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**A Better Approach to Resolving Variable Selection Uncertainty in Meta Analysis
for Benefits Transfer**

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A Better Approach to Resolving Variable Selection Uncertainty in Meta Analysis for Benefits Transfer

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Abstract. Because original high-quality non-market valuation studies can be expensive, perhaps prohibitively so, benefits transfer (BT) approaches are often used for valuing, e.g., the outputs of multifunctional agriculture. Here we focus on the use of BT functions, a preferred method, and address an under-appreciated problem – variable selection uncertainty – and demonstrate a conceptually superior method of resolving it.

We show that the standard method of value-function BT, using the full estimated model, may generate BT values that are too sensitive to insignificant variables, whereas models reduced by backward elimination of insignificant variables pay no attention to insignificant variables that may in fact have some influence on values. Rather than searching for the best single model for BT, Bayesian model averaging (BMA) is attentive to all of the variables that are *a priori* relevant, but uses posterior model probabilities to give systematically lower weight to less significant variables.

We estimate a full value model for wetlands in the US, and then calculate BT values from the full model, a reduced model, and by BMA. Variable selection uncertainty is exemplified by regional variables for wetland location. Predicted values from the full model are quite sensitive to region; reduced models pay no attention to regional variables; and the BMA predictions are attentive to region but give it relatively low weight. However, the suite of insignificant RHS variables, taken together, have non-trivial influence on BT values. BMA predicted values, like values from reduced models, have much narrower confidence intervals than values calculated from the full model.

Introduction

The problem of variable selection for benefits transfer

A common motivation for meta analysis is to generalize from a set of original studies in order to generate more reliable predictions of the value of a dependent variable. Benefits transfer (BT) is value prediction addressed to an explicit purpose – it uses an estimated meta function to predict the value of amenities produced by an actual or proposed site characterized by a suite of site and project descriptors.

Meta analytic equations of resource and amenity values often have many (say, more than 20) independent variables. At the outset, the set of potential RHS variables confronting analysts is quite large because BT-oriented clients are anxious to have parameter estimates for a rather complete set of descriptors in order to get BT values reflecting the particulars of policy sites; and an additional suite of variables is required to control for differences in methods and execution among the original valuation studies that form the data set for meta analysis.

Meta analysts have their own motivations for specifying models with relatively large sets of independent variables. Theoretical considerations provide relatively little guidance for

selecting among the large set of variables that plausibly might be related to value, and data deficiencies often force valuation researchers to use imperfect proxies for the variables suggested by theory, leaving meta analysts with relatively weak priors as to which of the observed variables will turn out to be important for predicting value.

Examples from recent wetlands valuation meta analyses include Borisova-Kidder (2006), who used 30 independent variables (including identifiers for valuation methods and regions within the US); Brander *et al.* (2006), who had 37 independent variables (including identifiers for valuation methods and countries); while Brouwer *et al.* (1999) analyzing only CV studies used 34 independent variables (including a substantial suite of identifiers for details in CV execution); and Woodward and Wui (2001) had 22 independent variables (including identifiers for valuation methods but not for regions within the US). Clearly, a list of all the unique variables potentially relevant to meta analysis of wetlands values would be longer than any of the above lists.

It is not uncommon that when the full model, i.e. $Y = f(\mathbf{X})$, where \mathbf{X} represents the vector of observed independent variables thought to be useful in predicting value, is estimated relatively few of the many independent variables are significant. Typically, researchers find that fewer than one-half of the independent variables are significant. Even that level of responsiveness to independent variables may be misleadingly high. Pursuit of significance and goodness of fit has led some investigators to use a long list of dummy variables (and, in some cases, interactions among dummy variables) with the inevitable result that just a few observations support parameter estimates for these variables, so we cannot be confident that the results are not influenced unduly by idiosyncrasies in a few studies.

BT values for policy sites are calculated from an estimated meta value function by inserting policy site values for the independent variables into the equation. Clearly, calculated values may be sensitive to the variable selection strategy used in meta analysis. If the full model (with 20 or more independent variables, many of them insignificant) is used, calculated BT values may be quite sensitive to insignificant variables that are *ipso facto* related only loosely to value. Reduced models (such as might be produced by backward elimination of insignificant variables) pay no attention to variables that fall below the threshold for significance but may nevertheless have some impact on true BT values. This would produce BT values strictly insensitive to some variables that make a difference to value, and disappoint clients seeking BT values tailor-made for the policy site.

