihood (that is, the density function of y^* conditional on ψ_M and $M = M^*$) times the prior density of ψ_M conditional on $M = M^*$. The function $g_{M^*}(\psi_M)$ is the distribution from which ψ_M is generated and $\pi(M^*)$ is the prior probability of model M^*. Holmes and Held (2006) choose $g_{M^*}(\psi_M)$ to be the conditional posterior of ψ_M given y^* and $M = M^*$, in which case ρ simplifies to:

$$\rho = \min\left\{1, \frac{\pi(M^n|M^*)}{\pi(M^*|M^n)} \frac{f_{M^*}(y^*)}{f_{M^n}(y^*)} \frac{\pi(M^*)}{\pi(M^n)}\right\} \tag{13}$$

where

$$f_{M^*}(y^*) = \int f_{M^*}(y^*, \psi_M) d\psi_M$$

This integral is the marginal likelihood in a linear model and can be calculated with standard operations (e.g. Zellner, 1971). If model M^* is neither equal to the BFT model nor to the NT model, then $f_{M^*}(y^*)$ can be written as $f_{M^*}(y^*) = f_P(y_P^*) \prod\limits_{j \in NP} f_{NP}(y_j^*)$, with:

$$\begin{aligned} f_P(y_P^*) \quad &= \quad \frac{1}{\Gamma(1/2)} \Gamma\left(\frac{N_P + 1}{2}\right) |V_{0P}|^{-1/2} |V_P|^{1/2} \frac{1}{\sqrt{K_P g_P}} \times \\ & \left| \frac{1}{K_P g_P} + y_P^{*\prime} y_P^* - \mu_P' V_P^{-1} \mu_P + \mu_{0P}' V_{0P}^{-1} \mu_{0P} \right|^{-(N_P+1)/2} \end{aligned}$$

where y^*_P is a vector concatenating all y^*_i for $i \in P$, $N_P = \sum_{j \in P} N_j$, and $(\mu_{0P}, V_{0P}, \mu_P, V_P)$ are:

$$
\begin{aligned}
V_{0P} &= g_P \begin{pmatrix} \sum_{j\in P} N_j & 0 & 0 \\ 0 & \sum_{j\in P}\sum_i (\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{q}_j - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i (\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \\ 0 & \sum_{j\in P}\sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{q}_{ij} - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \end{pmatrix}^{-1} \\
\mu_{0P} &= \begin{pmatrix} \bar{t}_P \\ 0 \\ 0 \end{pmatrix} \\
V_P &= \left(V_{0P}^{-1} + \begin{pmatrix} \sum_{j\in P} N_j & 0 & 0 \\ 0 & \sum_{j\in P}\sum_i (\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{q}_j - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i (\mathbf{q}_j - \bar{\mathbf{q}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \\ 0 & \sum_{j\in P}\sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{q}_{ij} - \bar{\mathbf{q}}_P) & \sum_{j\in P}\sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_P) \end{pmatrix} \right)^{-1} \\
\mu_P &= V_P \left(\begin{pmatrix} \sum_{j\in P}\sum_{j=1}^{N_j} y^*_{ij} \\ \sum_{j\in P}\sum_i (\mathbf{q}_j - \bar{\mathbf{q}}_P)' y^*_{ij} \\ \sum_{j\in P}\sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)' y^*_{ij} \end{pmatrix} + (V_{0P})^{-1}\mu_{0P} \right)
\end{aligned}
$$

and g_P and K_P are prior parameters defined in Section 2.3.2.

For $j \in NP$:

$$
\begin{aligned}
f_{NP}(y^*_j) &= \frac{1}{\Gamma(1/2)} \Gamma(\frac{N_j + 1}{2}) \left|V_{0j}\right|^{-1/2} \left|V_j\right|^{1/2} \frac{1}{\sqrt{K_j g_j}} \times \\
&\quad \left| \frac{1}{K_j g_j} + y^{*\prime}_j y^*_j - \mu_j' V_j^{-1} \mu_j + \mu_{0j}' V_{0j}^{-1} \mu_{0j} \right|^{-(N_j+1)/2}
\end{aligned}
$$

where:

$$
\begin{aligned}
V_{0j} &= g_j \begin{pmatrix} N_i & 0 \\ 0 & \sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_i)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_i) \end{pmatrix}^{-1} \\
\mu_{0j} &= \begin{pmatrix} \bar{t}_j \\ 0 \end{pmatrix} \\
V_j &= \left(V_{0j}^{-1} + \begin{pmatrix} N_j & 0 \\ 0 & \sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_i)'(\mathbf{s}_{ij} - \bar{\mathbf{s}}_i) \end{pmatrix} \right)^{-1} \\
\mu_j &= V_j \left(\begin{pmatrix} \sum_{j=1}^{N_j} y^*_{ij} \\ \sum_i (\mathbf{s}_{ij} - \bar{\mathbf{s}}_i)' y^*_{ij} \end{pmatrix} + (V_{0j})^{-1}\mu_{0j} \right)
\end{aligned}
$$

and where g_j and K_j are prior parameters defined in Section 2.3.2.

