

1     **Improving Bayesian Model Averaging for Ensemble Flood Modeling Using**  
2             **Multiple Markov Chains Monte Carlo Sampling**

3     **Tao Huang<sup>1</sup> and Venkatesh Merwade<sup>1</sup>**

4     <sup>1</sup>Lyles School of Civil Engineering, Purdue University, West Lafayette, Indiana, USA

5     Corresponding author: Tao Huang ([huan1441@purdue.edu](mailto:huan1441@purdue.edu))

6     **Key Points:**

- 7         ● Multiple Markov Chains Monte Carlo method is applicable for estimating Bayesian  
8             model averaging weights and variances.
- 9         ● The performance of Metropolis-Hastings algorithm is better than that of Expectation-  
10             Maximization algorithm in ensemble flood modeling.
- 11         ● Multiple Markov Chains Monte Carlo method can provide more information about the  
12             uncertainty of Bayesian model averaging parameters.

13

14 **Abstract**

15 As all kinds of physics-based and data-driven models are emerging in hydrologic and hydraulic  
16 engineering, Bayesian model averaging (BMA) is one of the popular multi-model methods used  
17 to account for various uncertainty sources in the flood modeling process and generate robust  
18 ensemble predictions. The reliability of BMA parameters (weights and variances) determines the  
19 accuracy of BMA predictions. However, the uncertainty in BMA parameters with fixed values,  
20 which are usually obtained from Expectation-Maximization (EM) algorithm, has not been  
21 adequately investigated in BMA-related applications over the past few decades. Given the  
22 limitations of the commonly used EM algorithm, Metropolis-Hastings (M-H) algorithm, which is  
23 one of the most widely used algorithms in Markov Chain Monte Carlo (MCMC) method, is  
24 proposed to estimate BMA parameters. Both numerical experiments and one-dimensional HEC-  
25 RAS models are employed to examine the applicability of M-H algorithm with multiple  
26 independent Markov chains. The performances of EM and M-H algorithms are compared based  
27 on the daily water stage predictions from 10 model members. Results show that BMA weights  
28 estimated from both algorithms are comparable, while BMA variances obtained from M-H  
29 algorithm are closer to the given variances in the numerical experiment. Moreover, the normal  
30 proposal used in M-H algorithm can yield narrower distributions for BMA weights than those  
31 from the uniform proposal. Overall, MCMC approach with multiple chains can provide more  
32 information associated with the uncertainty of BMA parameters and its performance is better  
33 than the default EM algorithm in terms of multiple evaluation metrics as well as algorithm  
34 flexibility.

35 **1 Introduction**

36 Application of different numerical models based on physical processes as well as data driven  
37 approaches are playing a crucial role in simulating hydrologic and hydraulic systems to provide  
38 flood risk information to the public (Dottori et al., 2021; FEMA, 2018; Teng et al., 2017; Xie et  
39 al., 2021). Given the temporal and spatial variability of flood events as well as the complexity of  
40 watersheds, the pursuit of a “perfect” model that can incorporate all hydrologic and hydraulic  
41 processes and handle different scenarios is encouraging, but this pursuit faces multiple  
42 challenges. The challenges in simulating flooding processes, including the limitations of  
43 governing mathematic principles, estimation of parameters, measurement of driving forces, and  
44 computational efficiency, are important issues that modelers need to take into consideration in  
45 order to provide reliable and robust predictions about flooding (Jafarzadegan et al., 2021;  
46 Kobarfard et al., 2022; Liu and Merwade, 2018; Merwade et al., 2008; F Pappenberger et al.,  
47 2005; Florian Pappenberger et al., 2006; Sharma et al., 2022; Teng et al., 2017). Additionally,  
48 “equifinality” in hydrologic and hydraulic modeling may lead to multiple models or different  
49 model configurations to yield similar results that match the observations equally well (Beven and  
50 Binley, 1992; Refsgaard et al., 2012; Von Bertalanffy, 1972). Thus, it is not recommended to  
51 rely on streamflow predictions and flood inundation maps obtained by a single model  
52 implementation (Duan et al., 2007; Huang and Merwade, 2023; Liu and Merwade, 2018;  
53 Romanowicz and Beven, 2003; Zounemat-Kermani et al., 2021).