Variable selection uncertainty

Variable selection uncertainty is one kind of model uncertainty. Suppose that $\mathbf{X} = (X_1, \dots, X_k)$ is a set of k observed independent variables such that Y may depend on any or all members of \mathbf{X} . Variable selection uncertainty arises when it is unclear *a priori* which if any model $Y = f(\mathbf{X}_i)$, where \mathbf{X}_i is a subset of \mathbf{X} , will provide the best predictions of Y (whatever we mean by best predictions). The goal of estimating BT values highlights the urgency of resolving the issue of variable selection uncertainty.

The variable selection problem is usually posed as selecting the “best” predictor subset \mathbf{X}_i for Y . The BT values dilemma (should we use values that overweight insignificant variables, or should such variables be given no weight at all in calculating BT values?) suggests that there may often be no single model $Y = f(\mathbf{X}_i)$ that is ideal in the sense of making the most effective use of the information in the data set.

Bayesian approaches to variable selection uncertainty allow us to formulate a more appropriate objective – rather than to find the best predictor subset of \mathbf{X} , the objective is to make the most effective use of posterior information in prediction (Clyde and George 2003). It seems intuitive that an effective method of predicting the value of Y would be attentive to all of the variables that are *a priori* relevant, but would give systematically lower weight to those that are less significant.

Bayesian model averaging (BMA) can consider all possible models $Y = f(\mathbf{X}_i)$, where \mathbf{X}_i is a subset of \mathbf{X} , using the estimated parameter values of each model weighted by the posterior probability that the model is the true model. Because the number of unique models, 2^k , grows exponentially with k , a representative sample of the possible models may be considered in the case where k is large. Insignificant variables have non-zero but relatively smaller influence on the predicted value of Y , because they appear in models whose posterior probability is low.

BMA is *a priori* a preferable alternative to model selection (i.e. to selecting a single “best” model) because theory suggests that it provides better average predictive performance than any single model (Hoeting *et al.* 1999). In meta analysis, BMA is finding increasing use as a solution to variable selection uncertainty. Moeltner and colleagues have introduced Bayesian methods to meta analysis for BT. Moeltner *et al.* (2007) and Moeltner and Woodward (2009) used Bayesian methods to overcome small sample problems. Moeltner and Woodward also apply BMA to address model uncertainty *ad hoc*, using posterior model probabilities to decide whether specific variables should be included in the final model or excluded. Yet, to our knowledge, there has been no published application of BMA to systematically address variable selection uncertainty in meta analysis for BT in a way that is attentive to all variables specified and to their posterior probabilities.

We demonstrate the use of BMA to address variable selection uncertainty, and present estimation results and BT value calculations showing that BMA narrows the confidence intervals on BT values and reduces but does not eliminate the influence of insignificant variables on calculated BT values.

Bayesian Model Averaging

General principles

BMA was first proposed in 1978 by Leamer, who pointed out that the information for estimating regression coefficients might be diluted if there is uncertainty about the model, because part of the information in the data is used to specify the model. To avoid this problem, BMA, rather than selecting a single model and generating a single point estimate, bases its inference on several or even all possible models by taking the average of the parameter of interest obtained from each model weighted by its posterior model probability. In this manner, less information is sacrificed to refine the model.

In the case of k independent variables in \mathbf{X} , there are $R = 2^k$ possible models, $\mathbf{M} = (M_1, \dots, M_r)$, each taking the form $Y = f(\mathbf{X}_i)$ where \mathbf{X}_i is a subset of \mathbf{X} . The posterior distribution of Y can be expressed as

$$p(Y | w) = \sum_{r=1}^R p(Y | M_r, w) p(M_r | w) \quad (1)$$

where w denotes the observed data, $p(Y | M_r, w)$ is the posterior distribution of Y under

model M_r , and $p(M_r | w)$ denotes the posterior probability that M_r is the true model given the data. The posterior model probability of model M_r can be expressed as

$$p(M_r | w) = \frac{p(w | M_r)p(M_r)}{\sum_{l=1}^R p(w | M_l)p(M_l)} \quad (2)$$

where

$$p(w | M_r) = \int p(w | Y, M_r)p(Y | M_r)dY$$

is the marginal likelihood of model M_r , and $p(w | Y, M_r)$ and $p(Y | M_r)$ are the likelihood and the prior for Y under model M_r .

