International Statistical Review (2018), 86, 1, 1–28 doi:10.1111/insr.12243

# **Bayesian Model Averaging: A Systematic Review and Conceptual Classification**

# Tiago M. Fragoso<sup>1</sup>, Wesley Bertoli<sup>2</sup> and Francisco Louzada<sup>3</sup>

<sup>1</sup>Fundação CESGRANRIO, Rua Santa Alexandrina, 1011, Rio de Janeiro 20261-903, Brazil

# **Summary**

Bayesian model averaging (BMA) provides a coherent and systematic mechanism for accounting for model uncertainty. It can be regarded as an direct application of Bayesian inference to the problem of model selection, combined estimation and prediction. BMA produces a straightforward model choice criterion and less risky predictions. However, the application of BMA is not always straightforward, leading to diverse assumptions and situational choices on its different aspects. Despite the widespread application of BMA in the literature, there were not many accounts of these differences and trends besides a few landmark revisions in the late 1990s and early 2000s, therefore not accounting for advancements made in the last decades. In this work, we present an account of these developments through a careful content analysis of 820 articles in BMA published between 1996 and 2016. We also develop a conceptual classification scheme to better describe this vast literature, understand its trends and future directions and provide guidance for the researcher interested in both the application and development of the methodology. The results of the classification scheme and content review are then used to discuss the present and future of the BMA literature.

Key words: Bayesian model averaging; systematic review; conceptual classification scheme; qualitative content analysis.

### 1 Introduction

It is very common that multiple models provide adequate descriptions of the distributions generating the observed data. In such situations, a better model must be selected according to some criteria, like model fit to the observed data set, predictive capabilities or likelihood penalizations such as information criterion. After selection is performed, inferences are made, and conclusions are drawn assuming the selected model as the true model.

There are downsides to this approach. The selection of one particular model may lead to overconfident inferences and riskier decision-making as it ignores the existent model uncertainty in favour of very particular distributions and assumptions on the model of choice. Therefore, modelling this source of uncertainty to appropriately select or combine multiple models is desirable.

<sup>&</sup>lt;sup>2</sup>Departamento Acadêmico de Matemática – Universidade Tecnológica Federal do Paraná, Avenida Sete de Setembro, 3165, Curitiba 80230-901, Brazil

<sup>&</sup>lt;sup>3</sup>Instituto de Ciências Matemáticas e de Computação — Universidade de São Paulo, Avenida Trabalhador São-carlense, 400, São Carlos 13566-590, Brazil E-mail: louzada@icmc.usp.br

Using Bayesian inference to this purpose has been suggested as a framework capable of achieving these goals (Leamer, 1978). Bayesian model averaging (BMA) is an extension of the usual Bayesian inference methods in which one does not only describe parameter uncertainty through the prior distribution but also model uncertainty obtaining posterior distributions for model parameters and for the model themselves using Bayes' theorem, allowing for direct model selection, combined estimation and prediction.

# 1.1 Background

Let each model in consideration be written as  $M_l$ ,  $l=1,\ldots,K$ , representing a set of probability distributions encompassing the likelihood function  $L(Y|\theta_l,M_l)$  of the observed data Y in terms of model-specific parameters  $\theta_l$  and a set of prior probability densities for said parameters, denoted in general terms by  $\pi(\theta_l|M_l)$  on which we omit eventual prior hyperparameters for the sake of clarity. Both the likelihood and priors are conditional on a particular model.

Given a model, one then obtains the posterior distribution for the model parameters by

$$\pi(\theta_l|Y, M_l) = \frac{L(Y|\theta_l, M_l)\pi(\theta_l|M_l)}{\int L(Y|\theta_l, M_l)\pi(\theta_l|M_l)d\theta_l},\tag{1}$$

and the integral in the denominator is calculated over the support set for each prior distribution and represents the marginal distribution of the observations over all parameter values specified in model  $M_l$ .

This quantity is essential for BMA applications and is called the model's marginal likelihood or model evidence and is denoted by

$$\pi(Y|M_l) = \int L(Y|\theta_l, M_l) \pi(\theta_l|M_l) d\theta_l.$$
 (2)

Bayesian model averaging adds a layer to this hierarchical modelling by assuming a prior distribution over the set of all considered models describing the prior uncertainty over each model's capability to accurately describe the data. This is modelled as a probability density over all the models with values  $\pi(M_l)$  for  $l=1,\ldots,K$ , then posterior model probabilities given the observed data are given by

$$\pi(M_l|Y) = \frac{\pi(Y|M_l)\pi(M_l)}{\sum_{m=1}^K \pi(Y|M_m)\pi(M_m)},$$
(3)

representing the backing of each considered model by the observed data.

This support can also be described through the use of Bayes factors. Given two models l and m, the Bayes factor of model l against model m is given by

$$BF_{lm} = \frac{\pi(M_l|Y)}{\pi(M_m|Y)},\tag{4}$$

which represents the relative strength of the evidence in favour of model l against that of model m. Given a baseline model, which we arbitrarily fix as model 1, it is clear that Equation 3 can be written in terms of Bayes factors by simply dividing by the baseline model's evidence, resulting in

$$\pi(M_l|Y) = \frac{BF_{l1}\pi(M_l)}{\sum_{m=1}^{K} BF_{m1}\pi(M_m)},$$
(5)

which means that one can estimate the posterior model probabilities by using estimates for Bayes factors and vice versa.

These model probabilities can mainly be used for two purposes. First, the posterior probabilities (3) can be used as a model selection criterion, the most likely model being selected. Second, consider a quantity  $\Delta$  present in all models, such as a covariate or future observation, it follows that its marginal posterior distribution across all models is given by

$$\pi(\Delta|Y) = \sum_{l=1}^{K} \pi(\Delta|Y, M_l) \pi(M_l|Y), \tag{6}$$

the expected value of the quantity conditional on the observations alone. Therefore, BMA allows for a direct combination of models to obtain combined parameter estimates or predictions (Roberts, 1965). This practice leads to predictions with lower risk under a logarithmic scoring rule (Madigan & Raftery, 1994) than using a single model.

However, the implementation and application of BMA is not without difficulties. A prior distribution over the considered models must be specified, which is non-trivial in most applications.

Additionally, calculating each model evidence (Equation 2) is difficult. Except in simple settings like in some generalised linear models with conjugate distributions, the evidence does not present a closed form and must be approximated, which presents plenty of challenges and is an active research field (Friel & Wyse, 2012).

Despite these difficulties, BMA was extensively applied in the last 20 years, mostly in combining multiple models for predictive purposes and selecting models, particularly covariate sets in regression models or network structure in Bayesian network models. The latter application induces another pitfall in the form of large model spaces. For instance, consider a regression model with p covariates. The number of possible models without any interaction coefficients is  $2^p$ , which represents a large number of models even for moderate values of p. This difficulty can be mostly addressed by prior filtering of all possible models or through stochastic search algorithms over the model space.

# 1.2 Objectives of this Review

The idea of selecting and combining models based on their posterior probabilities is not news, but a series of advances made in the 1990s made the implementation and application of these ideas a reality. Following Leamer (1978), most model selection and marginal probabilities were only obtainable for the linear model under very specific parameter priors. However, the seminal work by Raftery (1996) paved the way for a multitude of applications by providing a straightforward approximation for the evidence in generalised linear models.

There were also advances in the implementation of BMA in large model spaces, from a preliminary filtering based on posterior probability ratios (the Occam's window; Madigan & Raftery, 1994) to a stochastic search algorithm inspired in reversible jump Markov chain Monte Carlo (MCMC) (Green, 1995) with trans-dimensional jumps based on posterior model probabilities (the MC3 algorithm; Madigan *et al.*, 1995).

After the landmark reviews of Hoeting *et al.* (1999) and Wasserman (2000), there were no comprehensive reviews of the developments and applications of BMA in the last 17 years, which does not account for the developments in Bayesian inference brought by the MCMC

revolution in the late 1990s and 2000s. With this paper, we aim to cover this undocumented period, specifically we have the following goals:

- provide a conceptual classification scheme (CCS) to review and classify key components of the BMA literature;
- summarise research findings and identify research trends; and
- obtain useful guidance for researchers interested in applying BMA to complex models.

# 1.3 Outline

The remainder of this paper is structured as follows. In Section 2, we outline the literature search procedure and criteria employed to select the relevant BMA literature. The content of each selected article is then classified according to its main features using the CCS described in Section 3, obtaining the patterns we describe and discuss in Section 4. Computing resources are presented in Section 5. We conclude in Section 6 with some guidance on the directions of the BMA literature.

# 2 Survey Methodology

To better understand how BMA was applied, we chose to perform a content analysis of the published literature. The purpose of a content analysis is to systematically evaluate all forms of a recorded communication, identifying and classifying key contributions to a field and to clarify trends, practice and indicate research possibilities. To achieve this objective, we formulated a systematic review following the guidelines in Moher *et al.* (2009) specifying objective criteria for defining the relevant literature to revise and the appropriate ways to report our findings.

### 2.1 Literature Search Procedure

Aiming to perform a comprehensive search in the BMA literature, we combined four databases: Elsevier's Scopus and ScienceDirect (available at http://www.scopus.com and http://www.sciencedirect.com/, respectively), Thompsom Reuters's Web of Science (available at http://apps.webofknowledge.com) and the American Mathematical Society's MathSciNet database (available at http://www.ams.org/mathscinet/index.html).

We performed queries of the 'Bayesian model averaging' term restricted to the 1996–2016 period on the publications' title, abstract and keywords for queries in Scopus and ScienceDirect, topic (encompassing title, abstract, keywords and proprietary 'keywords plus') in Web of Science and 'Anywhere' in MathSciNet, as it presented fewer search options. The time period was chosen to cover most of the published literature not covered by previous works while still including seminal works.

Two exclusion criteria were employed over search results to select articles for further revision, namely:

- 1. Search results written in English, published in peer-reviewed journals as an article (which excludes conference proceedings, theses, dissertations, books, etc.) and available online.
- 2. Articles explicitly employing BMA, therefore excluding articles only listing BMA in keywords, alluding to BMA as a model combination procedure or applying BMA without further explanation or reference to the specific methodology employed.

