

Semiparametric Bayesian Analysis of Simultaneous Systems With an Application to Japanese Meat Demand¹

Jing Xi, Thomas Heckelei, and Ron C. Mittelhammer²

Washington State University

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Abstract

This paper motivates and applies a variant of the Bayesian Bootstrap Multivariate Regression by Heckelei and Mittelhammer (2003) to a Japanese meat demand specification with endogenous regressors. The methodology is first given an alternative and more elegant motivation and then extended to incorporate microtheoretic restrictions and to apply in the context of a simultaneous equation models. The results of the application are compared to results based on an earlier approach used by Heckelei, Mittelhammer, and Wahl (1996).

***JEL Classification:* C11, C15, C30**

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² Jing Xi is a graduate student in the Department of Economics, Thomas Heckelei is Assistant Professor, IMPACT Center and Department of Agricultural and Resource Economics and, and Ron Mittelhammer is a Professor in the Department of Agricultural and Resource Economics and in the Department of Statistics, Washington State University, USA. No senior authorship is assigned. Contact e-mail: heckelei@wsu.edu,

1. Introduction

Heckelei and Mittelhammer (2002) introduced a semiparametric methodology, the "Simultaneous Equations Bayesian Bootstrap" (SEBB), for Bayesian analysis of simultaneous equations that replaces the usual explicit specification of a parametric likelihood function with a bootstrapped representation of the likelihood of the parameters. Their methodology is based on simulated distributional mappings from the error distribution to the parameters of the model. The method is a completely computer-driven, simulation-based method for conducting Bayesian estimation and inference that fully avoids the oftentimes very difficult and even intractable derivations attendant to more complex Bayesian problems involving flexible combinations of prior distributions and likelihood functions. Moreover, the approach obviates the need for any specific functional specification of the likelihood function, thus eliminating the possibility of misspecification of the model in this regard and imparting a degree of model specification robustness to the analysis.

In this paper, a new full-rank distributional mapping from the error distribution to the parameters of the model is presented. This new full-rank mapping is more efficient in terms of information completeness because the projection from the error to the parameters is based on a full rank projection matrix rather than one of less-than-full rank, as was the mapping used by Heckelei and Mittelhammer (2002).

The paper is structured in the following way: First, the concept of a *Bayesian Data Information Mapping* (BDIM) is presented, which identifies a semiparametric analogue to the mapping of error distributions to parameters that occurs in standard parametric Bayesian contexts. Then a brief review of the relation between reduced form and structural parameter

distributions within the Bayesian paradigm is given. Third, the theory underlying the algorithm for obtaining posterior distributions of structural parameters using outcomes from an ignorance based posterior distribution of reduced form parameters is described. Fourth, a computational approach is described that allows for generating outcomes from the posterior distributions of structural parameters based on sample data. Finally, the functionality of the approach is illustrated by an empirical application to a Japanese meat demand system, providing a substantive illustration of the semiparametric technique and allowing a comparison of empirical results to both the previous semiparametric method suggested by Heckelei and Mittelhammer (2002) and to a Classical 3SLS estimation of parameters.

2. Bayesian Bootstrap Multivariate Regression (BBMR) Reconsidered and Extended

This section provides the methodological background underlying the semiparametric Bayesian analysis of the Japanese meat demand model presented later in the paper. Although the general concepts follow recent publications, several new contributions are made in this methodological section of the paper:

- 1) The BBMR approach introduced by Heckelei and Mittelhammer (2003) is motivated in a new and more elegant fashion based on the idea of a simultaneous mapping of error distributions to location and scale parameters.
- 2) The BBMR is extended from a multivariate regression setting characterized by identical regressor matrices across equations, as is typical in unrestricted reduced form specifications, to the case where regressor matrices differ by equations, as is often encountered in the specification of simultaneous systems of equations.

- 3) The method is modified to accommodate exact linear restrictions on model parameters.

2.1 Simultaneous BBMR Mapping

Consider the multivariate regression model with m equations given by

$$(2.1) \quad \mathbf{Y} = \mathbf{X} \mathbf{\Pi} + \mathbf{V},$$

where \mathbf{Y} is a $(n \times m)$ matrix of observations on m endogenous variables, \mathbf{X} is a $(n \times k)$ matrix of observations on k exogenous variables, $\mathbf{\Pi}$ is a $(k \times m)$ matrix of regression coefficients, and \mathbf{V} is a $(n \times m)$ matrix representing iid outcomes of a $1 \times m$ disturbance vector $\mathbf{V}_i = \mathbf{V}[\mathbf{i}, \cdot]$, $i = 1, \dots, n$, having some joint density function $g(\cdot | \mathbf{0}, \Sigma)$ with mean vector $\mathbf{0}$ and covariance matrix Σ . It is assumed that the covariance matrix Σ and the parameter matrix $\mathbf{\Pi}$ are not functionally related. Begin with the probability distribution of the residual vector and consider the transition to the likelihood function for the parameters, as is standard in Bayesian analyses of the linear model. Given the linear model structure (2.1) underlying the data generating process, the probability distribution of the random vector \mathbf{V} can be thought of as being transferred to the random vector $\mathbf{Y} - \mathbf{X}\mathbf{\Pi}$, where the Jacobian of this type of transformation is always the identity matrix and is thus immaterial in the transfer. In effect, the argument, \mathbf{V} , of the residual density function is replaced by the argument $\mathbf{Y} - \mathbf{X}\mathbf{\Pi}$ in establishing the joint probability density function of the random sample \mathbf{Y} , and in defining the likelihood function of the parameters. Specifically,