BMA inference for wetland values

We begin with a full model for meta analysis of wetlands values in the US. Earlier versions of this model were reported in Borisova-Kidder (2006), Chen (2010), and Randall *et al.* (2008). The full model was estimated by OLS using data from 72 observations and a log-linear specification, and while goodness of fit was respectable only 4 of 23 independent variables were significant (Tables 1 and 2). Backward elimination of insignificant variables increased adjusted-R² but would allow only 4 site and project descriptors to influence calculated BT values. Intuition suggests that the full model may accord too much influence to insignificant variables in calculated BT values, but the reduced model may err by using none of the information for variables that are statistically insignificant. So, we implemented BMA, hypothesizing that it would yield predicted BT preferred to those from the above models.

Like classical approaches, BMA can provide point estimates and confidence intervals for the quantities of interest, and can therefore support hypothesis testing. However, unlike classical approaches, inferences from BMA can account for the concerns of variable selection uncertainty. Since the quantity of interest in this study focuses on the estimated model parameters, the following value derivations are centered on these quantities.

A Bayesian approach to hypothesis testing considers the posterior probability that the model parameter, say β_1 , is not equal to zero. This posterior probability can be interpreted as the probability that a particular parameter is part of the true model. It is the sum of the posterior model probabilities of the models that include the corresponding variable X_1 , i.e.

$$p(\beta_1 \neq 0 | w) = \sum_{M_r: X_1 \in M_r} p(M_r | w). \quad (3)$$

The point estimate of β_1 , can be derived through the following equation:

$$E(\beta_1 | w) = \sum \hat{\beta}_1^r p(M_r | w). \quad (4)$$

This is a weighted average of model-specific point estimates, where $\hat{\beta}_1^r$ is the posterior mean of β_1 under model M_r , whose weight is $p(M_r | w)$. If the variable X_1 is not in model M_r , then $\hat{\beta}_1^r$ is set to zero.

The posterior standard deviation of β_1 can be derived by taking the square root of the following equation:

$$\text{Var}(\beta_1 | w) = \sum \{(\text{var}(\beta_1 | w, M_k) + (\beta_1^r)^2) p(M_r | w) - E(\beta_1 | w)^2\}. \quad (5)$$

Model Description

Basic Framework. Since there are $R = 2^k$ models in the model space $\mathbf{M} = (M_1, \dots, M_r)$, each model under consideration is of the form $Y = \alpha t_N + X_r \beta_r + \varepsilon$, where N denotes the number of observations, t_N is a $N \times 1$ vector of ones, X_r is a $N \times k_r$ matrix containing some (or all) columns of X , and ε is a N -vector of errors, which is assumed to be $N(0_N, h^{-1} I_N)$.

The Prior. The computational demand of BMA when the vector X is relatively large is an important concern. Using a Normal-Gamma natural conjugate prior greatly reduces the computational time for implementing BMA, since these types of priors lead to analytical posteriors that do not require posterior simulations. Because α and h are common parameters to all models, we use the following standard non-informative priors for these two parameters: $p(\alpha) \propto 1$, and $p(h) \propto \frac{1}{h}$.

We follow the suggestion of Fernandez *et al.* (2001) and Koop and Potter (2004) to standardize explanatory variables by subtracting their means. As a result, the intercept for each model can be interpreted as measuring the mean of w .

The natural conjugate Normal-Gamma prior then implies that the prior for β is

$p(\beta_r | h) \sim N(\underline{\beta}_r, h^{-1} \underline{V}_r)$. For the choice of $\underline{\beta}_r$, we follow standard BMA practice by centering the distribution of β on zero. With $\underline{\beta}_r = 0_{k_r}$, the null hypothesis is that the independent variables have no effects on wetland values.