Articles that did not comply with at least one of the criteria were excluded from the review. The articles were then selected according to the procedure illustrated in Figure 1. Using the

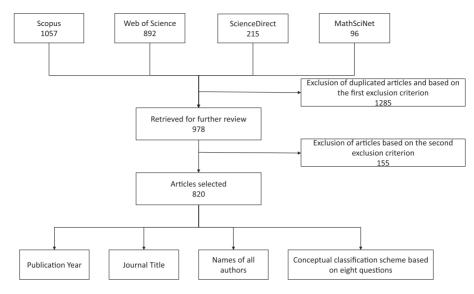


Figure 1. Literature search procedure and number of selected articles.

aforementioned queries, 1 057 articles were found in Scopus, 892 in Web of Science, 215 in ScienceDirect and 96 in MathSciNet. After the removal of duplicates and application of the first exclusion criterion, 882 articles were listed for further investigation and carefully revised, leading to the exclusion of 155 articles based on the second exclusion criterion, leaving 820 articles for classification. Interested readers can refer to our supplement that contains the overall alphabetical ordered list of articles.

# 2.2 Structure of the Data Set

The final data set consisting of 820 eligible articles was then classified according to four main categories:

- 1. Publication year
- 2. Names of all authors
- 3. Journal title
- 4. Responses to the eight items of the CCS

### 3 A Conceptual Scheme for BMA

Besides the systematic review of the literature, we also aimed to employ a content analysis of our findings, to provide further inside into the applications of BMA, to identify research trends and to elucidate possible research directions and opportunities. To achieve this objective, we immersed ourselves in the selected data set to better define characteristics in which current research that can be used to better understand the literature. This conventional content analysis (Hsieh & Shannon, 2005) allows for better understanding of the literature without preconceived notions.

We codified these formulated characteristics into a conceptual classification scheme inspired in the scheme developed in Hachicha & Ghorbel (2012) but adapted to characteristics relevant to the BMA literature. We then elaborated a CCS to classify the literature and refined the defined

categories as we revised all articles. An article's classification according to the CCS is useful to a researcher interested in the field, as it gives key characteristics on the methodology and formulation, leading to more efficient queries into the developments and applications of BMA. In the present work, we elaborated a CCS with eight items which, along with the possible responses can be found in Table 1 and thoroughly described in the succeeding text.

# 3.1 Usage

Being a framework for model selection and combination, BMA can be used to solve a wide range of problems. As such, we first classified each eligible article with respect to usage. Our content search resulted in five main categories of BMA usage.

The derivation of posterior model probabilities makes BMA a very straightforward model choice method. Said probabilities are easily interpretable under the Bayesian paradigm, and the model space can be as wide as necessary, and it requires no bookkeeping over the number

Table 1. List of questions and employed categories for the conceptual classification scheme.

- 1. How is BMA used?
  - 1.1. Model choice
  - 1.2. Combined parameter estimation
  - 1.3. Combined prediction
  - 1.4. Conceptual discussion and methodological improvements
  - 1.5. Review of current methods
- 2. What is the field of application?
  - 2.1. Statistics and Machine Learning
  - 2.2. Physical Sciences and Engineering
  - 2.3. Biological and Medical Sciences
  - 2.4. Economics and Humanities
- 3. How are model prior specified?
  - 3.1. Vague prior
  - 3.2. Used verbatim from the literature
  - 3.3. Elicitated from experts or from the problem
  - 3.4. No explicit use or reference/not applicable
- 4. How is the evidence estimated?
  - 4.1. Monte Carlo sampling and extensions
  - 4.2. Analytical approximations
  - 4.3. Markov chain Monte Carlo
  - 4.4. Ratio of densities
- 5. How do the authors real with high dimensionality?
  - 5.1. Dimensionality reduction
  - 5.2. Stochastic search via Markov chain Monte Carlo
- 6. Are Markov chain Monte Carlo-based methods employed?
  - 6.1. Yes
  - 6.2. No
- 7. Is the method validated through simulation studies?
  - 7.1. Yes
  - 7.2. No
- 8. Is the application validated through data-driven procedures?
  - 8.1. Cross validation and data splitting
  - 8.2. Leave-one-out or K-fold cross validation
  - 8.3. Posterior predictive checks
  - 8.4. None/not applicable

BMA, Bayesian model averaging.

of parameters or kind of penalty as required by the information criterion methods applied in the statistical literature. We therefore singled out articles that employ BMA as a model choice method.

Using the posterior model probabilities as weights, one can produce estimates averaged over all considered models (Equation 6), that can have a lower overall risk and take model uncertainty into consideration. There are two main kind of estimates. When  $\Delta$  in Equation 6 represents a parameter that is common to all considered models, one can obtain an averaged model estimate. On the other hand, when  $\Delta$  represents a future observation or yet to be collected data point, Equation 6 is used to obtain an average prediction. Albeit similar, both applications have distinct uses, so we classified articles on its use of BMA to obtain joint estimation and prediction, respectively.

As we previously mentioned, BMA is not as direct to apply. As such, there is a considerable technical literature in theoretical aspects and extensions of BMA. There is also retrospective studies in which BMA or any one of the applications mentioned earlier are revised in a specific area (model selection methods in economics, for instance), so we classified these articles as conceptual discussions and review articles, respectively.

# 3.2 Field of Application

Given the wide array of possible uses, we also classified every selected article according to its field of application. We employed a vague classification of BMA applications for two reasons. First, as stated in Section 1.2, we aim to summarise and point research trends, not to perform a detailed taxonomy of BMA usage. Second, as BMA (and Bayesian methods in general) find more penetration into applied research, we lack the expertise to discriminate between subfields. Restricting the present work to a more general view, we defined four fields of application.

An immediate field of application for BMA is the Statistics literature, which is in turn heavily borrowed and borrows upon the Machine Learning literature. Therefore, we classified papers that are more concerned with statistical modelling, theoretical developments and machine learning applications into a single category. After some pioneering works in the statistical literature, BMA found its way into the Biological and Life Sciences, composing of the studies in the fields of Medicine, Epidemiology, Biological Sciences such as Ecology and others. The seminal revision work by Geweke (1999) introduced BMA to the field of Economics and later on to other Humanities such as Political and Social Sciences. After a few years, some works started to appear in the fields of Engineering and Physical Sciences such as Meteorology and Physics.

### 3.3 Model Priors

Much of the study in Bayesian methods is concerned with the elicitation of prior distributions, representing the uncertainty in place before any data are observed. Elicitating an appropriate prior is a non-trivial task in any Bayesian setting, and such difficulties are compounded in model averaging because a probability measure for the model space is not obvious in principle. Throughout our review, we encountered four main approaches.

One can simply assume prior ignorance about which model is correct through a vague prior (i.e.  $\pi(M_l) \propto 1, l = 1, 2, ..., K$ ) that assumes no model is more likely a priori than any other and let the observed data carry all the information. This is not always desirable, and sometimes it is possible to perform some elicitation based on expert opinions or specific characteristics of a particular problem, resulting in elicitated priors.

In the case of elicitated, conjugate or simply convenient priors, sometimes a particular choice spreads through the literature, resulting in subsequent authors that use such priors verbatim, which we classified into a single category of a literature prior. Finally, as mentioned previously,

a number of authors bypass the problem entirely by neither explicitly stating their model priors nor providing references to clarify their assumptions yet still use BMA in some sense. We classified these cases as 'not available (NA)'.

### 3.4 Evidence Estimation

In the estimation of the marginal likelihood (Equation 2), the model evidence is non-trivial in any general setting because it usually involves complicated multidimensional integrands with sometimes complex support sets that can make the integration unfeasible. As such, many solutions have been proposed, which we classified into five categories.

The integral can be approximated by Monte Carlo methods or extensions such as importance sampling. Given an importance probability density  $w(\theta)$  defined over the same integration domain of Equation 2, the evidence can be approximated by taking R random samples  $\theta_1, \ldots, \theta_R$  from the probability distribution determined by  $w(\theta)$  and computing the weighted average

$$\widehat{\pi(Y|M_l)} = \frac{1}{R} \sum_{r=1}^{R} \frac{L(Y|\theta_r, M_l)\pi(\theta_r|M_l)}{w(\theta_r)},\tag{7}$$

which is guaranteed to converge to the evidence by the strong law of large numbers. Clearly, the ordinary Monte Carlo approximation can be performed by using the parameter prior as an importance density. Further extensions of this idea exist in the form of bridge sampling (Gelman & Meng, 1998) and other forms of integration. Because all draw upon the same Monte Carlo framework, we classified these methods into one category.

Still in the spirit of Monte Carlo methods but very distinct in practice, one could also sample from a Markov chain, using MCMC methods to approximate the evidence. Let  $\theta_l^{(1)}, \ldots, \theta_l^{(R)}$  be R posterior samples obtained from a MCMC chain and  $w(\theta)$  an importance density as defined previously, then one can use the 'importance sampling' estimator (Gelfand & Dey, 1994) given by

$$\widehat{\pi(Y|M_l)} = \left\{ \frac{1}{R} \sum_{r=1}^{R} \frac{w(\theta_l^{(r)})}{L(Y|\theta_l^{(r)}, M_l)\pi(\theta_l^{(r)}|M_l)} \right\}^{-1},$$
(8)

which is, in turn, a generalisation of the harmonic mean estimator of Newton and Raftery (1994) that uses the prior as an importance density. The estimator is shown to converge to the evidence as the sample size increases, but an importance function must be finely tuned to avoid estimators with unbounded variance.

Another flavour of MCMC posterior probability estimator comes through the use of transdimensional Markov chain methods like the reversible jump MCMC (RJMCMC) (Green, 1995) or stochastic searches through the model space like stochastic search variable selection (SSVS; George & McCulloch, 1993; 1997) employed in regression models.

In these methods, multiple models are sampled either through a Gibbs sampler or a Metropolis jump on the same MCMC chain. Consider the output of a MCMC procedure of R posterior samples, and let  $\gamma_r$  be a variable indicating which model the chain is visiting at step r,  $\gamma_r \in \{1, \ldots, K\}$ . The model posterior is estimated commonly by the sample mean

$$\widehat{\pi(Y|M_l)} = \frac{1}{R} \sum_{r=1}^{R} I(\gamma_r = l), \qquad (9)$$

where  $I(\cdot)$  is the indicator function or by some Rao-Blackwellized estimator when available (Guan & Stephens, 2011). When using MCMC samples, the quality of the approximation is not

guaranteed, and there are more sophisticated results ensuring its good behaviour (see Robert & Casella, 2013, for a complete treatment). In this paper, we classified all MCMC based methods into a single category.