$$(2.2) \quad g(\mathbf{V} | \Sigma) = g(\mathbf{Y} | \mathbf{X}, \mathbf{\Pi}, \Sigma), \text{ for } \mathbf{Y} = \mathbf{X}\mathbf{\Pi} + \mathbf{V},$$

by the direct substitution of $\mathbf{Y} - \mathbf{X}\boldsymbol{\Pi}$ for \mathbf{V} . This step in the process of defining the likelihood function is a dimension preserving transformation from \mathbb{R}^{nm} (the dimension of \mathbf{V}) to \mathbb{R}^{nm} (the dimension of \mathbf{Y}).

In making the subsequent transition to the likelihood function, one engages in a dimension-reducing transformation whereby the function $g(\mathbf{Y} | \mathbf{X}, \boldsymbol{\Pi}, \boldsymbol{\Sigma})$ of the nm elements in \mathbf{Y} is changed to a function of the $(km + m(m+1)/2)$ arguments in $\boldsymbol{\Pi}$ and $\boldsymbol{\Sigma}$, leading to the likelihood function

$$(2.3) \quad L(\boldsymbol{\Pi}, \boldsymbol{\Sigma} | \mathbf{Y}, \mathbf{X}).$$

For further motivation consider a modified version of (2.1) defined as

$$(2.4) \quad \mathbf{Y} = \mathbf{X}\boldsymbol{\Pi} + \mathbf{U}\mathbf{T} = (\mathbf{X} \quad \mathbf{U}) \begin{pmatrix} \boldsymbol{\Pi} \\ \mathbf{T} \end{pmatrix}$$

where the rows of the $(n \times m)$ matrix of residuals, \mathbf{U} , are iid outcomes from a probability distribution $g(\cdot | \mathbf{0}, \mathbf{I})$ having a mean vector of $\mathbf{0}$ and a covariance matrix of \mathbf{I} . The density of $\mathbf{V}_i = \mathbf{V}[\mathbf{i}, \cdot] = \mathbf{U}[\mathbf{i}, \cdot]\mathbf{T}$ is then $g(\mathbf{V}_i | \mathbf{0}, \mathbf{T}'\mathbf{T})$ for any conformable \mathbf{T} with full column rank, and the $(m \times m)$ matrix \mathbf{T} is a matrix for which $\boldsymbol{\Sigma} = \mathbf{T}'\mathbf{T}$, so that $\mathbf{V}_i = \mathbf{U}[\mathbf{i}, \cdot]\mathbf{T} \sim g(\mathbf{V}_i | \mathbf{0}, \boldsymbol{\Sigma}) \forall i$.

Now consider the admissible values of $\boldsymbol{\Pi}$ and \mathbf{T} . Note that in the absence of prior information to the contrary, the values of $\boldsymbol{\Pi}$ and \mathbf{T} are clearly coincident with the value of $\mathbf{V} = \mathbf{U}\mathbf{T}$ that satisfies the relationship $\mathbf{V} = \mathbf{U}\mathbf{T} = \mathbf{Y} - \mathbf{X}\boldsymbol{\Pi}$, given the data \mathbf{Y} and \mathbf{X} . This implies that one can view the likelihood weighting on $(\boldsymbol{\Pi}, \mathbf{T})$ as being coincident with the PDF weighting on the value of \mathbf{U} , say $U(\boldsymbol{\Pi}, \mathbf{T}) \equiv (\mathbf{Y} - \mathbf{X}\boldsymbol{\Pi})\mathbf{T}^{-1}$, that corresponds to $\boldsymbol{\Pi}$ and \mathbf{T} . That is,

$$(2.5) \quad L(\boldsymbol{\Pi}, \mathbf{T} | \mathbf{Y}, \mathbf{X}) \equiv g(U(\boldsymbol{\Pi}, \mathbf{T})).$$

Moreover, the joint posterior density of $(\mathbf{\Pi}, \mathbf{T})$ can then be represented in the form

$$(2.6) \quad p(\mathbf{\Pi}, \mathbf{T}) \propto L(\mathbf{\Pi}, \mathbf{T} | \mathbf{Y}, \mathbf{X}) p_{\mathbf{T}}(\mathbf{T}) \equiv g(\mathbf{U}(\mathbf{\Pi}, \mathbf{T})) p_{\mathbf{T}}(\mathbf{T})$$

where we are temporarily considering the case where an improper prior

$$(2.7) \quad p_{\mathbf{\Pi}}(\mathbf{\Pi}) \propto c > 0$$

is being used to convey ignorance regarding the values of the unknown $\mathbf{\Pi}$ parameters of the model, $p_{\mathbf{T}}(\mathbf{T})$ denotes the prior on \mathbf{T} (which could also be improper), and we are assuming that prior information on $\mathbf{\Pi}$ and \mathbf{T} are independent.