For the choice of \underline{V}_r , we use a benchmark prior called a *g - prior*, introduced by Zellner (1986), which takes the form $\underline{V}_r = (g_r X_r' X_r)^{-1}$. This prior is commonly used in the literature since it only requires researchers to elicit the scalar prior hyper-parameter g_r .

The Posterior and Marginal Likelihood. Using the natural conjugate Normal-Gamma prior, the posterior for β_r follows a multivariate t distribution with mean

$$E(\beta_r | w, M_r) = \bar{\beta}_r = \bar{V}_r X_r' w \text{ and covariance matrix } \text{var}(\beta_r | w, M_r) = \frac{v_s r}{v-2} \bar{V}_r, \text{ with } \bar{v} = N$$

degrees of freedom. Furthermore, $\bar{V}_r = ((1 + g_r) X_r' X_r)^{-1}$ and

$$\frac{1}{g_r + 1} w' P_{X_r} y + \frac{g_r}{g_r + 1} (w - \bar{w}_N)' (w - \bar{w}_N) \text{, where } P_{X_r} = I_N - X_r (X_r' X_r)^{-1} X_r' \text{. Using the}$$

g - prior, the marginal likelihood for model M_r is

$$p(w | M_r) \propto \left(\frac{g_r}{1 + g_r} \right)^{\frac{k_r}{2}} \left[\frac{1}{1 + g_r} w' P_{X_r} w + \frac{g_r}{1 + g_r} (w - w t_N)' (w - \bar{w}_N) \right]^{\frac{N-1}{2}}.$$

With this marginal likelihood, the posterior model probability can be calculated from the equation (2).

Since we do not favor any model *a priori*, equal prior model probability is assigned to each model. As a result, $p(M_r)$ and $p(M_l)$ will be canceled out in equation (2). We follow the suggestions of Fernandez et al. (2001) with the choice of value for g_r in the following form

$$g_r = \begin{cases} \frac{1}{K^2} & \text{if } N \leq K^2 \\ \frac{1}{N} & \text{if } N > K^2 \end{cases}$$

Markov Chain Monte Carlo Model Composition. Since the number of models ($R = 2^k$) under consideration might be quite large, it may be impossible for researchers to evaluate the posterior mean or model probability for every possible model. In this study, we apply a commonly-used algorithm, the Markov Chain Monte Carlo Model Composition (MC³), initially developed by Madigan and York (1995), to carry out BMA. The MC³ algorithm generates a candidate model from regions of the model space in the neighborhood of the current draw. In our application a candidate model M^* is generated from a set of models including the current model, $M^{(s-1)}$, all models with one explanatory variable deleted from the current model, and all models with one explanatory variable added to the current model.

The acceptance probability has the form: $\min \left[\frac{p(w | M^*)p(M^*)}{p(w | M^{(s-1)})p(M^{(s-1)})}, 1 \right]$.

If the candidate model is not accepted, this chain will remain at the current model $M^{(s-1)}$. Again, since we do not favor any model *a priori*, $p(M^*)$ and $p(M^{(s-1)})$ will be canceled out in the above equation.

Comparing Results: the Full Model, the Reduced Model, and BMA

Predictive performance: BT values

BT scenarios were specified for freshwater (scenarios 1 and 1a, Tables 3 and 4) and saltwater marshes (scenarios 2 and 2a), with Income, RecFish, ComFish, Bird, and Publish set at their median values, Acres at 10,000, Share at .125, the remaining wetlands services at .5, and the estimation method at CVM. Scenarios 1a and 2a specify a wetland in region 2, whereas in scenarios 1 and 2 the wetland is in the default region 4.

Note first that backward elimination of insignificant variables and BMA both generate BT value predictions with substantially narrower intervals than the full model (Table 4). Now, consider the variable R2 (= 1 if the study site is in region 2). R2 does not approach significance in the full model ($p = .54$), and does not appear in the reduced model (Table 2). Median BT values for typical wetlands calculated from the full model are \$300/acre/year for a freshwater marsh and \$81 for a saltwater marsh in region 4 (the default), but \$796 and \$214 respectively for wetlands in region 2. This seems a rather large response to a variable that is quite insignificant and, if the full model is used in BT, would suggest that wetlands conservation projects in region 2 are typically more than 2½ times more valuable per acre than those in region 4. Alternatively, BT values calculated from the reduced model make no distinction between wetlands in region 2 and region 4 (or any of the other regions). The

decision as to which model to use in BT clearly is highly consequential, yet standard BT methods call upon analysts and their clients to make such decisions without clear guidance.