Also of particular interest is the ratio of densities method popularised by Chib (1995), in which one exploits the fact that Equation 1 is valid for every parameter value, whereas the normalising constant stays the same. Chib (1995) suggests picking one particular parameter point  $\theta^*$  and estimate the evidence as

$$\widehat{\pi(Y|M_l)} = \frac{L(Y|\theta_l^*, M_l)\pi(\theta_l^*|M_l)}{\pi(\theta_l^*|Y, M_l)},\tag{10}$$

for l = 1, ..., K, and the parameter value  $\theta^*$  is chosen as to minimise estimation error.

Besides stochastic approximations, analytical approximations based on asymptotic results can be employed as shown in the seminal works by Kass and Raftery (1995) and Raftery (1996). Through a Taylor expansion around the posterior mode and imposing some regularity conditions, one can approximate the evidence through the so-called Laplace approximation. Namely, if  $\tilde{\theta}_l$  is the posterior mode for model l, then

$$\pi(Y|M_l) \approx (2\pi)^{\frac{p_l}{2}} \sqrt{|\Psi_l|} L(Y|\tilde{\theta}_l, M_l) \pi(\tilde{\theta}_l|M_l), \tag{11}$$

where  $p_k$  is the number of parameters in model l and  $\Psi_l$  is minus the inverse Hessian matrix of the log-posterior given by  $\log \left( L(Y|\tilde{\theta}_l, M_l) \pi(\tilde{\theta}_l|M_l) \right)$  for the model. Under regularity conditions, the approximation is  $O(n^{-1})$ . Let  $\hat{\theta}_l$  denote the maximum likelihood estimator for model l, then the Bayes factor between two models l and m can be reasonably approximated by the Bayesian information criteria (BIC), given by

$$2\log B_{lm} \approx 2\left(\log\left(L(\boldsymbol{Y}|\hat{\theta}_{l}, M_{l})\right) - \log\left(L(\boldsymbol{Y}|\hat{\theta}_{m}, M_{m})\right)\right) - (p_{l} - p_{m})\log N, \quad (12)$$

when both models are used to fit the same data set of sample size N. The BIC provides a good approximation for many generalised linear models and enjoys widespread use, even with the larger approximation error of O(1). Both methods are very similar in spirit, and as such, were put into the same classification.

Finally, many authors were able to compute the evidence in closed form, either by the shape or their models and distributional assumptions (as in the linear model) or through the use of convenient parameter prior distributions. Because we were more interested in the approximation of complex evidences in general settings, we classified these cases as NA.

### 3.5 Dimensionality

It is very common in current applications to encounter extremely wide model spaces in which the exhaustive fit of all models is unfeasible. We illustrate the problem with one of the most popular applications of model choice, variable selection in regression models. Let Y represent an observation and X represent a  $p \times 1$  vector of covariates that we aim to investigate the degree of association to Y through the linear model

$$Y = \beta X + e,\tag{13}$$

where  $\beta$  is a 1 × p parameter vector of fixed effects and e is a random effect. Finding the subset of covariates (most) associated with Y induces a model selection problem.

However, not considering any interaction terms, the number of possible subsets (and therefore models) is  $2^p$ , which grows geometrically with the number of covariates resulting in very large model spaces even for a moderate number of covariates precluding an exhaustive investigation of all models. The BMA literature answered to this problem through two main approaches: dimensionality reductions of the model space and stochastic searches through MCMC.

One of the first dimensionality reduction techniques was the leaps and bounds algorithm (Furnival & Wilson, 1974). The algorithm aims to select the best performing regression models based on the residual sum of squares, with the model with smaller sum being selected as more fit to the data. Exploiting relationships on the linear model and the branch and bound optimisation algorithm, the most parsimonious models can be obtained without an exhaustive search. In much of the literature, a preliminary search through the leaps and bounds algorithm is performed to subject only the most promising models to BMA.

Another popular criterion is the Occam's window (Madigan & Raftery, 1994). It proposes that only models with a relatively high posterior probability must be considered. As such, it reduces the model set comprised by the K models to the reduced set

$$A = \left\{ M_k : \frac{\max_l P(M_l | Y)}{P(M_k | Y)} \le c \right\},\tag{14}$$

where c is a tuning parameter chosen by the user. The Occam's window excludes all models whose model probability is smaller than the most likely model by a factor of c, usually set to 20 to emulate the popular 0.05 cut-off employed when filtering models based on p values. Note that, albeit straightforward to set up, the application of Occam's window relies on the easy calculation or approximation of the model posterior probabilities, which in turn relies on the model evidence. In our review, we classified all aforementioned preliminary filtering methods together.

Instead of reducing the model space beforehand, other approaches take the entire model head on and perform some kind of search, mostly through MCMC techniques. In these cases, not only the dimensionality problem is dealt with, but there is also a straightforward manner to estimate the posterior model probabilities through the proportion of times a model is visited throughout the search.

One of the first proposals for these searches in regression models was proposed by George and McCulloch (1993) called SSVS. The SSVS utilises a set of auxiliary random variables  $\gamma_l$ , l = 1, ..., p such that

$$\gamma_l = \begin{cases} 1, & \text{if variable } l \text{ belongs in the model} \\ 0, & \text{otherwise} \end{cases}$$
 (15)

Along with all other parameters, a prior distribution is assigned to these variables, and therefore, a posterior distribution is obtained through MCMC procedures. The stochastic search is performed by the updating of the indicator variables, each configuration representing a distinct model. SSVS just expands over an already implemented MCMC algorithm, making it a widely used and flexible methodology. It is however unwieldy for higher dimensions, as the number of update steps will grow with the number of covariates. To address this issue, the updating can be performed through Metropolis-Hastings step to consider only the most likely models as performed in Baragatti (2011).

A more general approach was proposed by Green (1995) in the RJMCMC algorithm, which just like in the current BMA setting, insert all models into a larger space in which a Markov

chain is constructed. Model search is then performed using two components: a proposal probability density for a model l given the current model  $M_m$  and an invertible differentiable mapping between the two spaces defined by the models. The chain then moves through models by means of a Metropolis-Hastings step. The construction of the acceptance probability required for the Metropolis-Hastings step is not straightforward, and we shall omit it for the sake of clarity. The interested reader is directed to Green (1995) for a complete treatment.

There is a similar relatively general model search procedure in the literature, the MCMC model composition (MC3; Madigan *et al.*, 1995) in which one applies the same idea of a Metropolis-Hastings step for model jumps from RJMCMC but in a simplified fashion. Let  $M_l$  and  $M_m$  be two models, MC3 performs a model change from model  $M_l$  to model  $M_m$  with acceptance probability

$$\alpha(m,l) = \min\left\{1, \frac{P(M_m|Y)}{P(M_l|Y)}\right\}. \tag{16}$$

Given that marginal probabilities are available, the implementation of MC3 is straightforward. For the purposes of our categorisation scheme, we considered all methods employing MCMC based searches similar and therefore were classified into a single category.

Throughout our literature review, we also encountered applications in which dimensionality was not an issue. In these cases, all models were fit to the data, and BMA performed posteriorly. As these articles obviously did not propose any way to mitigate dimensionality problems, we classified these articles as NA.

### 3.6 Markov Chain Monte Carlo Methods

It is impossible to ignore the revolution in Bayesian inference sparked by the dissemination of MCMC methods and software. MCMC made it possible to perform inference with very complex likelihood and prior structures and to obtain estimates of key posterior quantities based on straightforward outputs and grounded on solid theory, making it the default approach for many applied problems.

Such popularity comes in part from the popularisation of out-of-the-box MCMC software containing robust MCMC implementations to a wide range of problems like the widely used 'Bayesian inference using the Gibbs sampler' software (Spiegelhalter *et al.*, 1995) and the 'Just another Gibbs sampler' (Plummer, 2003). These software, commonly integrated with the R statistical software, made MCMC methods and Bayesian inference available to a broad audience. We aimed to track this spread of MCMC methods through the BMA literature by classifying each article on its usage of MCMC methods.

### 3.7 Simulation Studies

We classified articles on the practice of generating simulations from the proposed models or the use of artificial data sets. Simulation studies can be employed to investigate characteristics of the averaging process and desired properties like predictive power in the best case scenario, emulate physical systems to better understanding and generate predictions from diverse models for averaging. As such, we classified articles with respect to the presence of simulation studies.

### 3.8 Data-driven Validation

After BMA was applied, we also investigated how the process was validated using real data. The most traditional data-driven validation procedure consists of simply splitting the data set

into at least two disjoint sets, fitting the model to the data on the former and validating the fitted model on the latter. This kind of cross validation is very commonly used and articles practicing this kind of validation were put into a single category.

Another category was made for more sophisticated kinds of cross validation like K-fold cross validation. In this procedure, the data set is split into K disjoint subsets, and for each subset, the model is fit over the combined remainder K-1 subsets. The chosen subset is then used as a validation set, and the process is repeated in turn for the next subset. After going through all subsets, the validation measures employed (goodness-of-fit, predictive power, etc.) are somehow combined for an overall conclusion. Being significantly more complex than simple data splitting, we classified articles using K-fold cross validation or special cases like the popular leave-one-out cross validation into the same category.

Being a Bayesian procedure in nature, it is not unexpected that applications of BMA might use Bayesian goodness-of-fit measures like posterior predictive checks (Gelman *et al.*, 1996). For the predictive check, one chooses a test statistic over the observed data set and compares it with replicated data generated using the posterior distribution, and a model is said to do present good fit if, averaged over the posterior, the test statistic is not too extreme when compared with its value calculated over the observations. One usually generates the replicated data using posterior samples obtained from MCMC methods so that required averages are straightforward from the estimation procedure. This procedure is clearly distinct from the previous validation procedures mentioned and, therefore, categorised separately.

### 4 Results and Discussion

We first performed some descriptive statistics to investigate the growth and some trends in the BMA literature and then investigated the patterns in the light of our proposed CCS.