Now suppose that we have an outcome of the matrix \mathbf{U} . Then, any solution $\begin{pmatrix} \mathbf{\Pi} \\ \mathbf{T} \end{pmatrix}$ to the matrix equation $(\mathbf{X} \quad \mathbf{U}) \begin{pmatrix} \mathbf{\Pi} \\ \mathbf{T} \end{pmatrix} = \mathbf{Y}$ is necessarily expressible uniquely via an application of the generalized inverse of $(\mathbf{X} \quad \mathbf{U})$ given by

$$(2.8) \quad (\mathbf{X} \quad \mathbf{U})^- = \left[(\mathbf{X} \quad \mathbf{U})' (\mathbf{X} \quad \mathbf{U}) \right]^{-1} (\mathbf{X} \quad \mathbf{U})', \text{ to yield}$$

$$\begin{pmatrix} \mathbf{\Pi} \\ \mathbf{T} \end{pmatrix} = \left[(\mathbf{X} \quad \mathbf{U})' (\mathbf{X} \quad \mathbf{U}) \right]^{-1} (\mathbf{X} \quad \mathbf{U})' \mathbf{Y} = \begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{U} \\ \mathbf{U}'\mathbf{X} & \mathbf{U}'\mathbf{U} \end{bmatrix}^{-1} \begin{pmatrix} \mathbf{X}'\mathbf{Y} \\ \mathbf{U}'\mathbf{Y} \end{pmatrix},$$

Using the partitioned inverse and substituting $\mathbf{X}\hat{\mathbf{\Pi}} + \hat{\mathbf{V}}$ for \mathbf{Y} in the process, where $\hat{\mathbf{\Pi}}$ and $\hat{\mathbf{V}}$ are the least squares estimates of regression coefficients and residuals, yields the following mappings from \mathbf{U} to $\mathbf{\Pi}$ and \mathbf{T} :

$$(2.9) \quad \begin{pmatrix} \mathbf{\Pi} \\ \mathbf{T} \end{pmatrix} = \begin{pmatrix} \hat{\mathbf{\Pi}} - (\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{U} (\mathbf{U}'\mathbf{M}_{\mathbf{X}}\mathbf{U})^{-1} \mathbf{U}'\hat{\mathbf{V}} \\ (\mathbf{U}'\mathbf{M}_{\mathbf{X}}\mathbf{U})^{-1} \mathbf{U}'\hat{\mathbf{V}} \end{pmatrix} = \begin{pmatrix} \hat{\mathbf{\Pi}} - (\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\mathbf{U}\mathbf{T} \\ (\mathbf{U}'\mathbf{M}_{\mathbf{X}}\mathbf{U})^{-1} \mathbf{U}'\hat{\mathbf{V}} \end{pmatrix},$$

where $\mathbf{M}_x = \mathbf{I} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$. The expression in (2.9) is fully functionally equivalent to the BBMR results presented by Heckelei and Mittelhammer (2003), but in their paper the result is derived via a two-step procedure that first conditions Π on the value \mathbf{T} , and then mixes the conditioned Π values over the \mathbf{T} values implied by the representation of \mathbf{T} in equation (9). The resulting posterior automatically incorporates the standard ignorance prior on $\{\Pi, \Sigma\}$ given by $p(\Pi, \Sigma) \propto |\Sigma|^{-(m+1)/2}$ (for a formal proof, see Heckelei and Mittelhammer, 2003) so that the Π 's generated by mapping \mathbf{U} 's into the parameters via (9) can be interpreted as outcomes from the marginal posterior distribution of Π . For example, under the special case of a normal error distribution, the implied posterior distribution for Π coincides identically with the matrix-t posterior implied by a full parametric Bayesian analysis under the assumption of a multivariate normal error distribution, as demonstrated by Heckelei and Mittelhammer (2003).

Note that the conceptual development to this point provides an important practical contribution to computational *parametric* Bayesian methodology with considerable empirical relevance. In particular, one can construct a generic algorithm based on the preceding sampling strategy that allows sampling from an ignorance prior-based posterior distribution of the regression parameters associated with any given residual density, and the likelihood function that it implies, only assuming that the regression and covariance matrix parameters are functionally independent of one another. No case-by-case analytical derivations of posterior distributions for inference purposes are necessary – the procedure allows sampling from the posterior in any case. Informative prior information on the Π parameters can be straightforwardly incorporated into posterior analyses using an importance sampling approach.

A semiparametric version of the sampling methodology presented in the preceding section can be constructed through the use of a nonparametric representation of the residual distribution. We focus here on Efron's bootstrap, but in principle sampling from any empirical distribution function-type representation of the residual distribution (e.g., kernel density, empirical likelihood) might also be considered. Bootstrapped outcomes from least squares residuals, appropriately transformed to residuals with an identity covariance matrix, represent approximations to outcomes from the empirical distribution function of \mathbf{U} . These bootstrapped outcomes can be utilized for the outcomes of the errors in the sampling methodology outlined above. It is important to note that the bootstrap needs to preserve the covariance structure of the error by sampling complete rows from the matrix of least squares residuals.