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55 Considering the uncertainty involved in simulating the hydrology and hydraulics of flooding,  
56 multi-model ensemble methods should be applied to capture various uncertainty sources for  
57 making robust predictions (Bates and Granger, 1969; Dickinson, 1973; Newbold and Granger,

58 1974; Teng et al., 2017; Zounemat-Kermani et al., 2021). Over the past few decades, different  
59 kinds of multi-model methods, for example the simple average method (Makridakis et al., 1982),  
60 the weighted average method (Makridakis and Winkler, 1983; Singh et al., 2010; Tebaldi and  
61 Knutti, 2007; Winkler, 1989), the multi-model super-ensemble method (Ajami et al., 2006;  
62 Krishnamurti et al., 1999) and the neural network method (Acharya et al., 2014; Chattopadhyay  
63 and Chattopadhyay, 2008; Shamseldin and O'Connor, 1999; Shamseldin et al., 1997; Zounemat-  
64 Kermani et al., 2021), have been widely used in climate projections and hydrologic predictions.  
65 Among these multi-model ensemble approaches, the Bayesian model averaging (BMA) approach  
66 (Kass and Raftery, 1995; Leamer, 1978; Raftery et al., 2005) has been successfully applied to the  
67 flood modeling (Duan et al., 2007; Huang and Merwade, 2023; Liu and Merwade, 2018, 2019;  
68 Rings et al., 2012; Vrugt et al., 2008). More importantly, the BMA approach is able to produce  
69 accurate and reliable predictions due to its advantages over other multi-model techniques.  
70 Specifically, the BMA probability density function (PDF) of a predictive variable is a weighted  
71 average of PDFs from a model ensemble that covers multiple significant uncertainty sources.  
72 From the Bayesian perspective, the weight of a model member represents its relative prediction  
73 performance compared to the other model members and the sum of the nonnegative weights is  
74 equal to one, which is easy to interpret when performing the model evaluation and comparison  
75 (Raftery et al., 2005). Additionally, the BMA procedure can produce the prediction probability  
76 distribution which reflects the uncertainty associated with the mean prediction (Raftery et al.,  
77 1997). Finally, the relative impacts of individual uncertainty sources and the uncertainty  
78 propagation in the modeling process can be demonstrated and quantified through a hierarchical  
79 BMA (HBMA) framework (Chitsazan and Tsai, 2015; Huang and Merwade, 2023; Liu and  
80 Merwade, 2019).

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The performance of BMA predictions is primarily dependent on the accurate estimation of BMA parameters (weights and variances). However, the reliability associated with BMA parameters has not received enough attention. In past literature relevant to the applications of BMA approach, both the weights and variances obtained through the Expectation-Maximization (EM) algorithm are assigned fixed values (Cao et al., 2021; Darbandsari and Coulibaly, 2021; Dormann et al., 2018; Duan et al., 2007; Huang and Merwade, 2023; Liu and Merwade, 2018; Madadgar and Moradkhani, 2014; Moknatian and Mukundan, 2023; Tsai, 2010). These fixed values cannot represent the uncertainty in the BMA parameters, especially when different datasets are used for training or a specific training dataset does encompass the overall prediction capacity of certain models (Madadgar and Moradkhani, 2014; Refsgaard et al., 2012; Rojas et al., 2010; Tebaldi and Knutti, 2007). Although the EM algorithm has been provided to be able to provide good estimates of the BMA weight and variance for each model member with satisfactory computational efficiency (McLachlan and Krishnan, 2007; Vrugt et al., 2008), a few issues need to be addressed. First, the global optimal estimates of BMA parameters cannot be guaranteed especially for solving some high-dimensional problems (Duan et al., 2007; Vrugt et al., 2008). Second, the assumption that the conditional PDF of the variable of interest follows a normal distribution in the application of the default EM algorithm limits its wide application in other fields. Finally, a fixed value for the pre-processing parameter (e.g., transformation parameter in the Box-Cox method) used to transform the original datasets into the Gaussian space can add more uncertainty in the final predictions (Liu and Merwade, 2018).