# 4.1 Descriptive Statistics for the BMA Literature

We segmented our data set with respect to publication year to investigate the growth of the literature in terms of the number of published articles throughout the considered period. Because peer-reviewed articles can take a significant time from submission to publication, we smoothed the temporal trends using a 3-year moving average. The results can be observed in Figure 2.

One can interpret the growth shown in Figure 2 in three stages. First, in the 1996–2000 time period, there were a relatively small number of publications, not because of the lack of theoretical results, but rather for the absence of a systematic exposition to BMA and accessible computational tools. Then, with the publication of the revisions by Hoeting *et al.* (1999), Wasserman (2000) and Geweke (1999) and some computational tools implementing the results by Raftery (1996), Volinsky *et al.* (1997), Madigan and Raftery (1994) and Madigan *et al.* (1995) led to a popularisation of BMA resulting in a growth in publications in the 2000–2005 time period. Then, after 2005, there was a veritable increase in the number of publications, probably because of the widespread use of computational tools, more easily accessible computer power and the increasing availability of ready-to-use MCMC software.

We then divided the database according to the journal title, to identify fields with a more widespread application of BMA. There was no single periodical responsible for most of the literature, and it is clear that its applications have spread through diverse fields. The 100 titles with the higher counts of publications are listed in Table 2.

There are some clusters representing some patterns in the diffusion and application of BMA. As it is expected from a statistical methodology, there were many articles published in Statistics

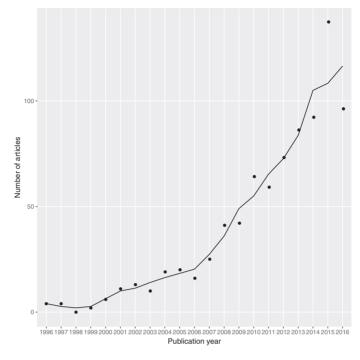


Figure 2. Number of published articles by year of publication and 3-year moving average.

and Machine Learning periodicals, adding up to 21 periodicals in the top 100. There is also a widespread application of BMA in the Economics literature, with 21 titles in the top 100 and a few periodicals in Meteorology and Climatology, following the seminal predictive framework proposed by Raftery *et al.* (2005).

We also classified each article with respect to the authors and co-authors and listed the top 10 most productive authors in Table 3 to infer the most massive contributions to the literature. There were no authors overwhelmingly present in the literature given its size, but one can single out the contributions of Adrian Raftery from the University of Washington. Raftery authored or co-authored 36 articles in our data set, a productive author that contributed both to the theoretical underpinnings of BMA (Kass & Raftery, 1995; Raftery, 1996) and to its applications, for instance, in genetics (Yeung *et al.*, 2005), engineering (Raftery *et al.*, 2010), economics (Eicher *et al.*, 2011) and proposed an ensemble prediction method in meteorology and climatology (Raftery *et al.*, 2005) that enjoys widespread use.

Of note, there are also Tilmann Gneiting who mainly contributed to ensemble methods in Meteorology, Merlyse Clyde, who applied BMA mostly in the context of variable selection for regression models using SSVS, Q. J. Wang, Xiaobao Li and Xuesong Zhang with contributions in Metereology and Hidrology and Theo S. Eicher, Martin Feldkircher and Gary Koop, who applied BMA to Economics.

### 4.2 Conceptual Classification Scheme

We present below some brief descriptive statistics and discussion on the classification patterns generated using the CCS to the data set, with some notes to trends and guidance to specific

Table 2. Number of publications on the 100 periodicals with most Bayesian model averaging articles.

Title	Articles published	Percentage
Water Resources Research	26	3.2
Journal of Hydrology	19	2.3
Monthly Weather Review	17	2.1
Journal of Applied Econometrics	13	1.6
Journal of the American Statistical Association	13	1.6
Computational Statistics and Data Analysis	10	1.2
International Journal of Forecasting	9	1.1
Journal of Econometrics	9	1.1
Journal of Health Economics	9	1.1
Public Library of Science — One	9	1.1
Statistics in Medicine	9	1.1
Ecological Modelling	8	1.0
Journal of Forecasting	8	1.0
Journal of International Money and Finance	8	1.0
NeuroImage	8	1.0
Canadian Journal of Fishery and Aquatic Sciences	7	0.8
Journal of Macroeconomics	7	0.8
Risk Analysis	7	0.8
Advances in Water Research	6	0.7
Biometrika	6	0.7
Ecological Economics	6	0.7
European Economic Review	6	0.7
Stochastic Environmental Research and Risk Assessment	6	0.7
Applied Economics	5	0.6
American Meteorological Society	5	0.6
Biometrics	5	0.6
Biometrics	5	0.6
Climate Dynamics	5	0.6
Environmetrics	5	0.6
Environmental Modelling and Software	5	0.6
Journal of Agricultural Biological and Environmental Statistics	5	0.6
Journal of Machine Learning Research	5	0.6
Annals of Applied Statistics	4	0.5
Bioinformatics	4	0.5
Bioinformatics	4	0.5
Biostatistics	4	0.5
Ecological Applications	4	0.5
Economics Bulletin	4	0.5
Environmental and Ecological Statistics	4	0.5
Fisheries Research	4	0.5
Genetic Epidemiology	4	0.5
Hydrology and Earth System Sciences	4	0.5
Journal of Banking and Finance	4	0.5
Journal of Computational and Graphical Statistics	4	0.5
Journal of Geophysical Research: Atmospheres	4	0.5
Journal of Money Credit and Banking	4	0.5
Journal of the Royal Statistical Society — Series B	4	0.5
Reliability Engineering and System Safety	4	0.5
Statistics and Computing	4	0.5
Technometrics	4	0.5
Applied Economics Letters	3	0.4
Asia-Pacific Journal of Atmospheric Sciences	3	0.4
Applied Stochastic Models in Business and Industry	3	0.4
BMC Medical Research Methodology	3	0.4

Table 2. Continued

Title	Articles published	Percentage
Conservation Biology	3	0.4
Cerebral Cortex	3	0.4
Econometrics Journal	3	0.4
Economic Modelling	3	0.4
Econometric Reviews	3	0.4
Economics and Sociology	3	0.4
Geographical Analysis	3	0.4
Global and Planetary Change	3	0.4
Geophysical Review Letters	3	0.4
International Journal of Climatology	3	0.4
Journal of Applied Metereology and Climatology	3	0.4
Journal of Applied Statistics	3	0.4
Journal of Applied Statistics	3	0.4
Journal of Business and Economic Statistics	3	0.4
Journal of Economic Surveys	3	0.4
Journal of Gerontology – Series A	3	0.4
Journal of the Royal Statistical Society – Series A	3	0.4
Journal of the Royal Statistical Society – Series C	3	0.4
Journal of Statistical Computation and Simulation	3	0.4
Journal of Statistical Software	3	0.4
Machine Learning	3	0.4
Economic Systems	3	0.4
Quartely Journal of the Royal Metereological Society	3	0.4
Review of Economics and Statistics	3	0.4
Statistical Science	3	0.4
Tellus – A	3	0.4
Annals of Human Genetics	2	0.2
American Journal of Agricultural Economics	2	0.2
Bayesian Analysis	2	0.2
BMC – Systems Biology	2	0.2
Canadian Journal of Statistics	2	0.2
Computational Statistics	2	0.2
Clinical Trials	2	0.2
	2	0.2
Environmental Modelling and Assessment Emerging Markets Finance and Trade	2	0.2
Environmental and Resource Economics	2	0.2
	2	0.2
Ensayos sobre politica economica	2	0.2
Energy, Sustainability and Society	2 2	
Freshwater		0.2
Forest Ecology and Management	2	0.2
Genetics Selection Evolution	2	0.2
Groundwater	2	0.2
Human Heredity	2	0.2
Hydrological processes	2	0.2
(Other)	350	42.7
NA's	1	0.1
Total	820	100

NA, not applicable.

applications of BMA. It is not useful to list the hundreds of revised articles, so we aim to provide illustrative works for each aspect of our revision as the interested reader can follow through its references and citations for his or her own purposes. Furthermore, the data set of all responses to the CCS can be obtained upon request from the corresponding author.

Name	Institution	(Co-)authored works
Adrian E. Raftery	University of Washington	36
Xuesong Zhang	Pacific Northwest National Laboratory	13
Frank Tsai	Lousiana State University	12
Tilmann Gneiting	Karlsruhe Institute of Technology	11
Q. J. Wang	CSIRO Land and Water	11
Merlyse Clyde	Duke University	10
Gary Koop	University of Strathclyde	10
Theo S. Eicher	University of Washington	8
Xiaobao Li	Lousiana State University	8
Martin Feldkircher	OeNB	7

Table 3. Top 10 authors in the Bayesian model averaging literature in number of publications.

# 4.2.1 Usage

The most common usage of BMA in the revised literature was model choice, with 326 works totaling almost 40% of all articles, and the overwhelming majority of the revised articles deal with model choice through variable selection in regression models. Overall, we could spot three overarching themes in model choice throughout the literature with eventual variations.

First, there is the application of the background introduced by Adrian Raftery and collaborators in the first half of the 1990s. These works perform dimensionality reduction of the model space through Occam's window or leaps and bounds and approximate the model evidence using BIC like Volinsky *et al.* (1997), in which variable selection and model averaging is performed for a Cox regression model. This set of techniques enjoys great popularity to this date due in part to its implementation in the BMA R package (Raftery & Painter, 2005). Second, there are many works concerned with model selection in the linear model, specially in economic applications. Either all  $2^p$  possible models are considered or there is a stochastic search using MC3, and model evidences are derived explicitly from a conjugate priors (Fernandez *et al.*, 2001b). Finally, there is model choice using stochastic search through MCMC methods, like RJMCMC over spaces with different numbers of covariates (Lunn, 2008) and SSVS (Brown *et al.*, 2002).

After model choice, the most popular usage was the combination of multiple models for prediction, which was performed in 225 articles (around 28% of the data set). While combining each model's prediction is straightforward in principle, we identified at least three different trends.