If M^* is the BFT model then $f_{M^*}(y^*) = f_P(y^*_P)$. If M^* is the NT model then $f_{M^*}(y^*) =$

$\prod_{j=1}^{J} f_{NP}(y_j^*)$.

Sample ψ_M^{n+1} from its posterior conditional distribution given $y^* = y^{*n}$ and $M = M^{n+1}$.

The variance parameters $(\lambda^{-2}, \{\lambda_j^{-2} : j \in NP\})$ are sampled first from inverted Gamma-2 distributions (Bauwens, Lubrano and Richard (1999), Appendix A), and then the intercept and slope parameters $\left(\underline{\alpha}_P, \gamma, \beta, \{(\underline{\alpha}_j, \gamma_j, \beta_j) : j \in NP\}\right)$ are sampled conditional on the variance parameters. In particular, λ^{-2} is sampled from an inverted Gamma-2 with $(N_P + 1)$ degrees of freedom and parameter equal to:

$$\frac{1}{K_P g_P} + y_P^{*\prime} y_P^* - \mu_P' V_P^{-1} \mu_P + \mu_{0P}' V_{0P}^{-1} \mu_{0P}$$

Each of the λ_j^{-2} is sampled indepedently from an inverse Gamma-2 with $(N_j + 1)$ degrees of freedom and parameter equal to:

$$\frac{1}{K_j g_j} + y_j^{*\prime} y_j^* - \mu_j' V_j^{-1} \mu_j + \mu_{0j}' V_{0j}^{-1} \mu_{0j}$$

The parameters $(\underline{\alpha}_P, \gamma, \beta)$ are sampled from a normal distribution with mean μ_P and variance $\lambda^{-2} V_P$. Each vector $(\underline{\alpha}_j, \gamma_j, \beta_j)$, for $j \in NP$, is sampled independently from a normal with mean μ_j and covariance matrix $\lambda_j^{-2} V_j$.

Sample $y^{*(n+1)}$ from its posterior conditional distribution given $\psi_M = \psi_M^{n+1}$ and $M = M^{n+1}$.

Each $\ln(WTP_{ij})$ is sampled independently from a truncated normal distribution with variance equal to λ_P^{-2} if $j \in P$ or equal to λ_j^{-2} if $j \in NP$. The mean is given by:

$$\begin{array}{rlcl} \underline{\alpha}_P + (\mathbf{s}_{ij} - \bar{\mathbf{s}}_P)\,\gamma + (\mathbf{q}_j - \bar{\mathbf{q}}_P)\beta & \text{if} \;\; j & \in & P \\ \underline{\alpha}_j + (\mathbf{s}_{ij} - \bar{\mathbf{s}}_j)\,\gamma_j & \text{if} \;\; j & \in & NP \end{array} \tag{14}$$

In the single-bounded model, the truncation area will be (t_{ij}, ∞) if the individual accepted to pay $\exp(t_{ij})$, or $(-\infty, t_{ij})$ if he declined. The procedure is the same with double-bounded data, except that the truncation area has to be changed accordingly. Note that in the case of open-ended data the observed value of $\ln(WTP_{ij})$ is used and hence step 4 of the algorithm is not needed.

Appendix B: Additional Tables and Graphs

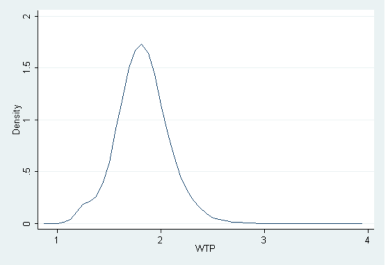

Figure 2: BMA Posterior density of median WTP for forest 30: 25 real observations

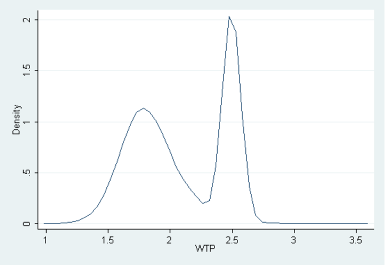

Figure 3: BMA Posterior density of median WTP for forest 30: 25 artificial observations