2.2 Incorporating Exact Restrictions on Parameters

The Bayesian framework developed above can be straightforwardly extended to incorporate non-degenerate prior distributions or inequality constraints using an importance sampling approach. However, the majority of econometric models derived from microeconomic theory require the imposition of *equality* restrictions. This is true for the Japanese meat demand model considered later in this paper. Consequently, the preceding BBMR approach is extended to impose g exact restrictions on $\mathbf{\Pi}$. For this purpose we rewrite model (2.1) in stacked form to obtain

$$(2.10) \quad \begin{aligned} \text{vec}(\mathbf{Y}) &= (\mathbf{I}_m \otimes \mathbf{X}) \text{vec}(\mathbf{\Pi}) + \text{vec}(\mathbf{V}) \\ \Leftrightarrow \mathbf{Y}_s &= \mathbf{X}_s \mathbf{\Pi}_s + \mathbf{V}_s \end{aligned}$$

where $\mathbf{Y}_s \equiv \text{vec}(\mathbf{Y})$, $\mathbf{X}_s \equiv (\mathbf{I}_m \otimes \mathbf{X})$, $\mathbf{\Pi}_s \equiv \text{vec}(\mathbf{\Pi})$, and $\mathbf{V}_s \equiv \text{vec}(\mathbf{V})$. Then the restrictions can be expressed as

$$(2.11) \quad \mathbf{r} = \mathbf{R}\boldsymbol{\Pi}_S,$$

where \mathbf{r} is $g \times 1$ and \mathbf{R} is $g \times km$. Now note that the generalized inverse of the full row rank matrix \mathbf{R} is given by

$$(2.12) \quad \mathbf{R}^- = \mathbf{R}'(\mathbf{R}\mathbf{R}')^{-1},$$

and using (2.12), we can rewrite $\boldsymbol{\Pi}_S$ in (2.11) as

$$(2.13) \quad \boldsymbol{\Pi}_S = \mathbf{R}^- \mathbf{r} + (\mathbf{I} - \mathbf{R}^- \mathbf{R}) \mathbf{h},$$

where \mathbf{h} is a $km \times 1$ vector that can be chosen arbitrarily. Substituting (2.13) into (2.10) and some algebraic rearrangement yields the equation system

$$(2.14) \quad (\mathbf{Y}_S - \mathbf{X}_S \mathbf{R}^- \mathbf{r}) = \mathbf{X}_S (\mathbf{I} - \mathbf{R}^- \mathbf{R}) \mathbf{h} + \mathbf{V}_S.$$

A singular value decomposition of $(\mathbf{I} - \mathbf{R}^- \mathbf{R})$, given by $\mathbf{P}\boldsymbol{\Lambda}\mathbf{P}'$, allows a transformation of the equation system to be defined as

$$(2.15) \quad \begin{aligned} (\mathbf{Y}_S - \mathbf{X}_S \mathbf{R}^- \mathbf{r}) &= \mathbf{X}_S \mathbf{P} \boldsymbol{\Lambda} \mathbf{P}' \mathbf{h} + \mathbf{V}_S \\ &= (\mathbf{X}_S \mathbf{P}_* \boldsymbol{\Lambda}_*) \mathbf{P}'_* \mathbf{h} + \mathbf{V}_S = (\mathbf{X}_S \mathbf{P}_*) \mathbf{P}'_* \mathbf{h} + \mathbf{V}_S, \\ &\Leftrightarrow \mathbf{Y}_{S^*} = \mathbf{X}_{S^*} \boldsymbol{\xi} + \mathbf{V}_S \end{aligned}$$

where $\mathbf{Y}_{S^*} \equiv (\mathbf{Y}_S - \mathbf{X}_S \mathbf{R}^- \mathbf{r})$, $\mathbf{X}_{S^*} \equiv \mathbf{X}_S \mathbf{P}_*$, $\boldsymbol{\xi} \equiv \mathbf{P}'_* \mathbf{h}$, the columns of \mathbf{P}_* are the eigenvectors

associated with the $km - g$ unit eigenvalues of the idempotent matrix $(\mathbf{I} - \mathbf{R}^- \mathbf{R})$, and $\boldsymbol{\Lambda}_*$ is a

diagonal matrix with these unit eigenvalues on the diagonal, which is then clearly a $km - g$

dimensional identity matrix, $\boldsymbol{\Lambda}_* = \mathbf{I}_{km-g}$.

The bootstrap procedure for sampling the residual distribution, suggested in the previous subsection, can now be applied to the transformed system (2.15).³ Subsequently, the bootstrapped outcomes of ξ can be transformed back to obtain restricted posterior outcomes of Π_S as

$$(2.16) \quad \Pi_S = \mathbf{P}_* \xi .$$

2.3 Extension to Systems with Varying Regressor Matrices

The approach outlined in the previous two subsections can be straightforwardly generalized to a restricted (incomplete) simultaneous equation system such as the Japanese meat demand model employed below. The main conceptual difference is that each equation potentially has different regressor matrices such that the blocks of \mathbf{X}_S are not necessarily identical in values or dimension, and so for example in (10) the block diagonal matrix $(\mathbf{I}_m \otimes \mathbf{X})$ would need to be replaced by the appropriate block diagonal matrix containing the differing regressor matrices along the diagonal block. For example, consider an incomplete simultaneous system of equation with one structural equation and $m-1$ reduced form equations⁴

$$(2.17) \quad \begin{aligned} \mathbf{y}_1 &= \mathbf{Y}_1 \boldsymbol{\gamma}_1 + \mathbf{X}_1 \boldsymbol{\beta}_1 + \boldsymbol{\varepsilon}_1 \\ \mathbf{Y}_1 &= \mathbf{X} \boldsymbol{\Pi}_1 + \mathbf{V}_1 \end{aligned}$$

The stacked form of this system, which would enter into the semiparametric mapping developed above, can be written as

³ One need to be aware, however, that the bootstrap sample of \mathbf{V}_S still needs to preserve the assumed covariance structure of the original system by sampling corresponding elements of all equations together.