103 Given the limitations of the default EM algorithm in the BMA analysis discussed above, the  
104 Markov Chain Monte Carlo (MCMC) sampling method (Robert et al., 1999) is proposed in this  
105 study to estimate the BMA parameters. It has been shown that the application of MCMC method  
106 for hydrology can provide a full view of the unknown parameter's posterior probability  
107 distribution (Gaume et al., 2010; Nguyen et al., 2021; Reis Jr and Stedinger, 2005; Sharma et al.,  
108 2022; Vrugt et al., 2008; Wang et al., 2017; Zhao et al., 2021), which can provide an explicit  
109 representation and quantification for the parameter uncertainty. Specifically, this method can be  
110 implemented by different algorithms to generate a sequence of stochastic samples that converge  
111 to the target probability density function of the unknown parameter (Luengo et al., 2020). In a  
112 previous study, differential evolution adaptive metropolis algorithm (Vrugt, 2016; Vrugt et al.,  
113 2008) was developed to estimate the BMA weights and an integrated variance of the hydrologic  
114 model ensemble. This study also introduced more parameters, such as the number of chain pairs  
115 used to generate the proposed sample and the jump size among different modes, in the algorithm.  
116 Furthermore, an overall variance across different model members was assumed and the  
117 autocorrelation of the samples in each chain was not evaluated, which would add more  
118 uncertainty to the estimates of BMA parameters.

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120 The Metropolis-Hastings (M-H) algorithm (Hastings, 1970; Metropolis et al., 1953) is one of the  
121 most widely used algorithms in the MCMC method, but its feasibility for estimating BMA  
122 parameters has not been investigated in previous literature. For the solution to some high-  
123 dimensional and multimodal problems (e.g., likelihood function in the BMA analysis), one single  
124 Markov chain may get stuck in a local optimal mode (Vats and Knudson, 2021), and hence  
125 multiple independent Markov chains is a possible option to explore the whole value space of

126 unknown parameters. Additionally, the MCMC method with the M-H algorithm does not require  
127 too many subjective judgments for setting-up of the sampling process and it is flexible in terms  
128 of modification based on the assumption of the target posterior distribution of the unknown  
129 parameter. Accordingly, the overall goal of this study is to investigate the feasibility of the M-H  
130 MCMC algorithm and assess any advantages over the default EM algorithm for estimating BMA  
131 parameters (weights and variances) of ensemble flood modeling. This broader goal is  
132 accomplished through the following objectives: (i) Apply BMA approach in flood modeling to  
133 estimate BMA parameters using different numbers of samples in each Markov chain with the M-  
134 H algorithm; (ii) compare the performance of EM and M-H MCMC algorithms for estimating the  
135 BMA parameters; (iii) estimate the BMA weights using different proposal distributions in the M-  
136 H algorithm; and (iv) investigate the impact of different conditional PDFs of the predictor  
137 variable on the BMA parameters. To examine the validity and applicability of the MCMC  
138 method with the M-H algorithm in the BMA analysis, both numerical experiments and hydraulic  
139 modeling using Hydrologic Engineering Center-River Analysis System (HEC-RAS) (Brunner,  
140 2016b; FEMA, 2018) are carried out in this study.

## 141 **2 Study area and data**

142 For hydraulic modeling to evaluate the uncertainty in the BMA parameters and verify the  
143 applicability of the MCMC method on the parameter estimation, two river reaches (see Figure 1  
144 and Table 1) in the states of Indiana and Texas of the United States are selected. Both reaches  
145 have existing HEC-RAS models from the Federal Emergency Management Agency's (FEMA)  
146 Flood Insurance Rate Map program and have both upstream and downstream streamflow  
147 measurements from the United States Geological Survey (USGS) gauges. These study reaches

148 are located in the midwestern and southern regions of the United States and provide distinct  
149 geomorphic characteristics, thus making them good test beds for the BMA analysis. The HEC-  
150 RAS models for all counties in Indiana are available from the Indiana Department of Natural  
151 Resources' hydrology and hydraulics library (INDNR, 2018), and the HEC-RAS models for the  
152 central and western regions in Texas can be accessed from FEMA's Estimated Base Flood  
153 Elevation Viewer (FEMA, 2015). Available HEC-RAS models from FEMA studies are 1D  
154 steady-state, but to reduce the uncertainty from the steady-flow assumption and also enable  
155 comparison of simulation output from the model ensemble to the observation from the USGS  
156 gauges, they are modified to perform 1D unsteady-flow simulation. The unsteady state  
157 modification did not involve any changes to the model structure and parameter, including the  
158 layout and geometry of river cross-sections and Manning's  $n$  for the main channel and the  
159 floodplain. Unsteady state simulations for 100 days from March to July 2021 covering a couple  
160 of flood events are performed. Daily streamflow data (upstream input for HEC-RAS) and water  
161 stage data (downstream output for the BMA analysis) used in this study are obtained from the  
162 corresponding USGS gauges at each study reach.