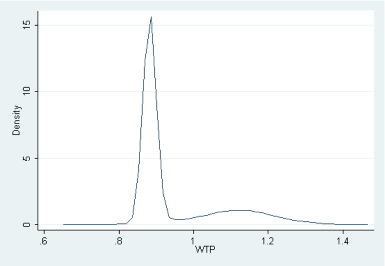

Figure 4: BMA Posterior density of median WTP for forest 33: 25 artificial observations

Forest	BMA BFT					NT				BFT			
	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
1	1.69	1.80	2.21	0.52	0.17	1.86	2.07	2.33	0.47	1.49	1.56	1.63	0.14
2	1.46	1.59	1.70	0.24	0.03	1.51	1.65	1.80	0.29	1.56	1.63	1.69	0.13
3	0.92	1.00	1.09	0.17	0.00	0.90	1.02	1.15	0.25	0.83	0.89	0.96	0.13
4	1.07	1.18	1.30	0.23	0.01	0.95	1.11	1.28	0.33	1.08	1.17	1.27	0.19
5	1.34	1.41	1.48	0.14	0.00	1.29	1.42	1.57	0.29	1.48	1.53	1.59	0.11
6	1.33	1.44	1.56	0.23	0.00	1.21	1.40	1.61	0.40	1.39	1.47	1.55	0.16
7	1.32	1.40	1.48	0.16	0.00	1.23	1.38	1.56	0.33	1.36	1.41	1.47	0.11
8	1.72	1.83	2.19	0.47	0.25	1.88	2.06	2.27	0.39	1.73	1.80	1.87	0.14
9	1.18	1.36	1.47	0.29	0.18	1.09	1.31	1.56	0.47	1.34	1.40	1.46	0.13
10	0.49	0.69	0.88	0.39	1.00	0.49	0.69	0.88	0.39	1.46	1.51	1.56	0.10
11	1.16	1.70	1.86	0.70	0.17	1.03	1.32	1.66	0.63	1.76	1.85	1.95	0.19
12	1.58	1.75	1.90	0.32	0.00	1.49	1.71	1.98	0.49	1.69	1.76	1.84	0.15
13	1.54	1.68	1.81	0.27	0.02	1.58	1.73	1.90	0.33	1.64	1.71	1.78	0.13
14	1.07	1.18	1.29	0.23	1.00	1.07	1.18	1.30	0.23	1.22	1.28	1.36	0.14
15	1.38	1.54	1.90	0.52	0.43	1.53	1.72	1.94	0.41	1.52	1.62	1.72	0.20
16	2.38	2.60	2.87	0.49	1.00	2.38	2.60	2.87	0.49	1.88	1.98	2.09	0.21
17	1.16	1.26	1.35	0.19	0.01	0.95	1.12	1.32	0.37	1.27	1.34	1.41	0.14
18	1.06	1.14	1.22	0.16	0.00	1.03	1.16	1.29	0.25	1.01	1.07	1.13	0.12
19	0.82	0.95	1.08	0.26	1.00	0.82	0.95	1.08	0.26	1.57	1.66	1.76	0.19