⁴ The Japanese meat demand model considered below is of this type with the exception that there are 5 structural equations.

$$(2.18) \quad \begin{pmatrix} \mathbf{y}_1 \\ \text{vec}(\mathbf{Y}_1) \end{pmatrix} = \begin{pmatrix} (\mathbf{Y}_1 & \mathbf{X}_1) & \mathbf{0} \\ \mathbf{0} & (\mathbf{I}_{m-1} \otimes \mathbf{X}) \end{pmatrix} \begin{pmatrix} \gamma_1 \\ \beta_1 \\ \Pi_1 \end{pmatrix} + \begin{pmatrix} \boldsymbol{\varepsilon}_1 \\ \text{vec}(\mathbf{V}_1) \end{pmatrix}$$

$$\Leftrightarrow \mathbf{y}^* = \mathbf{Z}^* \boldsymbol{\delta} + \mathbf{u}$$

From this point, the mapping of the residual distribution into parameters can proceed as described in sections 2.1 and 2.2.

One might wonder why the simultaneous nature of the random variables in the system specification does not require a different approach when mapping residual outcomes to parameters. This actually follows from the fact that in the Bayesian paradigm, the data are treated as fixed at their observed sample values. Consequently, the principle connection between the equations of a simultaneous equation system is the correlation of the errors across equations, which is fully represented by the approach.

3. Semiparametric Bayesian Analysis of Japanese Meat Demand

As a widely used systems approach for modeling consumption behavior for product groups, the LA/AIDS technique was chosen to estimate the parameters of the Japanese meat demand system. It combines the best of the theoretical features of both the Rotterdam and Translog models with the ease of estimation of the Linear Expenditure System (LES) in terms of allowing adding up, homogeneity and symmetry conditions to be imposed easily through linear restrictions on the parameters of the model. Moreover, the LA/AIDS provides an arbitrary first order approximation to any demand system, satisfies the axioms of choice exactly, and aggregates perfectly over consumers under certain conditions (Deaton and Muellbauer 1980a,b). The AIDS has been used extensively to test the economic theory of the consumer.

This application of the robust BDIM mapping analysis utilizes a linearized AIDS (LAIDS) model of Japanese meat demand, as originally specified by Hayes, et. al. (1990). The share equations of the system can be written as

$$(3.1) \quad w_i = \alpha_i + \sum_j \gamma_{ij} \log p_j + \beta_i \log(E/P), \quad i, j = 1, \dots, m,$$

where w_i is the share of group expenditure allocated to product i , p_j is the price of product j , E is the per capita expenditures on all five meats, and $P = \exp(\sum_j w_j \log p_j)$ denotes Stone's price index.

Additivity, homogeneity and symmetry define linear exact restrictions on the parameters of the LAIDS share equations implied by the utility maximization objective. Referring to the notation in equation (4.1) they are expressed as

$$(3.2) \quad \sum_i \alpha_i = 1; \quad \sum_i \gamma_{ij} = 0; \quad \sum_i \beta_i = 0,$$

$$(3.3) \quad \sum_j \gamma_{ij} = 0,$$

$$(3.4) \quad \gamma_{ij} = \gamma_{ji} \quad \forall i \neq j,$$

respectively. Provided that equations (3.2), (3.3), and (3.4) hold, the estimated demand functions add up to the total expenditure (3.2), are homogenous of degree zero in prices and income (3.3), and satisfy Slutsky symmetry (3.4) (Deaton and Muellbauer 1980b, p.314).

Hayes, et. al. (1990) estimated this model using Japanese expenditure and price data from 1965 to 1986 relating to five different meat groups: Wagyu beef, import quality beef, pork, chicken and fish. These meat groups are denoted by $i = 1, 2, 3, 4, 5$, respectively, in the model specification above. The empirical analysis in this paper follows and updates the line of analysis by Hayes, et. al. (1990), with the data set now spanning the years 1965 to 1999. Because the

meat expenditure shares (w_i) sum to one, the covariance matrix for the meat demand system composed of all five individual expenditure share equations is singular, so one of the equations is dropped to make the system equations estimable. In particular, the fish share equation was chosen for deletion in this study and the parameters for this equation were eventually recovered via symmetry, homogeneity and adding up constraints as expressed in (3.2)-(3.4). The application of an iterative estimation procedure makes the results invariant to the choice of equation for deletion (Barten 1969).

3.1 Data Description

The expenditure and price data were assembled from a variety of yearbooks and reports published by the Japanese ministry of Agriculture, Forestry, and Fisheries. Retail prices for pork and chicken meat are from the *Annual Report on the Family Income and Expenditure Survey*. Retail fish prices, from the same data resource, are calculated as averages of fresh and salted fish prices weighted by the proportional consumption levels of each fish type. Retail Wagyu and dairy beef prices are calculated by multiplying the respective wholesale prices by a markup coefficient of 2.1156, where the data source for these wholesale prices is *Statistics of Meat Marketing and Meat Statistics in Japan*.