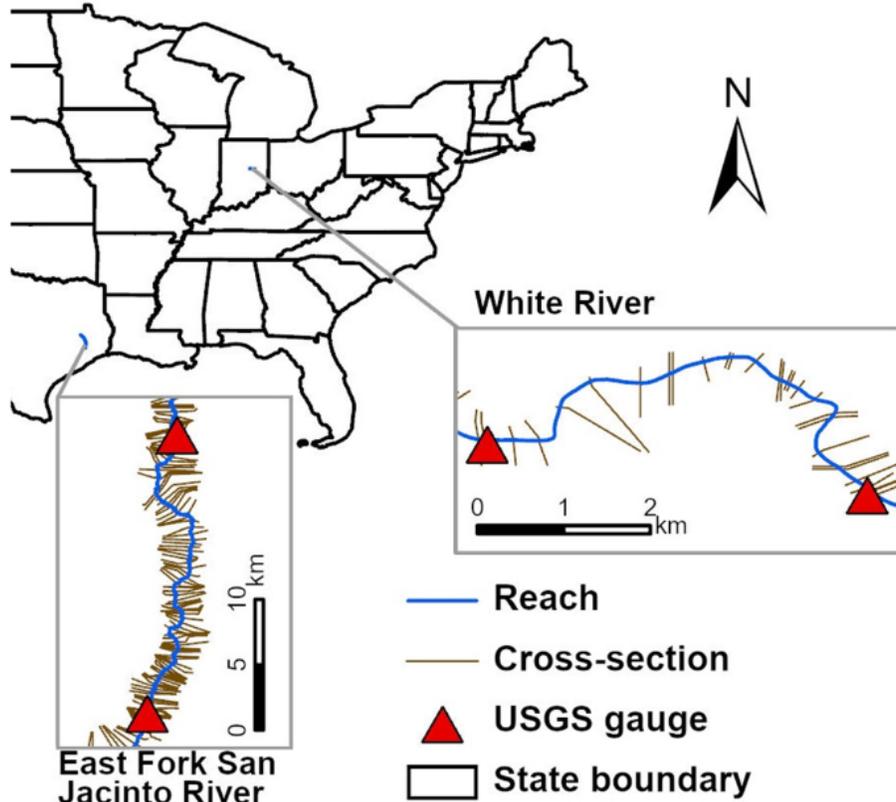


Figure 1. Layout map of study areas in Indiana and Texas, USA.

Table 1. Basic information of study area.

Study stream	Channel length (km)	Average channel width (m)	Channel slope (%)	Upstream USGS gauge	Downstream USGS gauge	Simulation Period (100 days)
White	6.76	64	0.0631	03348000	03348130	2021-3-15 to 2021-6-22
East Fork San Jacinto	50.11	76	0.0438	08070000	08070200	2021-4-15 to 2021-7-23

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### 168 3 Methodology

#### 169 3.1 Numerical Experiment and Hydraulic Modeling

##### 170 (1) Numerical experiment

171 Considering the complexity of residual patterns in hydrologic and hydraulic models (Beven,

172 2016), it is necessary to conduct numerical experiments based on pre-defined model errors as