20	0.90	1.06	1.24	0.33	1.00	0.90	1.06	1.23	0.33	1.21	1.26	1.31	0.10
21	1.01	1.40	1.81	0.80	0.54	0.98	1.22	1.49	0.51	1.40	1.44	1.49	0.09
22	1.07	1.20	1.33	0.26	1.00	1.07	1.20	1.33	0.26	1.51	1.60	1.70	0.19
23	1.76	1.99	2.23	0.47	0.00	1.69	2.13	2.80	1.11	1.21	1.27	1.34	0.13
24	2.03	2.23	2.47	0.44	0.01	2.15	2.57	3.24	1.09	1.56	1.63	1.71	0.16
25	1.33	1.44	1.51	0.19	0.02	1.06	1.24	1.43	0.37	1.35	1.39	1.44	0.09
26	1.41	1.61	1.83	0.42	0.02	1.36	1.56	1.80	0.45	1.45	1.62	1.81	0.37
27	1.89	2.04	2.17	0.28	0.00	1.69	1.95	2.27	0.57	1.92	2.01	2.10	0.18
28	1.30	1.37	1.44	0.14	0.00	1.26	1.43	1.62	0.36	1.35	1.40	1.46	0.11
29	1.95	2.22	2.53	0.58	0.00	2.11	2.64	3.65	1.54	1.60	1.69	1.79	0.18
30	1.80	1.94	2.08	0.28	1.00	1.81	1.94	2.08	0.28	1.56	1.65	1.75	0.20
31	1.23	1.35	1.49	0.26	0.00	1.20	1.36	1.54	0.34	1.49	1.59	1.71	0.22
32	1.12	1.33	1.75	0.63	0.84	1.11	1.31	1.54	0.43	1.47	1.52	1.58	0.11
33	2.26	2.46	2.70	0.44	1.00	2.26	2.46	2.70	0.44	1.77	1.86	1.95	0.18
34	1.37	1.57	1.78	0.41	0.78	1.36	1.54	1.75	0.39	1.41	1.47	1.53	0.12
35	1.51	1.64	1.78	0.26	0.00	1.46	1.62	1.80	0.34	1.91	2.02	2.14	0.23
36	0.71	0.96	1.33	0.62	0.96	0.71	0.96	1.21	0.49	1.66	1.80	1.96	0.29
37	1.30	1.47	1.66	0.35	1.00	1.30	1.47	1.66	0.36	1.64	1.76	1.88	0.24
38	1.40	1.52	1.63	0.22	0.00	1.38	1.53	1.70	0.32	1.39	1.45	1.52	0.13
39	1.46	2.08	2.37	0.91	0.21	1.36	1.65	2.00	0.64	1.65	1.79	1.95	0.31
40	1.31	1.46	1.63	0.32	1.00	1.31	1.46	1.63	0.32	1.73	1.81	1.89	0.16
41	1.50	1.69	1.85	0.34	0.03	1.26	1.48	1.72	0.47	1.23	1.30	1.37	0.15
42	2.38	2.65	2.93	0.55	0.00	2.17	2.42	2.73	0.56	1.91	2.03	2.17	0.25