Additionally, since the LA/AIDS model employed here only serves as a subsystem of a larger market model, a reduced form necessary for iterative 3SLS estimation does not exist and was replaced by regressing right hand side endogenous variables on instrumental variables. Note that the four remaining share equations are regarded as the structural equations in this model. For further details on the data underlying the instrumental variables, readers are referred to Hayes, et. al. (1990).

3.2 Robust Bayesian Analysis of the LAIDS Model

Two different Bayesian mappings of the restricted structural form coefficients were calculated with symmetry, homogeneity and adding up constraints enforced. These include the 3SLS reduced form (3SLS-RF) mapping, the details of which can be found in Heckeley (1995), and the full rank BBRES mapping described above.

To elucidate the application of the methodology underlying these two mappings, rewrite the LA/AIDS of Japanese meat demand in matrix notation as

$$(4.5) \quad \mathbf{W} = \mathbf{1}_{35} \odot \boldsymbol{\alpha} + \mathbf{Z}\boldsymbol{\delta} + \mathbf{U}$$

where \mathbf{W} is a (35×5) matrix of budget shares, $\mathbf{1}_{35}$ is a (35×1) vector of 1's, $\boldsymbol{\alpha}$ is a (1×5) vector of intercept terms, \odot denotes a Hadamard (elementwise) product, \mathbf{Z} is a (35×6) matrix of right hand side endogenous variables consisting of $\ln(P_i)$, $i=1, \dots, 5$ and $\ln(E/P)$, $\boldsymbol{\delta}$ is a (6×5) matrix of parameters (consisting of the values of γ_{ij} and $\beta_{i,j}$, $i, j=1, \dots, 5$), and \mathbf{U} is a (35×5) matrix of structural errors. The projection of all right hand side endogenous variables of the LA/AIDS subsystem (prices and expenditure), \mathbf{Z} , through the instrument space represented by \mathbf{X} constitutes the relevant reduced form representation that completes the specification of the system.

In brief, we describe the posterior 3SLS reduced form mapping employed by Heckeley 1995, which is related to similar mappings by Zellner, Bauwens and van Dijk (1988) for normally distributed errors. It involves bootstrapping reduced form parameters via the BBMR algorithm presented in section 2.1 (see also Heckeley and Mittelhammer, 2003). Those are then used to construct values of the right hand side endogenous variables of the structural equations, just as one would do in an explicit 2SLS or 3SLS classical procedure. For each outcome of reduced form parameters, and corresponding updated endogenous variables, a classical iterative

restricted 3SLS estimation of the structural parameters is obtained. The collected outcomes of those parameters for all bootstrap samples represent outcomes from this posterior mapping.

Symmetry and homogeneity restrictions for the remaining four equations (recall the share equation for fish has been deleted) model can be formulated as $\mathbf{R} \text{vec}(\delta) = \mathbf{r}$, where \mathbf{R} and \mathbf{r} are a matrix and a vector with dimensions 10×28 and 10×1 , respectively, representing 6 symmetry and 4 homogeneity restrictions for the 28 coefficients contained in the demand system. Those restrictions are imposed for all results presented below but their use is here illustrated for the Bayesian 3SLS-RF mapping. The first iteration of the restricted 3SLS-RF mapping procedure is given by

$$(4.6) \quad \delta^{\text{R3SLS}} = \text{vec}(\delta^{\text{R2SLS}}) + \hat{\mathbf{C}} \mathbf{R}' (\mathbf{R} \hat{\mathbf{C}} \mathbf{R}')^{-1} (\mathbf{r} - \mathbf{R} \text{vec}(\delta^{\text{2SLS}}))$$

where

$$\hat{\mathbf{C}} = [\mathbf{Z}_{*b} \hat{\mathbf{\Omega}}^{-1} \mathbf{Z}_{*b}']^{-1},$$

$$\mathbf{Z}_{*b} = \mathbf{I}_4 \otimes \mathbf{Z}_*, \text{ with } \mathbf{Z}_* \text{ being the updated } \mathbf{Z} \text{ from the BBMR algorithm,}$$

$$\hat{\mathbf{\Omega}} = (\mathbf{W} - \mathbf{Z}_* \delta^{\text{2SLS}})' (\mathbf{W} - \mathbf{Z}_* \delta^{\text{2SLS}}) / n$$

where δ^{2SLS} is a 2SLS-Bayesian-mapping used to construct an appropriate starting value. In subsequent iterations, the updated values of $\hat{\mathbf{C}}$ and $\hat{\mathbf{\Omega}}$ replace the corresponding values in previous iterations and act as new starting values until convergence is achieved.

3.3 Empirical Results

The estimated intercept, price, and expenditure parameters obtained from estimating the Japanese meat demand system using the Classical 3SLS estimator, and the Bayesian 3SLS-RF and full rank BBRES methods, are presented in Table 1, along with standard deviations

corresponding to the parameters. Note that for the two Bayesian methods, the means of the marginal posterior distributions of the parameter estimates are reported, which represent the best Bayesian estimates of the parameters under a quadratic loss criterion. The standard deviations reported for the Bayesian estimates correspond to the standard deviations of the marginal posterior distributions. Thus, the interpretation of Bayesian estimates and standard deviations are markedly different than the results reported for the Classical 3SLS approach.