173 this is the first study to apply the MCMC method for estimating BMA parameters. Given the  
 174 basic assumption of EM algorithm and the relatively small size (less than 10) of the model  
 175 ensemble in practice (Cao et al., 2021; Huo et al., 2019; Moknatian and Mukundan, 2023;  
 176 Raftery et al., 2005; Tian et al., 2021; Tsai, 2010; Vrugt et al., 2008), a total of 10 sets of  
 177 hydrologic data (100 days of daily observed water stage data, denoted as  $D$ , of the White river in  
 178 Indiana) that contain random errors (denoted as  $\varepsilon$ ) are generated. These synthetic datasets are  
 179 created assuming a normal distribution with zero mean and standard deviations ranging from  
 180 0.06 m (0.2 ft) to 0.30 m (1 ft) with an increment of 0.06m (0.2 ft). These 10 datasets (see Table  
 181 2) will serve as the predictions obtained from the flood model ensemble. Next, both EM and M-  
 182 H MCMC algorithms are applied to these predictions to estimate the BMA parameters (weight  
 183 and variance) of each candidate model. Due to the randomness in model errors, it is expected that  
 184 the value of BMA parameters will vary to some extent even though the standard deviations of the  
 185 normal distribution are the same. For example, both Model 1 ( $f_1$ ) and Model 2 ( $f_2$ ) have the same  
 186 standard deviation of 0.06 m in Table 2.

187 Table 2. BMA ensemble model members for numerical experiments.

No.	Model Predictions (m)	No.	Model Predictions (m)
1	$f_1 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.06^2)$	2	$f_2 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.06^2)$
3	$f_3 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.12^2)$	4	$f_4 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.12^2)$
5	$f_5 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.18^2)$	6	$f_6 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.18^2)$
7	$f_7 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.24^2)$	8	$f_8 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.24^2)$
9	$f_9 = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.30^2)$	10	$f_{10} = D + \varepsilon$ , where $\varepsilon \sim N(0, 0.30^2)$

188 Note:  $D = 100$  days of daily water stage data, and  $\varepsilon =$  random model errors that follow a normal  
 189 distribution.

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## 191 (2) Ensemble Flood Modeling in 1D HEC-RAS

192 A 1D HEC-RAS model is a simplified representation of the river network, i.e., river centerlines,  
 193 left and right bank lines, and horizontal cross-sections along the reach. During the simulation  
 194 process, the water surface elevation at discrete cross-sections is estimated for given boundary  
 195 conditions. Using the water surface elevations from all cross-sections, a 2D inundation extent  
 196 map can be generated by interpolating the positive differences between the topographical data  
 197 (e.g., digital elevation model) and the water surface layer. More technical details about the 1D  
 198 HEC-RAS can be referred to the software manual (Brunner, 2016a, 2016b). In terms of the  
 199 model configuration, a HEC-RAS project is a collection of multiple files including the river  
 200 geometry, relevant parameters, and boundary conditions. Based on previous studies about the  
 201 uncertainty in the modeling of FEMA’s flood inundation maps, an uncertainty range of  $\pm 20\%$   
 202 around values of channel roughness and upstream flow input used in the model are considered in  
 203 simulations (Huang and Merwade, 2023; Liu and Merwade, 2019). Accordingly, the ensemble is  
 204 made up of 10 sets of model predictions from the HEC-RAS ensemble (see Table 3), 9 of which  
 205 are obtained based on different combinations of geometry files (including channel roughness)  
 206 and unsteady flow files (including upstream flow series), and the last one is the average of  
 207 simulations from the other 9 members.

208 Table 3. Model configurations in HEC-RAS for BMA analysis.

<b>Model Configuration No.</b>	<b>Channel Roughness</b>	<b>Upstream Flow Input</b>	<b>HEC-RAS Plan Files</b>
1	0.8n	0.8Q	g01 & u01
2	0.8n	Q	g01 & u02
3	0.8n	1.2Q	g01 & u03
4	N	0.8Q	g02 & u01
5	N	Q	g02 & u02
6	N	1.2Q	g02 & u03
7	1.2n	0.8Q	g03 & u01

Model Configuration No.	Channel Roughness	Upstream Flow Input	HEC-RAS Plan Files
8	1.2n	Q	g03 & u02
9	1.2n	1.2Q	g03 & u03
10	Average of simulations from No.1-No.9		

209 Note: n is the Manning's n value for the main channel in the original HEC-RAS models, Q is the  
 210 streamflow from USGS gauge stations, g\*\* represents a geometry file of a HEC-RAS project,  
 211 and u\*\* represents a flow data file of a HEC-RAS project.  
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### 213 3.2 Bayesian modeling averaging (BMA) analysis