Table 8: Real data with full samples. Labels defined in Table 3

Forest	BMA BFT					NT				BFT			
	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
1	1.86	2.07	2.33	0.47	1.00	1.87	2.07	2.33	0.46	1.46	1.53	1.61	0.15
2	1.21	1.55	1.69	0.48	0.10	0.98	1.33	1.75	0.77	1.53	1.60	1.68	0.15
3	0.95	1.04	1.13	0.18	0.00	0.90	1.02	1.15	0.25	0.84	0.91	0.98	0.14
4	1.06	1.18	1.31	0.25	0.03	0.95	1.11	1.28	0.33	1.13	1.23	1.34	0.21
5	1.37	1.45	1.53	0.16	0.00	1.29	1.43	1.58	0.29	1.42	1.49	1.55	0.12
6	1.25	1.39	1.49	0.24	0.00	1.21	1.40	1.61	0.40	1.39	1.48	1.57	0.18
7	1.34	1.43	1.52	0.17	0.00	1.22	1.38	1.55	0.33	1.33	1.39	1.45	0.12
8	1.73	2.03	2.26	0.53	0.87	1.87	2.06	2.27	0.39	1.71	1.79	1.87	0.16
9	1.13	1.40	1.55	0.40	0.32	1.09	1.32	1.55	0.47	1.30	1.37	1.43	0.13
10	0.48	0.69	0.87	0.39	1.00	0.49	0.69	0.88	0.39	1.40	1.46	1.51	0.11
11	1.34	1.55	1.77	0.38	0.02	1.03	1.31	1.66	0.63	1.78	1.88	1.98	0.21
12	1.41	1.53	1.89	0.48	0.01	1.49	1.71	1.98	0.49	1.68	1.76	1.85	0.17
13	1.35	1.49	1.77	0.40	0.02	0.95	1.35	1.82	0.86	1.65	1.72	1.80	0.15
14	0.99	1.12	1.24	0.25	0.04	1.07	1.18	1.29	0.23	1.19	1.27	1.35	0.16
15	1.48	1.62	1.86	0.38	0.16	1.53	1.72	1.93	0.40	1.53	1.63	1.74	0.22
16	2.38	2.60	2.87	0.49	1.00	2.38	2.60	2.86	0.48	1.83	1.94	2.05	0.22
17	1.16	1.29	1.39	0.23	0.02	0.95	1.13	1.32	0.37	1.27	1.34	1.42	0.15
18	0.99	1.07	1.15	0.16	0.00	1.03	1.15	1.29	0.26	1.00	1.06	1.12	0.12
19	0.84	1.01	1.22	0.37	0.54	0.82	0.95	1.08	0.26	1.54	1.64	1.74	0.21
20	0.95	1.23	1.31	0.36	0.31	0.90	1.06	1.23	0.33	1.21	1.26	1.32	0.10
21	1.22	1.32	1.41	0.18	0.00	0.98	1.22	1.48	0.51	1.36	1.41	1.46	0.10
22	1.12	1.29	1.42	0.30	0.19	1.07	1.20	1.33	0.26	1.48	1.58	1.69	0.20
23	1.45	2.13	2.81	1.44	0.96	1.70	2.14	2.79	1.09	1.17	1.25	1.32	0.14
24	2.16	2.57	3.26	1.10	1.00	2.15	2.57	3.23	1.08	1.58	1.66	1.75	0.17
25	1.30	1.38	1.45	0.14	0.01	1.06	1.24	1.44	0.37	1.34	1.39	1.44	0.10
26	1.40	1.58	1.78	0.37	0.00	1.36	1.56	1.80	0.44	1.44	1.61	1.81	0.37
27	1.56	1.69	2.08	0.61	0.31	1.69	1.95	2.28	0.58	1.85	1.95	2.05	0.19
28	1.25	1.33	1.48	0.19	0.06	1.27	1.43	1.62	0.36	1.33	1.38	1.44	0.12
29	2.10	2.64	3.63	1.55	1.00	2.11	2.64	3.66	1.55	1.42	1.51	1.62	0.20
30	1.29	1.81	2.36	1.10	0.93	1.43	1.84	2.36	0.92	1.39	1.50	1.61	0.22
31	1.24	1.37	1.53	0.28	0.00	1.20	1.35	1.53	0.34	1.31	1.41	1.53	0.22
32	1.22	1.33	1.50	0.27	0.00	1.11	1.31	1.54	0.43	1.35	1.41	1.47	0.12
33	1.56	2.11	2.76	1.20	0.86	1.72	2.14	2.75	1.03	1.58	1.68	1.77	0.19
34	1.37	1.53	1.75	0.39	0.88	1.37	1.54	1.75	0.39	1.32	1.38	1.44	0.12
35	1.53	1.70	1.85	0.32	0.00	1.46	1.62	1.79	0.33	1.69	1.81	1.93	0.24
36	0.71	0.97	1.32	0.60	0.94	0.72	0.96	1.20	0.48	1.60	1.75	1.91	0.31
37	1.20	1.43	1.64	0.44	0.74	1.30	1.47	1.65	0.35	1.43	1.56	1.70	0.27
38	1.36	1.45	1.57	0.21	0.00	1.38	1.53	1.70	0.32	1.33	1.40	1.47	0.14
39	1.31	1.63	1.94	0.62	0.04	1.36	1.65	2.01	0.66	1.58	1.73	1.90	0.32
40	1.32	1.45	1.68	0.37	0.06	1.31	1.46	1.64	0.33	1.75	1.83	1.92	0.18
41	1.16	1.26	1.48	0.32	0.00	1.26	1.48	1.72	0.47	1.19	1.26	1.33	0.15
42	2.17	2.42	2.74	0.56	1.00	2.17	2.43	2.74	0.57	1.90	2.03	2.17	0.27