First, there is the straightforward application of BMA by fitting all models to the data, calculating model evidences, generating a prediction from each model's predictive distribution culminating in a combined prediction. This practice leads to lower risk predictions under a logarithmic loss (Madigan & Raftery, 1994) and is relatively widespread in the literature, with applications in Ecology (Wintle *et al.*, 2003) and Genetics (Annest *et al.*, 2009). Second, there is a compromise between variable selection and prediction through an application of BMA to select the models or covariates with highest posterior model probability, and the selected model is then used to derive predictions. This procedure employs the techniques developed for variable selection in favour of prediction, like SSVS (Lamon & Clyde, 2000) or RJMCMC (Jacobson & Karlsson, 2004). Finally, there is an alternative use of BMA ideas proposed in Raftery *et al.* (2005) for meteorological applications that differs somewhat of usual applications and that we will briefly discuss below.

The authors consider the problem of combining forecasts from K models,  $f_1, \ldots, f_K$  into one combined prediction. For each forecast, there is a probability density function for the quantity one wished to forecast y denoted by  $g_l(y|f_l)$  for  $l=1,\ldots,K$ . Raftery  $et\ al.\ (2005)$  then propose to construct a combined density function using the weighted average

$$g(y|f_1,...,f_K) = \sum_{l=1}^K w_l g_l(y|f_l),$$
(17)

in which  $\sum_{l=1}^K w_l = 1$ , and the weights are interpreted in an analogous fashion to the posterior model probabilities in usual BMA. Assuming then each density as a normal, the authors estimate the weights using the expectation–maximization (EM) algorithm. This method has spread widely on the specialised literature, and albeit no strong theoretical optimality seems to exist, it enjoys adequate performance in Meteorological and Climatological applications.

Bayesian model averaging is used for combined estimation in 174 articles (around 21%) throughout our revision. Albeit similar in purpose with combined prediction, we classified a work as a combined estimation article if its purpose was to estimate a common parameter to all models, but not a future observation. Combined estimators were employed to estimate a variety of quantities that might be appropriately modelled by plenty of models, such as population size (King & Brooks, 2001), toxicity in clinical trials (Yin & Yuan, 2009), breeding values in genetics (Habier *et al.*, 2010) and the probability of an economic recession (Guarín *et al.*, 2014).

Conceptual discussions and methodological articles amounted for 74 data points (around 9% of the data set). This category presents a clear heterogeneity, as it comprises theoretical and conceptual advances in many directions. Articles in this category are, however, very similar with respect to its purpose to introduce an application of BMA to an existing problem or extend BMA to overcome limitations in some settings.

The former articles refer to seminal theoretical works like Raftery (1996) that introduced the BIC approximation to the Bayes factor and paved the way for many subsequent works. There were also pioneer works discussing the introduction of BMA to applied fields, like the methodology discussed in Fernandez *et al.* (2001a) for variable selection in economical applications. Its use of Zellner's (1986) g-prior for the regression coefficients (allowing for explicit model evidences) and MC3 composition for model space search were quickly adopted by many authors in very diverse economical studies. The introduction of BMA to the problem of selecting network structures in Bayesian networks (Friedman & Koller, 2003) also had a great impact in the Machine Learning literature, spawning a wealth of approximations for the ideal Bayesian averaged network. Finally, there were also novel developments in BMA that made it usable within a field. For instance, the variational Bayes approximation for the evidence proposed in Friston *et al.* (2007) sparked plenty of BMA applications to neurological data sets. On the other hand, the latter articles deal with extensions of BMA to different Bayesian applications, like the BMA under sequential updating discussed in Raftery *et al.* (2010).

The last category we employed to classify articles on usage pertains to review articles on BMA or the applications of model averaging to specific fields or models. There are 21 such articles in our data set, amounting to less than 3% of the total. Some of the revision articles sparked the application of BMA in general like the seminal works by Hoeting *et al.* (1999) and Wasserman (2000), whereas more specific revisions exposed the methodology in other fields like Economics (Geweke, 1999), Genetics (Fridley, 2009) and Physics (Parkinson & Liddle, 2013). There are also revisions on model selection (Kadane & Lazar, 2004) and model uncertainty (Clyde & George, 2004) in which BMA figures as a technique.

# 4.2.2 Field of application

As stated in Section 3.2, we classified the data set into four main categories to give a broad idea of the application of BMA in different fields. We divided our data set into four categories regarding applications in the Biological and Life Sciences, Humanities and Economics, Physical Sciences and Engineering and Statistics and Machine Learning, respectively in order to infer if there was an increased penetration of BMA in either field.

The field with most articles was Life Sciences and Medicine, with 262 works corresponding to 31.9% of all reviewed publications. Within these publications, there are some trends of note. In the medical sciences, BMA was used mostly for model choice purposes, as in variable selection of factors associated with false positives in diagnostic kits (Ranyimbo & Held, 2006), weight loss (Phelan *et al.*, 2009), leukaemia progression (Oehler *et al.*, 2009), structure in Bayesian networks for patient-specific models (Visweswaran *et al.*, 2010) and the combined estimation as in Yin and Yuan (2009). BMA was also used extensively in Ecology, with applications to landscape ecology and geographical information systems (Barber *et al.*, 2006), prediction of species distribution (Thomsom *et al.*, 2007), capture—recapture models (Arnold *et al.*, 2010) and evolution (Silvestro *et al.*, 2014).

The massive number of genetic variables obtained from biomarkers like microarrays and single nucleotide polymorphisms (SNPs) that relate with observed characteristics through complex interactions fostered a rich Bayesian model selection literature in Genetics. BMA was employed to combine and select genetic information from metabolic pathways (Conti *et al.*, 2003), quantitative trait loci (Boone *et al.*, 2008), candidate SNPs for lung cancer risk (Swartz *et al.*, 2013) and a revision of Bayesian model selection models that was performed in Fridley (2009). There is also the seminal work by Meuwissen *et al.* (2001) that introduced a class of SSVS-like estimation procedure in quantitative genetics that gained much traction in the Animal and Plant Sciences literature, concerned with the prediction of genetic merit for selection (Kizilkaya *et al.*, 2010; Boddhireddy *et al.*, 2014). There also seems to be an increase of model averaging in neuroscience using the methods introduced by Penny *et al.* (2010).

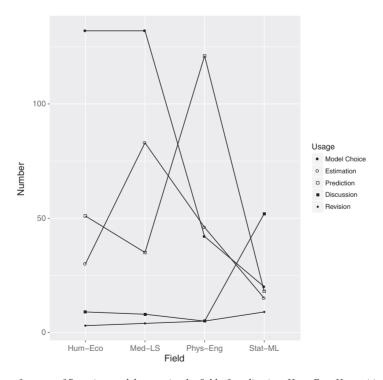
The Humanities and Economy field had 225 articles (27.4% of the data set), with the overwhelming majority being in economical applications. The earliest application to economics in our data set is the revision of Bayesian modelling by Geweke (1999). The most adopted framework for model selection using BMA was introduced in Fernandez *et al.* (2001a), describing conjugate priors and a model search procedure that enjoys a broad application to many economical questions to this date, although there were also articles applying the framework introduced by Adrian Raftery and collaborators through the R package that this group developed like Goenner (2010) and applications of SSVS (Vrontos *et al.*, 2008). Forecasting using BMA in economical settings was discussed in Koop and Potter (2004) and was adopted by many subsequent articles. There were also some occasional applications to Political Science mostly on variable selection as in trade interdependence in conflict (Goenner, 2004) and some forecasting, like the study of the 2000 american presidential election in Sidman *et al.* (2008).

The application of BMA in the Physical Sciences and Engineering amounted for 219 articles, about 26.7% of the total. Most of this field was made of applications to forecasting problems in Meteorology and Climatology stemming from the seminal work of Raftery *et al.* (2005) in the field, using the ideas of BMA into an ensemble forecast with posterior model probabilities estimated using the EM algorithm. There were also some works in Physics, like the study of dark matter in Liddle *et al.* (2006) and the revision of BMA methods in astrophysics in Parkinson and Liddle (2013).

Finally, there were 114 articles in the Statistics and Machine Learning field. There are some methodological articles, like Raftery (1996) on the BIC approximation and revisions on BMA

like the highly influential Hoeting *et al.* (1999) and Wasserman (2000) and model uncertainty (Kadane & Lazar, 2004; Clyde & George, 2004). There were also some developments in model choice to more statistically sophisticated models like generalised linear models (Morales *et al.*, 2006), transformations (Hoeting *et al.*, 2002) and generalised auto-regressive conditional heteroskedasticity models (Chen *et al.*, 2011). In the Machine Learning literature, BMA was mostly used along with Bayesian networks (Friedman & Koller, 2003), with theoretical developments allowing for the direct estimation of the averaged network without the necessity of the usual estimation procedure of estimating and combining all posteriors (Dash & Cooper, 2004; Cerquides & De Mántaras, 2005).

Because our revision spans through very diverse fields with very different questions, we investigated how these research questions were reflected in usage throughout the fields. A graphical summary can be observed in Figure 3. Combined prediction is more common in the Physical Sciences field, which is mostly explained by the abundance of prediction articles using the ensemble method by Raftery *et al.* (2005). Economics research questions seemed to focus more on the search for influent factors and determinants, leading to model and variable selection. Because economics dominated the Humanities and Economics field, one can observe a large number of model choice papers. Model selection was also very present in the Life Sciences and Medicine field, with more than half the revised articles. There is, however, an interest in combined estimation that is larger than other fields. Finally, most of the Statistics and Machine Learning literature revised concerns methodological advancements and discussions.



**Figure 3.** Number of usages of Bayesian model averaging by field of application. Hum–Eco, Humanities and Economics; Med–LS, Medicine and Life Sciences; Phys–Eng, Physical Sciences and Engineering; Stat–ML, Statistics and Machine Learning.

# 4.2.3 Model priors

Prior elicitation is a current and open research subject in Bayesian inference as a whole, with distinct currents advocating completely subjectivist researcher-driven prior distributions to completely agnostic and data-driven priors and many types of compromise in between. As discussed in Section 1.1, this problem is compounded in BMA settings, as the space of the conceivable models is a more abstract parametric space, thus harder to describe in terms of a probability measure.