214 BMA (Kass and Raftery, 1995; Raftery et al., 2005) is a statistical method that averages the  
 215 predictions from an ensemble of multiple competing models instead of from a single “perfect”  
 216 model through the corresponding BMA weights. According to the law of total probability, the  
 217 PDF of the BMA probabilistic prediction of the variable of interest (daily water stage in this  
 218 study) is given by Equations (1) - (2).

$$219 \quad p(y | D) = \sum_{k=1}^K p(f_k | D) \cdot p_k(y | f_k, D) = \sum_{k=1}^K w_k \cdot p_k(y | f_k, D) \quad (1)$$

$$220 \quad \sum_{k=1}^K w_k = 1 \quad (2)$$

221 where  $y$  is the predictor variable;  $D = [y_1^{obs}, y_2^{obs}, \dots, y_T^{obs}]$  is the observed hydrologic data (daily  
 222 water stage data from the USGS gauges) with data length  $T$ ;  $f_k$  is the prediction of the  $k^{\text{th}}$  model.

223  $p(f_k | D) = w_k$  is the posterior probability of the predictions of  $k^{\text{th}}$  model given the observation  
 224 data. The weight ( $w_k$ ) reflects how well a specific model prediction matches the observed data,  
 225 and hence better-performance models have higher weights, which is nonnegative and goes up to

226 one.  $p_k(y|f_k, D)$  is the posterior distribution of  $y$  given both the predictions of the  $k^{\text{th}}$  model and  
 227 the observation data.

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229 Based on Equation (1), a log-likelihood function is constructed for estimating the BMA weight  
 230 and variance that can maximize the likelihood. By convention, it is assumed that the conditional  
 231 probability  $p_k(y|f_k, D)$  follows a normal distribution. Thus, the log-likelihood function is  
 232 shown in Equation (3).

$$233 \quad L(\theta) = \sum_{t=1}^T \log \left( \sum_{k=1}^K w_k \cdot p_k(y_t | f_{k,t}, \sigma_k) \right) = \sum_{t=1}^T \log \left( \sum_{k=1}^K w_k \cdot \frac{1}{\sigma_k \sqrt{2\pi}} e^{-\frac{1}{2} \left( \frac{y_t - f_{k,t}}{\sigma_k} \right)^2} \right) \quad (3)$$

234 where  $\theta$  is the unknown BMA parameters (weight and variance of each model member),  $w_k$  is  
 235 the BMA weight of  $k^{\text{th}}$  model,  $f_{k,t}$  is the prediction of the  $k^{\text{th}}$  model at time step  $t$ ,  $y_t$  is the  
 236 predictor variable at time step  $t$ , and the mean and standard deviation of the normal distribution,  
 237  $f_{k,t}$  and  $\sigma_k$ .

238 Because some of the hydrologic variables (e.g., water stage, streamflow, rainfall, etc.) are  
 239 nonnegative, the corresponding distributions tend to be skewed to some extent (Sloughter et al.,  
 240 2007). Hence the assumption of normal distribution does not rigorously hold in this case. To  
 241 explore the effect of conditional PDFs on the estimates of BMA parameters, it is assumed that  
 242 the conditional probability  $p_k(y|f_k, D)$  follows a gamma distribution (PDF = 0 for  $y \leq 0$ ) with  
 243 two parameters ( $\alpha$  and  $\beta$ ) (Qi et al., 2021; Vrugt et al., 2008; Vrugt and Robinson, 2007), and the  
 244 log-likelihood function is shown in Equation (4). The gamma distribution is not symmetric

245 around the mean like the normal distribution. Specifically, its mean is identical to  $\mu = \alpha\beta = f_k$ ,  
 246 and its variance is identical to  $\sigma_k^2 = \alpha\beta^2 = \beta f_k$ , which depends on the specific prediction ( $f_k$ )  
 247 and hence is heteroscedastic.

$$248 \quad L(\theta) = \sum_{t=1}^T \log \left( \sum_{k=1}^K w_k \cdot p_k(y_t | f_{k,t}, \sigma_k) \right) = \sum_{t=1}^T \log \left( \sum_{k=1}^K w_k \cdot \frac{1}{\Gamma(\alpha)\beta^\alpha} y_t^{\alpha-1} e^{-\frac{y_t}{\beta}} \right) \quad (4)$$

249 where  $\alpha$  is the shape parameter of gamma distribution and  $\alpha = f_{k,t}^2 / \sigma_k^2$ , and  $\beta$  is the scale  
 250 parameter of gamma distribution and  $\beta = \sigma_k^2 / f_{k,t}$ .