The BT value predictions using BMA suggest a much smaller influence of R2 than the full model. Yet the BMA process that accords R2 and the other RHS variables weights reflecting their posterior probabilities has some more substantial effects on BT values. As the difference between median BT values for scenarios 1 and 1a, and 2 and 2a, shrinks, value attributed to S1 rises considerably, and the median BT values for saltwater marsh rise in both regions but moreso in the default region. It is clear that the 18 variables other than the 4 significant ones and R2 collectively provide information that has non-trivial influence on calculated BT values.

Conclusions

Theory suggests that, given variable selection uncertainty, BMA is *a priori* a preferable alternative to model selection (i.e. to selecting a single “best” model) because it provides better average predictive performance than any single model (Hoeting *et al.* 1999). Here, we argue that variable selection uncertainty is a serious, if unappreciated, problem in meta analysis for benefits transfer, and we demonstrate that BMA generates predicted BT values that reduce but do not eliminate the influence of insignificant variables. The precision of BT value predictions, as indicated by confidence intervals, is similar for BMA and backward elimination of insignificant variables, and both provide much more precise value predictions than the full model. Collectively, the set of insignificant variables may have, as intuition suggests they often should, non-trivial influence on predicted BT values. We conclude that Bayesian Model Averaging provides a superior method of resolving variable selection uncertainty in meta analysis for benefits transfer.

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Table 1. Variables in Full Model

Variable	Description
<i>Dependent variable</i>	
LNVALUE	Logarithm of value per acre of wetland, U.S. year 2003 dollars
INTERCEPT	
<i>Socio-economic variables</i>	
INCOME	Annual household income, U.S.
<i>Wetland size</i>	
ACRES	No. of wetland acres (,000) valued
SHARE	Share of wetland acres in the area by FIPS codes as reported by the NRI 1997 data
<i>Wetland types</i>	
FRESHWATER MARSH	1 if a freshwater marsh, 0 if not
SALTWATER MARSH	1 if a saltwater marsh, 0 if not
SWAMP	1 if a swamp, 0 if not
PRAIRIE POTHOLE	1 if a prairie pothole, 0 if not
<i>Wetland functions</i>	
WATER SUPPLY	1 if water supply augmented, 0 if not
QUALITY	1 if water quality improvement, 0 if not
FLOOD	1 if flood reduction, 0 if not
RECFISH	1 if recreational fisheries improved, 0 if not
COMFISH	1 if commercial fisheries improved, 0 if not
BIRD	1 if bird/wildlife-related recreation, 0 if not
AMENITY	1 if amenities augmented, 0 if not
HABITAT	1 if habitat is augmented, 0 if not
<i>Methodological variables</i>	
CVM	1 if study used Contingent Valuation Method, 0 if not
HP	1 if study used Hedonic Pricing Method, 0 if not
TCM	1 if study used Travel Cost Method, 0 if not
RC	1 if study used Replacement Cost Method, 0 if not
PFMPNFI	1 if study used Production Function or Market Prices or Net Factor Income Method, 0 if not
EA	1 if study used Energy Analysis Method, 0 if not
PUBLISH	1 if study is a journal article, 0 if not
<i>Regions</i>	
R1	1 if study conducted in Northern crescent or Northern great plains, 0 if not
R2	1 if study conducted in Fruitful rim or Southern seaboard, 0 if not
R3	1 if study conducted in Heartland or Mississippi portal, 0 if not
R4	1 if study conducted in Prairie gateway=1 or Eastern uplands, 0 if not