The most common answer to this uncertainty is to assume a uniform distribution over the model space through a vague prior. Such practice is, by far the most common and is adopted by more than 50% of the revised articles, in 408 publications. Given a finite number of K models, the authors simply assume  $\pi(M_l) = \frac{1}{K}$  for  $l = 1, \ldots, K$  or an equivalent formulation like assuming a Bernoulli prior with prior inclusions equal to  $\frac{1}{2}$  in SSVS. In the case of an infinite number of models like in mixture problems, some authors adopt the alternative proposed in Richardson and Green (1997) of fixing a maximum number of classes and assuming a uniform distribution over the restricted model space.

Some authors circumvent the problem by adopting more traditional prior distributions verbatim from the literature. This practice was present in 130 articles, around 15% of all publications, and there seems to be a few trends. Some of this adoption is caused by convenient conceptual frameworks – Many authors in the economics literature simply adopted the prior, evidence estimation and model search proposed by Fernandez *et al.* (2001a) verbatim. With the diffusion of BMA software, less attention was paid to the priors as many authors simply used whatever was default in these implementations.

We also observed 75 articles that tackled the problem and derived model priors for posterior BMA. Some noteworthy examples in the literature include Medvedovic and Sivaganesan (2002) that elicited model priors by the expected behaviour of the cell cultures under study, the analytical considerations of the Bayesian networks of interest in Friedman and Koller (2003), the combination of multiple stakeholders in Mäntyniemi *et al.* (2013) and the proposal of a cross-model correlations to elicit model priors in Garthwaite and Mubwandarikwa (2010).

The remainder 207 articles amount to those that did not specify or apply any model priors. Albeit odd by Bayesian standards, these articles still apply BMA, but priors are not specified. The most common reason in our data set is of the applications of the ensemble forecast method introduced in Raftery *et al.* (2005) that just estimates a 'posterior' weight using the EM algorithm with no mention of priors. There is also the adoption of default options in software packages for BMA for which we tracked down the default settings when possible, but that was not always possible.

### 4.2.4 Evidence estimation

The estimation of the marginal likelihood leading to the posterior model probability presents a considerable difficulty to be overcome in the applications of model averaging. As data sets get more complex, thus requiring more complex models, we aimed to investigate how the BMA literature deals with the problem of estimating the model evidence.

The integral in Equation 2 is not available in closed form for most likelihoods besides in the (generalised) linear regression model with conjugate priors. These models are, however, very popular, and its widespread adoption explains most of the 368 articles that we classified as NA in our CCS.

With respect to approximations, most revised articles approximated the evidence by analytical means, as carried out in 190 articles. Although inferior to the Laplace approximation in

theory (Kass & Raftery, 1995; Raftery, 1996) and simulations (Boone *et al.*, 2005), most articles use the BIC approximation, as its value is given by most software available for parameter estimation in generalised linear models, making for a straightforward application of BMA. Its immediate availability from the maximum likelihood estimates, combined with some theory and available software for a wide class of generalised linear models justify its popularity. Its popularity also makes it the most widely misused approximation. We encountered 'approximations' based on other information criteria as a way to improve over the BIC, frequently using the Akaike information criterion, the deviance information criterion (DIC) and other more *ad hoc* information criteria.

Markov chain Monte Carlo methods were used to estimate the evidence in 196 articles. The vast majority of there works use RJMCMC or SSVS methods, and as such, the posterior model probabilities are estimated by the sample average of an indicator variable for each model. There were, however, plenty of articles that employed the importance sampling approach by Gelfand and Dey (1994) and the much criticised harmonic mean estimator (Newton & Raftery, 1994), as they are simpler to implement in complex models than the trans-dimensional proposals and transformation required for RJMCMC. Still in spirit with MCMC but using a different technique, 18 articles used the ratio of densities (Chib, 1995) approach.

We also encountered 48 articles in which the evidence was estimated through the use of Monte Carlo integration techniques (using independent samples, in contrast with the dependent Markov chain samples used in MCMC), but there was no unifying trend over the practice. Most authors used importance methods, like sampling-importance-resampling, in which a size n sample is taken from the prior distributions and used to construct importance weights using the likelihood. Posterior samples are then obtained from resampling m < n values with replacement using the constructed weights. With these samples, posterior inference and evidence estimation are direct even for complex models, like the stochastic differential equation model used in Bunnin  $et\ al.\ (2002)$ .

# 4.2.5 Dimensionality

As data sets get more massive and models more complex to aggregate different sources of information, it is common that large model spaces emerge. For instance, in the Genomics literature, the development of high throughput marker chips generated millions of SNP variables one desires to associate with a response variable inducing a dimensionality problem. As mentioned in Section 3.5, we investigated two approaches: previous filtering and stochastic search through Markov chains.

Between these two approaches, stochastic search was the most prevalent one, with 149 articles. Among these papers, there are three main trends. With the abundance of BMA in regression models, plenty of the literature was concerned with variable selection, which led to the widespread application of dedicated methods like SSVS that allows for a direct measure of association strength through the marginal posterior inclusion probabilities. A typical example of SSVS can be encountered in Blattenberger *et al.* (2012) applied to the search for risk factors related to the use of cell phones while driving. The MC3 (Madigan *et al.*, 1995) was also widely applied in variable selection settings, mainly in the economics literature following the seminal work by Fernandez *et al.* (2001b). MC3 in turn is very similar in spirit with the RJMCMC methods, which were mostly employed in our revision to choose between complex models instead of variable selection, like performed in Wu and Drummond (2011).

Some authors chose to perform a prior dimensionality reduction in the model space and then apply the model averaging, as performed in 131 articles in our data set, most of them on variable selection for regression models. Among these prior reductions, the most popular was the Occam's window criterion (Madigan & Raftery, 1994), probably because of its implementation in the BMA R package. In some works, some applied the leaps and bounds algorithm (Furnival & Wilson, 1974) prior to the Occam's window to select highly likely variable subsets without the need of an exhaustive calculation.

However, there were cases where authors performed exhaustive calculations for all possible models, and there were many cases where the number of models under consideration were small, leading to the 540 articles marked as NA in our data set.

### 4.2.6 Markov chain Monte Carlo methods

We investigated the application of MCMC methods throughout our data set. For this particular classification, we excluded 24 works that either presented purely revisions or conceptual discussions and did not apply any estimation methodology and articles in which BMA was applied but poorly described to the point we could not tell whether MCMC methods were used anywhere. The remainder 796 articles were classified to their usage of MCMC or lack thereof. In our data set, 379 articled applied MCMC methods, whereas 417 did not.

The temporal pattern of MCMC usage, separated by publication year can be found in Figure 4. Although we suspected that MCMC would become more popular after the popularisation of freely available software, it seems like MCMC methods were not as prevalent in the literature as expected, and its usage did not increase much even with more available

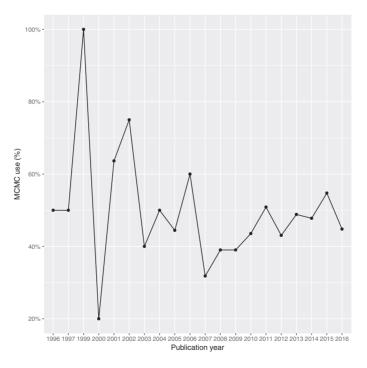


Figure 4. Markov chain Monte Carlo (MCMC) methods usage in the data set.

software and cheaper computational power. MCMC was applied in approximately half the articles published in any given year with the exception of the early years of the 2000s.

### 4.2.7 Simulation studies

Our data set was also classified with respect to the presence of simulation studies. Overall, 21 articles were not clear on their usage of simulations and were therefore excluded from this classification. Of the remaining articles, the majority composed of 504 articles did not perform any form of simulations, whereas 295 did some sort of simulation study.

A more detailed classification by year of publication can be encountered in Figure 5. As in the MCMC classification, the increased computational power did not seem to have an effect on the realisation of simulation studies. One can also observe that simulations seem to be unpopular overall, never accounting for more than half the published papers in any given year.

### 4.2.8 Data-driven validation

We classified the literature on the use of data-driven validation of the results obtained by model averaging. The majority of articles (483 papers) did not perform any validation whatso-ever. Among the articles that performed some kind of data-based validation, the overwhelming majority of 266 articles used cross validation by splitting the data set into two disjoint subsets, fitting the desired models to one of the subsets and validating their performance on the other. The slightly more sophisticated K-fold cross validation was only applied in 33 articles.

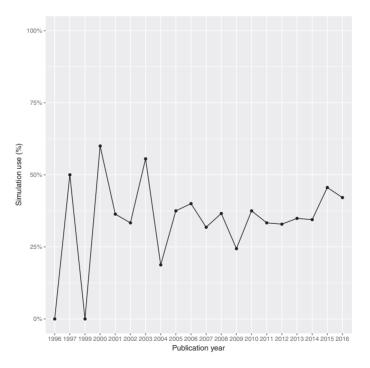


Figure 5. Proportion of simulation studies.

Curiously, even though BMA is a Bayesian technique, there was only a single application of posterior predictive checks (Barber *et al.*, 2006), a set of data-driven Bayesian goodness-of-fit criteria based on the posterior distribution deriving conclusions rooted in the Bayesian paradigm.

# **5 Computing Resources**

Actually, there is various computing resources useful for BMA. Probable the most popular resource is the R package 'BMA', authored by Adrian Raftery, Jennifer Hoeting, Chris Volinsky, Ian Painter and Ka Yee Yeung and maintained by Hana Sevcikova (hanas@uw.edu). It is a package for BMA for linear models, generalised linear models and cox survival regression modelling. Variable selection is also included. Interested readers can obtain its up to data reference manual at https://cran.r-project.org/web/packages/BMA/BMA.pdf.

Another two BMA R packages are the BMA Library (BMS) and the BMA using Bayesian adaptive sampling, particularly for linear regression. They can be found in https://cran.r-project.org/web/packages/BMS/index.html and https://cran.r-project.org/web/packages/BAS/index.html, respectively.

More web resources for BMA can be found in http://bms.zeugner.eu/resources/, for the following softwares: Fortran, Gauss, Gretl, Matlab (Octave) and R.

# 6 Concluding Remarks

This work performed a methodical literature review of BMA studies in the 1996–2016 time period. After a thorough search, we employed a conventional content analysis and proposed a novel CCS that we applied to the literature, revising and classifying 820 articles from a large variety of publications spanning a wide range of applications.