The interpretation of the parameter estimates themselves is less intuitive than interpreting elasticities implied by them, which we do ahead. However, in the way of comparison between the various parameter estimation results, at least two general patterns emerge. First of all, the 3SLS and 3SLS-RF results are notably more similar in magnitude and signs compared to the BBRES results. Secondly, the full rank BBRES Bayesian estimates, and the estimates generated by the 3SLS-RF, are overall quite similar in posterior precision in the sense that the spread of the marginal posterior distribution about the posterior means is generally similar, with only isolated instances where one of the methods exhibits a somewhat smaller posterior standard deviation than the other. Given that BBRES is a full rank mapping, whereas the 3SLS-RF is less than full rank, it appears that data information leakage in this particular empirical instance is quite minor. While not directly comparable because of the difference in interpretation between the Classical and Bayesian paradigms, it is also noteworthy that the BBRES precision, in terms of apparent spread around parameter estimates, is notably less than the apparent spread of the Classical 3SLS estimates.

The mean level price elasticity estimates implied by the three estimation methods are presented in Table 2. The formula used is based on Chalfant's method of calculating the elasticities, and the direct price elasticities are indicated in the table in bold font. All of the direct

price elasticities calculated by either Bayesian method have the correct negative signs, and the magnitudes of the elasticities appear to be plausible. However, the import quality beef elasticity, which is quality comparable to beef quality in the United States, appears to be somewhat high, being in the elastic range, for the 3SLS-RF results. Likewise, the direct price elasticity for chicken, being nearly elastic, appears to be also on the high side in the 3SLS-RF results. In both of these cases, the BBRES results appear to be more defensible. Comparing the Classical 3SLS results to the Bayesian results, the Classical pork direct price elasticity estimate has a wrong sign and a very large variance. Also, the Wagyu beef direct price elasticity appears to be unreasonably small, given the high priced, luxury good nature of the commodity.

The expenditure elasticities implied by the three estimation methods are presented in Table 3. The expenditure elasticity on Wagyu beef is negative, and *a priori* of the wrong sign for both the 3SLS and Bayesian 3SLS-RF estimation methods. Only the full rank BBRES Bayesian procedure produced the *a priori* correct positive sign on the expenditure elasticity for this luxury good, although even the BBRES estimate appears to be somewhat low. Of the remaining expenditure elasticities, the elasticities for IQ Beef, Chicken, and Fish are very similar in magnitude across all of the estimation procedures, and the BBRES Pork expenditure elasticity is lower than the elasticity estimates of the other two methods by only a relatively small amount.

4. Summary and Conclusions

Viewing the empirical results holistically across all commodities, across direct price and expenditure elasticities, and in terms of the precision of the information associated with the empirical results, it would appear that the BBRES methodology provides arguably the most *a priori* defensible and useful results. We note that all of the empirical Bayesian results reported in

this paper have been based on the use of an ignorance prior for the parameters of the demand system. It would be a simple matter to incorporate informative prior information on the parameters of the demand system (over and above the exact Neoclassical restrictions already imposed) through the use of an importance-sampling scheme that would lead to weighted average posterior means and posterior standard deviations. The Bayesian bootstrapping methodology is very flexible in this regard, while adding very little to the computational difficulties of calculating posterior moments. On the other hand, adding prior information, even in simple inequality form, provides both a computational and interpretational challenge within the Classical paradigm.

Overall, this paper demonstrated that Bayesian analysis of an econometric model containing multiple equations, exact restrictions, and a relatively large number of unknown parameters is relatively straightforward using the notion of Bayesian data information mappings. The approach relegates complicated analytical Bayesian posterior analyses to a relatively straightforward exercise in computer simulation. Moreover, adding the step of bootstrapping residuals in the process of simulating the error distribution imparts a distributional robustness to the Bayesian approach, making the assumption of a parameter family of densities for the residual term unnecessary, and making the Bayesian analysis a semiparametric one. Research is ongoing in this area to generalize the approach to models characterized by more complicated error generating processes, and to nonlinear mappings.