### 251 **3.3 Expectation-Maximization (EM) Algorithm**

252 Generally, it is not easy to obtain an analytical solution for the BMA log-likelihood function (see  
 253 Equation (3)) so the EM algorithm is recommended, and has been commonly used in previous  
 254 BMA applications (Duan et al., 2007; Huang and Merwade, 2023; Liu and Merwade, 2018;  
 255 Madadgar and Moradkhani, 2014; McLachlan and Krishnan, 2007; Moknatian and Mukundan,  
 256 2023; Parrish et al., 2012; Raftery et al., 2005). To find a numerical solution that can maximize  
 257 the log-likelihood function, this algorithm alternates iteratively between the E (i.e., Expectation)  
 258 step (see Equation (5)) and the M (i.e., Maximum) step (see Equations (6) and (7)). The value of  
 259 log-likelihood function is updated with the weight and variance estimated through each iteration.  
 260 The iteration will not stop until the difference between the previous value and the current value  
 261 of the log-likelihood function is within a pre-assigned threshold ( $10^{-4}$  is taken in the study). The  
 262 EM algorithm can guarantee that the likelihood function will be increasing monotonically at each  
 263 iteration (Saul and Lee, 2002; Wu, 1983), and thus the parameters that maximize the likelihood  
 264 can be obtained from the last M step. A few previous studies pointed out that the EM algorithm

265 can only converge to the local optimum rather than the global optimal results (Duan et al., 2007;  
 266 McLachlan and Krishnan, 2007; Vrugt et al., 2008), but this issue has not been addressed  
 267 adequately in the literature.

$$268 \quad z_{k,t}^i = \frac{w_k^{i-1} g_k(y_t | f_{k,t}, \sigma_k^{i-1})}{\sum_{k=1}^K w_k^{i-1} \cdot g_k(y_t | f_{k,t}, \sigma_k^{i-1})} \quad (5)$$

$$269 \quad w_k^i = \frac{1}{T} \sum_{t=1}^T z_{k,t}^i \quad (6)$$

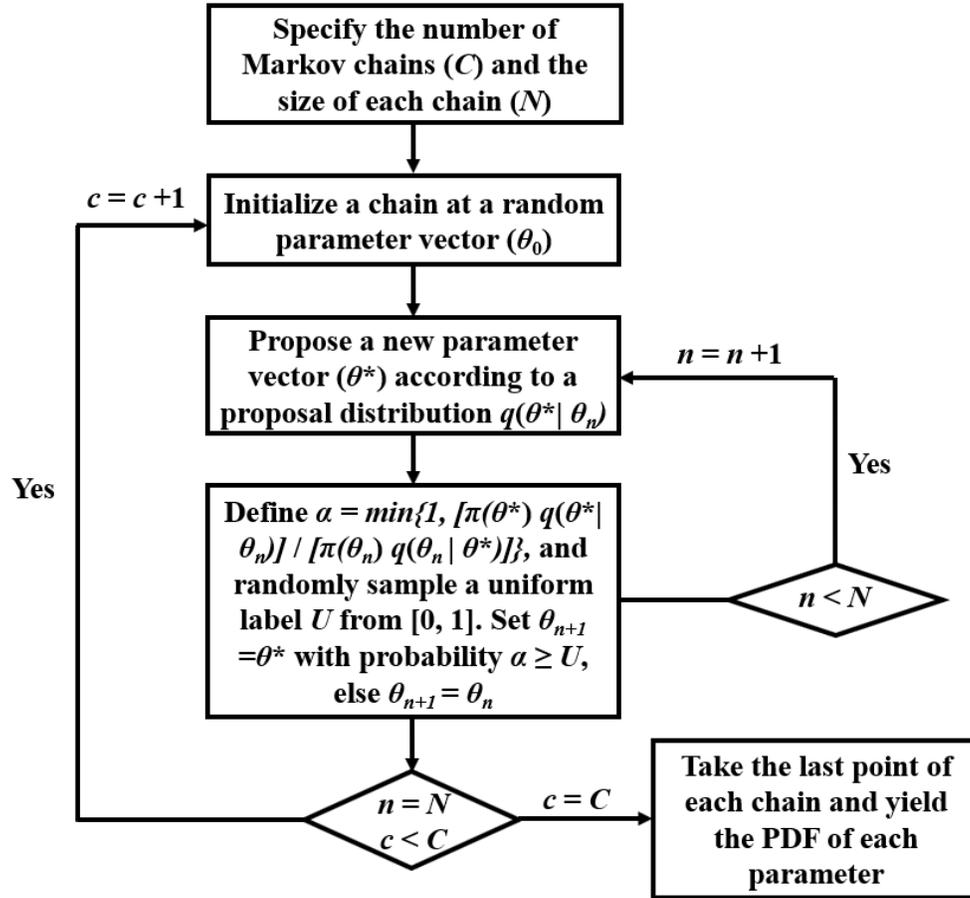
$$270 \quad \sigma_k^i = \sqrt{\frac{\sum_{t=1}^T z_{k,t}^i \cdot (y_t - f_{k,t})^2}{\sum_{t=1}^T z_{k,t}^i}} \quad (7)$$