Table 2. Parameter estimates

	FULL (OLS)		Backward Elimination		Bayesian Model Averaging		
	Coefficient	Std Error	Coefficient	Std Error	Mean (βD)	Std Error (βD)	Pr ($\beta \neq 0 D$)
Intercept	0.890	(2.37)	0.836	(1.55)			
Income	0.145**	(0.06)	0.134***	(0.03)	0.1067	(0.0462)	0.9122
Acres	-1.589E-7	(2.68E-7)			-6.22E-09	(6.04E-08)	0.0509
Share Freshwatermarsh	-4.824	(4.07)			-0.1249	(0.8482)	0.0584
Saltwatermarsh	-1.653	(1.12)	-1.444*	(0.87)	-0.0464	(0.5857)	0.1436
Prairiepothole	-2.969**	(1.33)	-3.220***	(0.94)	-1.4275	(1.1689)	0.6887
Watersupply Quality	-4.430***	(1.56)	-4.045***	(1.04)	-2.4768	(1.2475)	0.8810
Flood	0.821	(1.01)			0.0033	(0.1726)	0.0476
RecFish	1.106	(0.80)			1.6851	(0.8489)	0.8706
ComFish	0.195	(0.71)			0.0207	(0.1724)	0.0535
Bird	0.852	(0.65)			0.0581	(0.2397)	0.0915
Amenity	0.596	(0.82)			0.0111	(0.1674)	0.0504
Habitat	-0.335	(0.74)			0.0069	(0.1274)	0.0479
Publish	-0.792	(1.11)			-0.0154	(0.1847)	0.0509
EA	0.516	(0.78)			0.0477	(0.2451)	0.0750
PFMPNFI	-0.209	(0.97)			0.0013	(0.1315)	0.0461
CVM	5.985***	(1.86)	6.685***	(1.34)	6.3377	(1.4921)	0.9960
HP	-1.446	(1.04)			-0.5250	(0.8853)	0.3121
TCM	-0.242	(0.91)			0.0325	(0.2120)	0.0626
R1	0.213	(1.79)			9.77E-04	(0.2619)	0.0444
R2	-0.274	(1.35)			-0.0084	(0.2314)	0.0450
R3	0.564	(1.79)			0.0076	(0.1497)	0.0488
N	0.977	(1.61)			-0.0076	(0.1912)	0.0514
Num. of Var.	1.232	(1.56)			-0.0118	(0.2066)	0.0523
R ² (Adj-R ²)		72		72			
		23		5			
	0.5920 (0.3965)		0.551 (0.502)				

Table 3. Scenarios for Benefits Transfer

Variables ↓\Scenarios →	1	2	1a	2a
Intercept	1	1	1	1
Income	43	43	43	43
Acres	10000	10000	10000	10000
Share	0.125	0.125	0.125	0.125
Freshwatermarsh	1	0	1	0
Saltwatermarsh	0	1	0	1
Prairiepothole	0	0	0	0
Watersupply	0.5	0.5	0.5	0.5
Quality	0.5	0.5	0.5	0.5
Flood	0.5	0.5	0.5	0.5
RecFish	0.319	0.319	0.319	0.319
ComFish	0.278	0.278	0.278	0.278
Bird	0.38	0.38	0.38	0.38
Amenity	0.5	0.5	0.5	0.5
Habitat	0.5	0.5	0.5	0.5
Publish	0.694	0.694	0.694	0.694
EA	0	0	0	0
PFMPNFI	0	0	0	0
CVM	1	1	1	1
HP	0	0	0	0
TCM	0	0	0	0
R1	0	0	0	0
R2	0	0	1	1
R3	0	0	0	0

Table 4. Calculated BT Values

Estimation Method	Scenario	Median	90% CI Lower	90% CI Upper	Width of CI
Full model	S1	299.891	28.750	3369.504	3340.754
	S1a	796.296	157.299	3903.496	3746.196
	S2	80.480	5.396	1200.661	1195.265
	S2a	213.697	32.830	1351.405	1318.574
Backward Elimination	S1	732.400	457.299	1174.946	717.648
	S1a	-	-	-	-
	S2	100.342	45.318	220.843	175.525
BMA	S2a	-	-	-	-
	S1	678.775	405.915	1133.263	727.348
	S1a	676.838	399.021	1157.026	758.005
	S2	239.861	129.375	462.843	333.468
	S2a	236.494	126.500	460.986	334.486