Although much was discussed in the formulation of the proposed classification scheme and its results when applied to the selected literature, some limitations to the present work still exist. First, our search was limited to peer-reviewed articles published in digitally available periodicals. As such, many developments in BMA possibly published in conference proceedings, dissertations or theses and books might have been overlooked. Second, said periodicals were restricted to the titles listed on the four databases mentioned in Section 2.1, and albeit an effort was made to be as inclusive with the literature as possible, non-listed titles were not included except when cited in selected articles and passed the exclusion criteria. Finally, the search was initiated through specific queries on these databases, and as such, relevant articles might have been overlooked when we restricted terms.

Limitations aside, the present literature revision provides relevant insights into the current BMA literature and some indications of future developments. With no aspiration to be exhaustive, we point out a few, namely, we have six observations as follows.

The methodology provides for a very flexible account of model uncertainty that can in principle be applied to any problem, but not much was performed in model choice using BMA aside from variable selection in regression models, with the exception of BMA in Bayesian networks present in the Machine Learning literature of the early 2000s. We found the DIC to be one of the many information criteria incorrectly used in the literature in the place of the BIC for the weighted sum resulting in the Bayes factor in Equation 5. This substitution has, to the best of our knowledge, no analytical justification, and albeit DIC can be successfully used as a model choice criterion on a particular parametric family, it can not be as easily employed when multiple families are considered.

Not much was performed in methodological developments in the statistical literature aside from the seminal works in the late 1990s, limiting its application mostly to (generalised) linear regression models in spite of more complex models being proposed in the same time period. For instance, the problem of evidence estimation is still either circumvented by using convenient likelihoods and conjugate priors or solved through the BIC approximation, which, being reliant on plenty of regularity conditions, might not be adequate for more complex model. Much of the developments in MCMC after the textbook algorithms (i.e. straightforward applications of the Gibbs's sampler and Metropolis-Hastings algorithms) were also mostly absent from our data set. However, we have observed some trends with sequential (as sampling-importance-resampling) and variational methods that are newer and interesting, although they are still restricted to a few publications and sub-areas. For now, these variational methods are those used recently in neurosciences.

There was no significant discussion on computational costs of BMA. There are distinct computational problems derived from dealing with very large data sets, very large and complex model spaces and in the fit of complex models that were not approached in the revised literature.

The vague prior is still the most used model prior, and albeit convenient, it might not be the best choice for all problems. Not much was performed in prior elicitation or the reference priors for BMA.

Neither simulation studies nor validation methods were popular in the literature. This presents a very serious issue, as BMA usually deals with many models drawing from sometimes very distinct assumptions and therefore reaching distinct conclusions. Using BMA without any validation might lead to an overconfidence in the conclusions, the very problem that model averaging is proposed to mitigate.

We discussed model priors to great length in our manuscript. Model priors are rather universal in the applications of BMA, because there is not much one can do to elicitate a particular model space on each application, whereas parameter priors, however, are not. As we mentioned before, applications of BMA span different fields with very distinct models and parameter prior choices, many were motivated by particular applications and relevant literature on the field itself. A discussion of specific parameter priors for each kind of application can be interesting as a future research topic.

# Acknowledgements

The authors thank the Editorial Boarding and referees for their comments and suggestions that led to a substantial improvement of the final version of the manuscript. Brazilian organisations are also acknowledged for partial funding of this work. Tiago M. Fragoso thanks Coordenção de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) and the Universidade de São Paulo – Universidade Federal de São Carlos joint graduate program in Statistics. Wesley Bertoli thanks the Universidade Tecnológica Federal do Paraná and the State of Paraná's Fundação Araucária. Francisco Louzada thanks the Conselho Nacional de Pesquisa (CNPq) and Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP).

### References

Annest, A., Bumgarner, R. E, Raftery, A. E & Yeung, K. Y. (2009). Iterative bayesian model averaging: a method for the application of survival analysis to high-dimensional microarray data. *BMC Bioinf.*, **10**(1), 1–72.

Arnold, R., Hayakawa, Y. & Yip, P. (2010). Capture–recapture estimation using finite mixtures of arbitrary dimension. *Biometrics*, **66**(2), 644–655.

- Baragatti, M. (2011). Bayesian variable selection for probit mixed models applied to gene selection. *Bayesian Anal.*, 6(2), 209–229.
- Barber, J. J, Gelfand, A. E & Silander, J. A. (2006). Modelling map positional error to infer true feature location. *Can. J. Stat.*, 34(4), 659–676.
- Blattenberger, G., Fowles, R., Loeb, P. D. & Clarke, W. A. (2012). Understanding the cell phone effect on vehicle fatalities: a bayesian view. *Appl. Econ.*, **44**(14), 1823–1835.
- Boddhireddy, P., Kelly, M., Northcutt, S., Prayaga, K., Rumph, J. & DeNise, S. (2014). Genomic predictions in angus cattle: comparisons of sample size, response variables, and clustering methods for cross-validation. *J. Anim. Sci.*, **92**(2), 485–497.
- Boone, E. L, Simmons, S. J, Bao, H. & Stapleton, A. E. (2008). Bayesian hierarchical regression models for detecting qtls in plant experiments. *J. Appl. Stat.*, **35**(7), 799–808.
- Boone, E. L, Ye, K. & Smith, E. P. (2005). Assessment of two approximation methods for computing posterior model probabilities. *Comput. Stat. Data Anal.*, **48**(2), 221–234.
- Brown, P. J., Vannucci, M. & Fearn, T. (2002). Bayes model averaging with selection of regressors. *J. R. Stat. Soc. Ser.B (Statistical Methodology)*, **64**(3), 519–536.
- Bunnin, F. O., Guo, Y. & Ren, Y. (2002). Option pricing under model and parameter uncertainty using predictive densities. *Stat. Comput.*, **12**(1), 37–44.
- Cerquides, J. & De Mántaras, R. L. (2005). Tan classifiers based on decomposable distributions. *Mach. Learn.*, **59**(3), 323–354.
- Chen, C. W., Liu, F. C. & Gerlach, R. (2011). Bayesian subset selection for threshold autoregressive moving-average models. *Comput. Stat.*, **26**(1), 1–30.
- Chib, S. (1995). Marginal likelihood from the Gibbs output. J. Am. Stat. Assoc., 90(432), 1313–1321.
- Clyde, M. & George, E. I. (2004). Model uncertainty. Stat. Sci., 19, 81-94.
- Conti, D. V., Cortessis, V., Molitor, J. & Thomas, D. C. (2003). Bayesian modeling of complex metabolic pathways. *Hum. Heredity*, **56**(1-3), 83–93.
- Dash, D. & Cooper, G. F. (2004). Model averaging for prediction with discrete Bayesian networks. *The J. Mach. Learn. Res.*, **5**, 1177–1203.
- Eicher, T. S, Papageorgiou, C. & Raftery, A. E. (2011). Default priors and predictive performance in Bayesian model averaging, with application to growth determinants. *J. Appl. Econometrics*, **26**(1), 30–55.
- Fernandez, C., Ley, E. & Steel, M. F. J. (2001a). Benchmark priors for Bayesian model averaging. *J. Econometrics*, **100**(2), 381–427.
- Fernandez, C., Ley, E. & Steel, M. F. (2001b). Model uncertainty in cross-country growth regressions. *J. Appl. Econometrics*, **16**(5), 563–576.
- Fridley, B. L. (2009). Bayesian variable and model selection methods for genetic association studies. *Genet. Epidemiol.*, **33**(1), 27–37.
- Friedman, N. & Koller, D. (2003). Being Bayesian about network structure. A Bayesian approach to structure discovery in Bayesian networks. *Mach. Learn.*, **50**(1-2), 95–125.
- Friel, N. & Wyse, J. (2012). Estimating the evidence-a review. Stat. Neerlandica, 66(3), 288-308.
- Friston, K., Mattout, J., Trujillo-Barreto, N., Ashburner, J. & Penny, W. (2007). Variational free energy and the laplace approximation. *Neuroimage*, **34**(1), 220–234.
- Furnival, G. M & Wilson, R. W. (1974). Regressions by leaps and bounds. Technometrics, 16(4), 499-511.
- Garthwaite, P. H. & Mubwandarikwa, E. (2010). Selection of weights for weighted model averaging. *Aust. & N. Z. J. Stat.*, **52**(4), 363–382.
- Gelfand, A. E. & Dey, D. K. (1994). Bayesian model choice: asymptotics and exact calculations. *J. R. Stat. Soc. Ser. B (Methodological)*, 501–514.
- Gelman, A. & Meng, X. (1998). Simulating normalizing constants: from importance sampling to bridge sampling to path sampling. *Stat. Sci.*, **13**, 163–185.
- Gelman, A., Meng, X. & Stern, H. (1996). Posterior predictive assessment of model fitness via realized discrepancies. Stat. Sin., 6(4), 733–760.
- George, E. I. & McCulloch, R. E. (1993). Variable selection via Gibbs sampling. J. Am. Stat. Assoc., 88(423), 881–889.
- George, E. I. & McCulloch, R. E. (1997). Approaches for Bayesian variable selection. Stat. Sin., 7(2), 339–373.
- Geweke, J. (1999). Using simulation methods for Bayesian econometric models: inference, development, and communication. *Econometric Rev.*, **18**(1), 1–73.
- Goenner, C. F. (2004). Uncertainty of the liberal peace. J. Peace Res., 41(5), 589–605.
- Goenner, C. F. (2010). Discrimination and mortgage lending in Boston: the effects of model uncertainty. *The J. Real Estate Finance Econ.*, **40**(3), 260–285.
- Green, P. J. (1995). Reversible jump Markov chain Monte Carlo computation and Bayesian model determination. *Biometrika*, **82**(4), 711–732.