Table 9: Real data with 25 observations for forests 2, 13, 30 and 33. Full samples for other forests. Labels defined in Table 3

Forest	BMA BFT					NT				BFT			
	Est. Int.			R	Pr	Est. Int.			R	Est. Int.			R
1	1.67	1.98	2.31	0.64	0.62	1.86	2.08	2.33	0.47	1.46	1.53	1.61	0.15
2	1.30	1.47	1.63	0.33	0.02	1.19	1.50	1.90	0.70	1.53	1.60	1.68	0.15
3	0.90	0.99	1.08	0.18	0.00	0.90	1.02	1.15	0.25	0.84	0.91	0.98	0.14
4	1.05	1.17	1.29	0.24	0.01	0.95	1.11	1.28	0.33	1.13	1.23	1.34	0.21
5	1.31	1.38	1.45	0.15	0.00	1.29	1.42	1.57	0.29	1.43	1.49	1.55	0.12
6	1.27	1.38	1.50	0.23	0.00	1.21	1.40	1.61	0.40	1.40	1.48	1.58	0.18
7	1.28	1.37	1.45	0.17	0.00	1.22	1.38	1.55	0.33	1.34	1.39	1.45	0.12
8	1.72	1.85	2.13	0.40	0.16	1.87	2.06	2.27	0.39	1.72	1.80	1.88	0.16
9	1.14	1.34	1.51	0.37	0.44	1.10	1.32	1.56	0.46	1.31	1.37	1.44	0.13
10	0.49	0.69	0.88	0.39	1.00	0.49	0.69	0.88	0.39	1.41	1.46	1.52	0.11
11	1.16	1.72	1.90	0.74	0.15	1.02	1.32	1.66	0.64	1.78	1.89	1.99	0.21
12	1.63	1.81	2.00	0.37	0.00	1.49	1.71	1.98	0.49	1.69	1.77	1.86	0.17
13	1.57	1.72	1.88	0.31	0.00	1.36	1.75	2.30	0.94	1.65	1.73	1.81	0.15
14	1.07	1.18	1.29	0.23	1.00	1.07	1.18	1.29	0.23	1.19	1.27	1.35	0.15
15	1.42	1.70	1.93	0.51	0.89	1.53	1.72	1.93	0.40	1.53	1.63	1.74	0.21
16	2.38	2.60	2.86	0.49	1.00	2.38	2.60	2.87	0.49	1.84	1.95	2.06	0.22
17	1.12	1.22	1.31	0.19	0.01	0.95	1.13	1.32	0.36	1.27	1.34	1.42	0.15
18	1.07	1.15	1.24	0.17	0.00	1.03	1.16	1.29	0.26	1.00	1.06	1.12	0.12
19	0.82	0.95	1.08	0.26	1.00	0.82	0.95	1.09	0.26	1.54	1.64	1.74	0.20
20	0.91	1.06	1.25	0.35	1.00	0.90	1.06	1.24	0.33	1.21	1.26	1.32	0.10
21	1.02	1.60	1.78	0.76	0.47	0.98	1.22	1.48	0.50	1.36	1.41	1.46	0.10
22	1.07	1.20	1.33	0.25	1.00	1.07	1.20	1.33	0.25	1.49	1.59	1.69	0.20
23	1.71	1.98	2.26	0.55	0.00	1.69	2.14	2.78	1.09	1.17	1.24	1.32	0.14
24	2.10	2.31	2.58	0.49	0.00	2.15	2.57	3.23	1.08	1.58	1.66	1.75	0.17
25	1.30	1.39	1.48	0.18	0.02	1.06	1.24	1.44	0.38	1.35	1.39	1.44	0.10
26	1.37	1.56	1.78	0.40	0.01	1.36	1.57	1.80	0.44	1.44	1.61	1.81	0.37
27	1.90	2.04	2.18	0.29	0.00	1.69	1.95	2.27	0.58	1.86	1.96	2.05	0.19
28	1.27	1.34	1.41	0.15	0.00	1.27	1.43	1.62	0.36	1.33	1.39	1.45	0.12
29	1.98	2.29	2.68	0.71	0.02	2.10	2.64	3.67	1.57	1.43	1.52	1.62	0.20
30	1.61	1.94	2.31	0.69	0.96	1.61	1.93	2.30	0.69	1.39	1.50	1.61	0.22
31	1.27	1.40	1.56	0.29	0.00	1.20	1.35	1.53	0.34	1.32	1.43	1.54	0.22
32	1.12	1.34	1.77	0.65	0.84	1.11	1.31	1.54	0.43	1.36	1.42	1.48	0.12
33	1.95	2.26	2.66	0.71	1.00	1.94	2.25	2.66	0.71	1.60	1.69	1.78	0.19
34	1.36	1.55	1.75	0.39	0.96	1.36	1.54	1.75	0.39	1.32	1.38	1.45	0.13
35	1.46	1.60	1.74	0.28	0.00	1.46	1.62	1.79	0.33	1.71	1.82	1.95	0.24
36	0.72	0.99	1.44	0.72	0.83	0.71	0.96	1.20	0.49	1.61	1.75	1.91	0.31
37	1.31	1.47	1.66	0.35	1.00	1.31	1.47	1.66	0.35	1.44	1.56	1.70	0.26
38	1.35	1.48	1.61	0.25	0.00	1.38	1.53	1.70	0.32	1.34	1.40	1.47	0.14
39	1.47	1.86	2.27	0.79	0.06	1.36	1.65	2.01	0.65	1.58	1.73	1.90	0.32
40	1.31	1.46	1.65	0.34	1.00	1.31	1.46	1.63	0.32	1.75	1.84	1.93	0.18
41	1.49	1.70	1.88	0.38	0.02	1.26	1.48	1.72	0.46	1.19	1.26	1.34	0.15
42	2.26	2.54	2.85	0.59	0.00	2.17	2.42	2.74	0.57	1.90	2.03	2.17	0.27

Table 10: Real data with 50 observations for forests 2, 13, 30 and 33. Full samples for other forests. Labels defined in Table 3