Table 1. Parameter Estimates for the Japanese Meat Demand System

Share		Classical 3SLS		3SLS-RF		BBRES	
		Estimate	Std. Err.	Posterior Mean	Posterior Std. Dev.	Posterior Mean	Posterior Std. Dev.
Wagyu Beef	α_1	0.682	0.113	0.593	0.095	0.334	0.090
	γ_{11}	0.045	0.065	0.012	0.041	-0.008	0.034
	γ_{12}	0.038	0.044	0.045	0.020	-0.014	0.017
	γ_{13}	-0.031	0.166	-0.032	0.020	0.014	0.024
	γ_{14}	-0.026	0.118	-0.012	0.010	0.018	0.015
	γ_{15}	-0.026	0.053	-0.013	0.016	-0.010	0.013
	β_1	-0.142	0.027	-0.121	0.022	-0.061	0.021
IQBeef	α_2	0.130	0.101	0.109	0.067	0.090	0.076
	γ_{21}	0.038	0.058	0.045	0.020	-0.014	0.017
	γ_{22}	-0.005	0.039	-0.015	0.018	0.006	0.013
	γ_{23}	-0.090	0.147	-0.070	0.014	-0.031	0.015
	γ_{24}	-0.007	0.105	-0.016	0.007	-0.035	0.008
	γ_{25}	0.065	0.047	0.057	0.009	0.074	0.008
	β_2	-0.004	0.024	0.001	0.016	0.005	0.018
Pork	α_3	-0.762	0.172	-0.659	0.136	-0.412	0.113
	γ_{31}	-0.031	0.099	-0.032	0.020	0.014	0.024
	γ_{32}	-0.090	0.067	-0.070	0.014	-0.031	0.015
	γ_{33}	0.214	0.251	0.133	0.034	0.091	0.042
	γ_{34}	-0.001	0.179	0.042	0.022	0.016	0.030
	γ_{35}	-0.092	0.080	-0.073	0.013	-0.090	0.013
	β_3	0.216	0.040	0.192	0.032	0.135	0.026
Chicken	α_4	-0.241	0.061	-0.202	0.044	-0.214	0.052
	γ_{41}	-0.026	0.035	-0.012	0.010	0.018	0.015
	γ_{42}	-0.007	0.024	-0.016	0.007	-0.035	0.008
	γ_{43}	-0.001	0.090	0.042	0.022	0.016	0.030
	γ_{44}	0.048	0.064	0.012	0.016	0.036	0.021
	γ_{45}	-0.014	0.029	-0.027	0.007	-0.034	0.008
	β_4	0.076	0.014	0.066	0.010	0.069	0.012
Fish	α_5	1.191	0.160	1.158	0.100	1.202	0.145
	γ_{51}	-0.026	0.053	-0.013	0.016	-0.010	0.013
	γ_{52}	0.065	0.047	0.057	0.009	0.074	0.008
	γ_{53}	-0.092	0.080	-0.073	0.013	-0.090	0.013
	γ_{54}	-0.014	0.029	-0.027	0.007	-0.034	0.008
	γ_{55}	0.067	0.075	0.056	0.009	0.060	0.012
	β_5	-0.145	0.038	-0.138	0.023	-0.147	0.034

2. Price Elasticities for the Japanese Meat Demand System

	Classical R3SLS		3SLS-RF		BBRES	
	Price Elasticity	Standard Error	Posterior Mean of Price Elasticity	Posterior Standard Deviation	Posterior Mean of Price Elasticity	Posterior Standard Deviation
Wagyu beef - Wagyu beef	-0.263	0.876	-0.757	0.419	-1.041	0.466
IQ beef	0.695	0.577	0.523	0.207	-0.100	0.231
Pork	-0.081	2.200	-0.077	0.181	0.323	0.311
Chicken	-0.184	1.557	-0.006	0.098	0.310	0.194
Fish	0.722	0.697	0.552	0.189	0.332	0.209
IQ beef - Wagyu beef	0.369	0.578	0.796	0.365	-0.138	0.169
IQ beef	-1.044	0.372	-1.268	0.327	-0.949	0.130
Pork	-0.867	1.434	-1.259	0.231	-0.302	0.132
Chicken	-0.068	1.009	-0.296	0.119	-0.348	0.080
Fish	0.651	0.453	1.026	0.236	0.685	0.138
Pork - Wagyu beef	-0.272	0.627	-0.255	0.107	0.020	0.148
IQ beef	-0.654	0.371	-0.411	0.074	-0.256	0.087
Pork	0.027	1.476	-0.515	0.172	-0.609	0.241
Chicken	-0.112	1.017	0.122	0.117	0.026	0.171
Fish	-1.246	0.459	-0.916	0.131	-0.964	0.123
Chicken - Wagyu beef	-0.374	0.426	-0.198	0.111	0.152	0.177
IQ beef	-0.179	0.279	-0.217	0.077	-0.504	0.099
Pork	-0.165	1.067	0.310	0.250	0.047	0.353
Chicken	-0.509	0.754	-0.928	0.181	-0.652	0.254
Fish	-0.667	0.337	-0.679	0.100	-0.862	0.128
Fish - Wagyu beef	-0.027	0.544	0.001	0.030	0.002	0.023
IQ beef	0.141	0.473	0.117	0.016	0.157	0.014
Pork	-0.119	0.442	-0.084	0.022	-0.114	0.022
Chicken	-0.002	0.510	-0.025	0.013	-0.038	0.013
Fish	-0.736	0.354	-0.762	0.033	-0.746	0.049

3. Expenditure Elasticities for the Japanese Meat Demand System

	Classical R3SLS		Bayesian 3SLS		BBRES	
	Expenditure Elasticity	Standard Error	Posterior Mean of Expenditure Elasticity	Posterior Standard Deviation	Posterior Mean of Expenditure Elasticity	Posterior Standard Deviation
Wagyu beef	-0.889	0.354	-0.610	0.297	0.177	0.284
IQ beef	0.958	0.230	1.004	0.151	1.048	0.173
Pork	2.257	0.235	2.114	0.188	1.783	0.156
Chicken	1.895	0.171	1.782	0.122	1.820	0.144
Fish	0.743	0.067	0.757	0.041	0.739	0.060

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