- Guan, Y. & Stephens, M. (2011). Bayesian variable selection regression for genome-wide association studies and other large-scale problems. *The Ann. Appl. Stat.*, 5, 1780–1815.
- Guarín, A., González, A., Skandalis, D. & Sánchez, D. (2014). An early warning model for predicting credit booms using macroeconomic aggregates. *Ensayos Sobre Política Económica*, **32**(SPE73), 77–86.
- Habier, D., Tetens, J., Seefried, F., Lichtner, P. & Thaller, G. (2010). The impact of genetic relationship information on genomic breeding values in german holstein cattle. *Genet. Sel. Evol.*, **42**(1), 1–5.
- Hachicha, W. & Ghorbel, A. (2012). A survey of control-chart pattern-recognition literature (1991–2010) based on a new conceptual classification scheme. Comput. Ind. Eng., 63(1), 204–222.
- Hoeting, J. A., Madigan, D., Raftery, A. E. & Volinsky, C. T. (1999). Bayesian model averaging: a tutorial. Stat. Sci., 14, 382–401.
- Hoeting, J. A., Raftery, A. E. & Madigan, D. (2002). Bayesian variable and transformation selection in linear regression. J. Comput. Graphical Stat., 11(3), 485–507.
- Hsieh, H.-F. & Shannon, S. E. (2005). Three approaches to qualitative content analysis. *Qual. Health Res.*, **15**(9), 1277–1288.
- Jacobson, T. & Karlsson, S. (2004). Finding good predictors for inflation: a Bayesian model averaging approach. J. Forecasting, 23(7), 479–496.
- Kadane, J. B & Lazar, N. A. (2004). Methods and criteria for model selection. *J. Am. Stat. Assoc.*, **99**(465), 279–290. Kass, R. E. & Raftery, A. E. (1995). Bayes factors. *J. Am. Stat. Assoc.*, **90**(430), 773–795.
- King, R. & Brooks, S. (2001). On the Bayesian analysis of population size. Biometrika, 88(2), 317-336.
- Kizilkaya, K., Fernando, R. & Garrick, D. (2010). Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymorphism genotypes. J. Animal Sci., 88(2), 544–551.
- Koop, G. & Potter, S. (2004). Forecasting in dynamic factor models using Bayesian model averaging. The Econometrics J., 7(2), 550–565.
- Lamon, E. C. & Clyde, M. A. (2000). Accounting for model uncertainty in prediction of chlorophyll a in lake okeechobee. J. Agric. Biol. Environ. Stat., 5, 297–322.
- Leamer, E. E. (1978). Specification Searches New York: Wiley.
- Liddle, A. R., Mukherjee, P., Parkinson, D. & Wang, Y. (2006). Present and future evidence for evolving dark energy. *Phys. Rev. D*, **74**(12), 123506.
- Lunn, D. J. (2008). Automated covariate selection and Bayesian model averaging in population pk/pd models. J. Pharmacokinet. Pharmacodyn., 35(1), 85–100.
- Madigan, D. & Raftery, A. E. (1994). Model selection and accounting for model uncertainty in graphical models using Occam's window. *J. Am. Stat. Assoc.*, **89**(428), 1535–1546.
- Madigan, D., York, J. & Allard, D. (1995). Bayesian graphical models for discrete data. Int. Stat. Rev./Revue Int. de Stat., 63, 215–232.
- Mäntyniemi, S., Haapasaari, P., Kuikka, S., Parmanne, R., Lehtiniemi, M., Kaitaranta, J. & Hilborn, R. (2013). Incorporating stakeholders' knowledge to stock assessment: central baltic herring. *Can. J. Fish. Aquat.Sci.*, **70**(4), 591–599.
- Medvedovic, M. & Sivaganesan, S. (2002). Bayesian infinite mixture model based clustering of gene expression profiles. *Bioinformatics*, 18(9), 1194–1206.
- Meuwissen, T. E., Hayes, B. J. & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, **157**(4), 1819–1829.
- Moher, D., Liberati, A., Tetzlaff, J. & Altman, D. G. (2009). Preferred reporting items for systematic reviews and meta-analyses: the prisma statement. Ann. Internal Med., 151(4), 264–269.
- Morales, K. H., Ibrahim, J. G., Chen, C.-J. & Ryan, L. M. (2006). Bayesian model averaging with applications to benchmark dose estimation for arsenic in drinking water. *J. Am. Stat. Assoc.*, **101**(473), 9–17.
- Newton, M. A. & Raftery, A. E. (1994). Approximate Bayesian inference with the weighted likelihood bootstrap. *J. R. Stat. Soc. Ser. B (Methodological)*, **56**, 3–48.
- Oehler, V. G, Yeung, K., Choi, Y. E, Bumgarner, R. E, Raftery, A. E & Radich, J. P. (2009). The derivation of diagnostic markers of chronic myeloid leukemia progression from microarray data. *Blood*, **114**(15), 3292–3298.
- Parkinson, D. & Liddle, A. R. (2013). Bayesian model averaging in astrophysics: a review. *Stat. Anal. Data Mining: The ASA Data Sci. J.*, **6**(1), 3–14.
- Penny, W. D, Stephan, K. E, Daunizeau, J., Rosa, M. J, Friston, K. J, Schofield, T. M & Leff, A. P. (2010). Comparing families of dynamic causal models. *PLoS Comput. Biol.*, **6**(3), e1000709–e1000709.
- Phelan, S., Liu, T., Gorin, A., Lowe, M., Hogan, J., Fava, J. & Wing, R. R. (2009). What distinguishes weight-loss maintainers from the treatment-seeking obese? Analysis of environmental, behavioral, and psychosocial variables in diverse populations. *Ann. Behav. Med.*, **38**(2), 94–104.
- Plummer, M. (2003). Jags: a program for analysis of Bayesian graphical models using gibbs sampling. In *Proceedings* of the 3rd International Workshop on Distributed Statistical Computing, Vol. 124, pp. 1–125. Technische Universit at Wien.

- Raftery, A. E. (1996). Approximate Bayes factors and accounting for model uncertainty in generalised linear models. *Biometrika*, **83**(2), 251–266.
- Raftery, A. E, Gneiting, T., Balabdaoui, F. & Polakowski, M. (2005). Using Bayesian model averaging to calibrate forecast ensembles. *Mon. Weather Rev.*, 133(5), 1155–1174.
- Raftery, A. E, Kárnỳ, M. & Ettler, P. (2010). Online prediction under model uncertainty via dynamic model averaging: application to a cold rolling mill. *Technometrics*, **52**(1), 52–66.
- Raftery, A. E & Painter, I. S. (2005). BMA: an R package for Bayesian model averaging. R News, 5(2), 2-8.
- Ranyimbo, A. & Held, L. (2006). Estimation of the false negative fraction of a diagnostic kit through Bayesian regression model averaging. *Stat. Med.*, **25**(4), 653–667.
- Richardson, S. & Green, P. J. (1997). On Bayesian analysis of mixtures with an unknown number of components. *J. R. Stat. Soc. Ser. B (Methodological)*, **59**, 731–792.
- Robert, C. & Casella, G. (2013). Monte Carlo Statistical Methods. New York: Springer Science & Business Media.
- Roberts, H. V. (1965). Probabilistic prediction. J. Am. Stat. Assoc., 60(309), 50-62.
- Sidman, A. H., Mak, M. & Lebo, M. J. (2008). Forecasting non-incumbent presidential elections: lessons learned from the 2000 election. *Int. J. Forecasting*, **24**(2), 237–258.
- Silvestro, D., Zizka, G. & Schulte, K. (2014). Disentangling the effects of key innovations on the diversification of Bromelioideae (Bromeliaceae). *Evolution*, **68**(1), 163–175.
- Spiegelhalter, D. J, Thomas, A., Best, N. G & Gilks, W. R. (1995). Bugs: Bayesian inference using Gibbs sampling, version 0.50. MRC Biostatistics Unit, Cambridge.
- Swartz, M. D, Peterson, C. B, Lupo, P. J, Wu, X., Forman, M. R, Spitz, M. R, Hernandez, L. M, Vannucci, M. & Shete, S. (2013). Investigating multiple candidate genes and nutrients in the folate metabolism pathway to detect genetic and nutritional risk factors for lung cancer. *Plos One*, **8**(1), 1–9.
- Thomson, J. R, Mac Nally, R., Fleishman, E. & Horrocks, G. (2007). Predicting bird species distributions in reconstructed landscapes. *Conserv. Biol.*, **21**(3), 752–766.
- Visweswaran, S., Angus, D. C, Hsieh, M., Weissfeld, L., Yealy, D. & Cooper, G. F. (2010). Learning patient-specific predictive models from clinical data. *J. Biomed. Inf.*, **43**(5), 669–685.
- Volinsky, C. T., Madigan, D., Raftery, A. E. & Kronmal, R. A. (1997). Bayesian model averaging in proportional hazard models: assessing the risk of a stroke. *J. R. Stat. Soc. Ser. C (Applied Statistics)*, **46**(4), 433–448.
- Vrontos, S. D., Vrontos, I. D. & Giamouridis, D. (2008). Hedge fund pricing and model uncertainty. J. Banking & Finance, 32(5), 741–753.
- Wasserman, L. (2000). Bayesian model selection and model averaging. J. Math. Psychology, 44(1), 92-107.
- Wintle, B. A, McCarthy, M. A, Volinsky, C. T & Kavanagh, R. P. (2003). The use of Bayesian model averaging to better represent uncertainty in ecological models. *Conserv. Biol.*, 17(6), 1579–1590.
- Wu, C.-H. & Drummond, A. J. (2011). Joint inference of microsatellite mutation models, population history and genealogies using transdimensional Markov chain Monte Carlo. *Genetics*, **188**(1), 151–164.
- Yeung, K. Y, Bumgarner, R. E. & Raftery, A. E. (2005). Bayesian model averaging: development of an improved multi-class, gene selection and classification tool for microarray data. *Bioinformatics*, 21(10), 2394–2402.
- Yin, G. & Yuan, Y. (2009). Bayesian model averaging continual reassessment method in phase I clinical trials. J. Am. Stat. Assoc., 104(487), 954–968.
- Zellner, A. (1986). On assessing prior distributions and bayesian regression analysis with g-prior distributions. In *Bayesian Inference and Decision Techniques: Essays in Honor of Bruno de Finetti*, Ed. Zellner, A., pp. 233–243. Amsterdam: North-Holland.

# **Supporting Information**

Additional supporting information may be found online in the supporting information tab for this article.

[Received October 2015, accepted October 2017]

Copyright of International Statistical Review is the property of Wiley-Blackwell and its content may not be copied or emailed to multiple sites or posted to a listserv without the copyright holder's express written permission. However, users may print, download, or email articles for individual use.