			BMA BFT				NT			BFT		
Forest	True	What if	Est. Int.			Pr	Est. Int.			Est. Int.		
1	0.77		0.73	0.76	0.79	0.00	0.71	0.77	0.82	0.74	0.77	0.80
2	0.79		0.76	0.79	0.81	0.01	0.52	0.83	1.12	0.66	0.69	0.72
3	0.55		0.49	0.52	0.55	0.00	0.45	0.51	0.56	0.57	0.61	0.65
4	0.98		0.90	0.95	1.01	0.00	0.89	0.96	1.04	0.78	0.84	0.90
5	0.88		0.84	0.87	0.90	0.00	0.78	0.84	0.90	0.73	0.76	0.79
6	1.23		1.18	1.23	1.28	0.00	1.10	1.20	1.30	0.93	0.97	1.02
7	0.64		0.60	0.62	0.64	0.00	0.54	0.62	0.69	0.62	0.65	0.67
8	0.92		0.87	0.92	0.95	0.02	0.79	0.86	0.92	0.86	0.89	0.93
9	0.54		0.51	0.53	0.55	0.00	0.46	0.60	0.74	0.56	0.58	0.61
10	0.67		0.64	0.65	0.67	0.00	0.46	0.58	0.68	0.61	0.64	0.66
11	1.49		1.23	1.45	1.55	0.48	1.21	1.32	1.45	1.13	1.18	1.24
12	1.00		0.96	1.00	1.04	0.00	0.94	1.03	1.13	0.95	0.98	1.02
13	1.06		1.02	1.06	1.24	0.06	0.97	1.23	1.54	0.94	0.97	1.00
14	2.20		2.10	2.18	2.27	0.00	1.99	2.14	2.30	2.01	2.11	2.22
15	1.06		1.04	1.08	1.13	0.00	1.00	1.10	1.21	0.84	0.88	0.93
16	0.41	1.92	0.32	0.46	0.59	1.00	0.33	0.46	0.59	1.40	1.46	1.53
17	1.22		1.16	1.21	1.26	0.01	1.14	1.29	1.44	0.90	0.94	0.98
18	1.20		1.11	1.16	1.20	0.01	1.06	1.15	1.24	1.02	1.07	1.12
19	2.70		2.60	2.71	2.83	0.00	2.40	2.66	2.97	2.73	2.88	3.03
20	0.83		0.77	0.80	0.83	0.01	0.69	0.77	0.84	0.88	0.91	0.94
21	1.10		1.05	1.08	1.11	0.00	0.93	1.06	1.19	1.09	1.12	1.16
22	3.70	1.01	1.03	2.64	15.30	1.00	0.98	2.54	43.36	1.26	1.32	1.38
23	1.09		1.00	1.05	1.10	0.07	0.88	1.04	1.23	1.33	1.40	1.46
24	1.62		1.56	1.62	1.69	0.01	1.48	1.62	1.78	1.73	1.80	1.87
25	0.84		0.80	0.82	0.84	0.00	0.78	0.86	0.95	0.78	0.80	0.83
26	1.12		1.07	1.15	1.24	0.00	1.07	1.16	1.25	1.11	1.22	1.34
27	1.02		0.99	1.02	1.06	0.00	0.93	1.01	1.09	0.93	0.97	1.01
28	1.15		1.11	1.14	1.17	0.00	1.10	1.17	1.25	0.92	0.95	0.98
29	2.33		2.25	2.34	2.45	0.01	2.24	2.51	2.84	2.13	2.25	2.38
30	1.79	2.50	1.47	2.19	2.59	0.54	1.42	1.81	2.39	2.77	2.94	3.13
31	1.14		1.07	1.12	1.18	0.00	1.01	1.11	1.21	0.88	0.94	1.00
32	1.00		0.95	0.98	1.03	0.04	0.93	1.02	1.11	1.05	1.09	1.13
33	1.18	0.88	0.85	0.89	1.25	0.21	0.90	1.13	1.33	0.73	0.77	0.81
34	0.85		0.79	0.82	0.85	0.01	0.78	0.87	0.96	0.92	0.95	0.99
35	0.94		0.91	0.95	1.00	0.00	0.89	0.95	1.02	0.70	0.74	0.79
36	0.56		0.53	0.57	0.71	0.02	0.60	0.72	0.83	0.48	0.52	0.56
37	3.32		3.18	3.36	3.55	0.00	2.89	3.18	3.53	3.48	3.74	4.02
38	0.52		0.49	0.51	0.52	0.00	0.47	0.52	0.58	0.56	0.58	0.61
39	0.80		0.75	0.81	0.86	0.01	0.69	0.79	0.90	0.72	0.78	0.85
40	1.85		1.80	1.87	1.95	0.00	1.80	1.96	2.13	1.56	1.62	1.68
41	0.66		0.61	0.63	0.68	0.01	0.69	0.77	0.84	0.82	0.86	0.90
42	1.55		1.52	1.58	1.65	0.01	1.49	1.61	1.74	1.42	1.50	1.58

Table 11: Simulated data with 25 observations for forests 2, 13, 30 and 33. Full sample sizes for other forests. Labels defined in Table 6

			BMA BFT				NT			BFT		
Forest	True	What if	Est. Int.			Pr	Est. Int.			Est. Int.		
1	0.77		0.73	0.76	0.78	0.00	0.71	0.77	0.82	0.74	0.77	0.80
2	0.79		0.76	0.79	0.81	0.00	0.55	0.75	0.92	0.66	0.69	0.72
3	0.55		0.49	0.52	0.55	0.00	0.45	0.51	0.57	0.57	0.61	0.65
4	0.98		0.90	0.95	1.01	0.00	0.89	0.96	1.04	0.78	0.84	0.90
5	0.88		0.84	0.87	0.89	0.00	0.78	0.84	0.91	0.74	0.76	0.79
6	1.23		1.18	1.23	1.28	0.00	1.11	1.20	1.30	0.93	0.97	1.02
7	0.64		0.60	0.62	0.64	0.00	0.54	0.62	0.69	0.63	0.65	0.67
8	0.92		0.89	0.92	0.95	0.00	0.79	0.86	0.92	0.87	0.90	0.93
9	0.54		0.51	0.53	0.55	0.02	0.46	0.60	0.74	0.56	0.58	0.61
10	0.67		0.63	0.65	0.67	0.00	0.46	0.58	0.68	0.62	0.64	0.66
11	1.49		1.22	1.38	1.55	0.69	1.21	1.32	1.45	1.13	1.18	1.24
12	1.00		0.96	1.00	1.03	0.00	0.94	1.03	1.12	0.95	0.98	1.02
13	1.06		1.02	1.06	1.09	0.00	0.93	1.12	1.32	0.94	0.97	1.00
14	2.20		2.10	2.18	2.27	0.00	1.99	2.14	2.30	2.00	2.10	2.20
15	1.06		1.04	1.08	1.13	0.00	1.00	1.11	1.21	0.84	0.88	0.93
16	0.41	1.92	0.33	0.46	0.59	1.00	0.32	0.46	0.58	1.40	1.46	1.53
17	1.22		1.16	1.21	1.26	0.01	1.14	1.29	1.45	0.90	0.94	0.98
18	1.20		1.12	1.16	1.20	0.00	1.06	1.15	1.24	1.02	1.07	1.12
19	2.70		2.60	2.71	2.83	0.00	2.40	2.66	2.99	2.72	2.87	3.02
20	0.83		0.78	0.80	0.83	0.00	0.70	0.76	0.84	0.88	0.91	0.94
21	1.10		1.05	1.08	1.11	0.00	0.93	1.06	1.19	1.09	1.12	1.15
22	3.70	1.01	1.05	2.46	12.16	1.00	1.08	2.45	9.76	1.26	1.32	1.38
23	1.09		0.99	1.05	1.11	0.06	0.87	1.05	1.24	1.33	1.39	1.45
24	1.62		1.56	1.62	1.68	0.00	1.49	1.62	1.78	1.72	1.79	1.86
25	0.84		0.80	0.82	0.84	0.00	0.78	0.86	0.95	0.78	0.80	0.83
26	1.12		1.07	1.15	1.24	0.00	1.07	1.16	1.25	1.11	1.22	1.34
27	1.02		0.99	1.02	1.06	0.00	0.93	1.01	1.09	0.93	0.97	1.01
28	1.15		1.11	1.14	1.17	0.00	1.10	1.17	1.25	0.92	0.95	0.98
29	2.33		2.25	2.35	2.50	0.03	2.23	2.51	2.84	2.13	2.25	2.37
30	1.79	2.50	1.61	1.92	2.58	0.71	1.60	1.86	2.22	2.75	2.93	3.11
31	1.14		1.07	1.12	1.18	0.01	1.02	1.11	1.21	0.89	0.94	1.01
32	1.00		0.95	0.98	1.03	0.03	0.93	1.02	1.11	1.05	1.09	1.13
33	1.18	0.88	0.86	1.05	1.28	0.53	1.00	1.15	1.31	0.74	0.77	0.81
34	0.85		0.79	0.82	0.86	0.02	0.78	0.87	0.96	0.92	0.95	0.99
35	0.94		0.91	0.95	1.00	0.00	0.89	0.95	1.02	0.71	0.75	0.79
36	0.56		0.53	0.56	0.60	0.00	0.60	0.71	0.83	0.48	0.52	0.56
37	3.32		3.18	3.36	3.56	0.00	2.89	3.18	3.51	3.46	3.72	3.99
38	0.52		0.49	0.50	0.52	0.00	0.47	0.52	0.58	0.56	0.58	0.61
39	0.80		0.75	0.81	0.86	0.00	0.69	0.80	0.90	0.72	0.78	0.84
40	1.85		1.80	1.87	1.94	0.00	1.80	1.96	2.13	1.56	1.62	1.68
41	0.66		0.60	0.63	0.67	0.00	0.69	0.77	0.84	0.82	0.86	0.90
42	1.55		1.51	1.58	1.65	0.00	1.50	1.61	1.74	1.41	1.49	1.57

Table 12: Simulated data with 50 observations for forests 2, 13, 30 and 33. Full sample sizes for other forests. Labels defined in Table 6