271 where  $z_{k,t}^i$  is the latent variable depending on the performance of the  $k^{\text{th}}$  model at time  $t$  in the  $i^{\text{th}}$   
 272 iteration of the EM algorithm,  $w_k^i$  and  $\sigma_k^i$  is the BMA weight and standard deviation of the  $k^{\text{th}}$   
 273 model in the  $i^{\text{th}}$  iteration, respectively.

### 274 3.4 Metropolis-Hastings (M-H) Algorithm

275 In the conventional BMA analysis, optimal estimates of BMA weights and variances yielded  
 276 from the EM algorithm are fixed values. These fixed values cannot be considered with certainty  
 277 to be the global optimal solutions and provide enough information about the uncertainty  
 278 associated with the estimates of the BMA parameters. Therefore, the MCMC method with the  
 279 M-H algorithm is proposed to estimate the most likely values of the BMA parameters and  
 280 produce their underlying posterior distributions. The MCMC sampling is usually conducted  
 281 based on one single chain, but one single Markov chain may get stuck in a local mode for a high

282 dimensional problem (in the order of 20 unknown variables in this study). Thus, multiple  
283 independent chains are also tried in this study to explore the parameter space simultaneously and  
284 adequately, and then posterior distribution of each parameter is generated by using the local  
285 mode yielded by each chain. The flowchart in Figure 2 shows the procedure of the M-H  
286 algorithm with multiple MCMC chains. Without enough prior knowledge about the target  
287 distribution of the BMA parameters, a uniform distribution ranging from 0 to 1 or the normal  
288 distribution with a standard deviation of 0.1 is proposed to generate new samples of weights. A  
289 uniform distribution ranging from 0 to  $1.5 \times RMSE$  (root mean square error) is proposed to  
290 generate new samples of standard deviations during the MCMC sampling process. Since the  
291 dimensions and units of BMA standard deviations are different for different hydrologic variables  
292 of interest, it is difficult to propose another generalized proposal distribution and hence only a  
293 uniform proposal distribution is used in this study. The benefits of these assumptions mentioned  
294 above are that the proposal (prior) distribution is symmetric, and hence  $q(\theta^* | \theta_n) = q(\theta_n | \theta^*)$ .  
295 Thus, the posterior density distribution of the parameters,  $\pi(\theta | D)$ , is directly equal to the  
296 likelihood function (see Equations (3) and (4)). The improved method can maintain the  
297 ergodicity based on multiple Markov chains and is expected to provide a full view of the  
298 posterior distributions of the BMA parameters. Moreover, multiple sizes of each MCMC chain  
299 are attempted to investigate its effect on the estimates of BMA parameters. In addition, compared  
300 with the traditional EM algorithm, which requires the assumption of a conditional normal PDF,  
301 the MCMC simulation is easy to set up without any major algorithmic modifications when using  
302 different conditional PDFs for the variable of interest in the BMA analysis.



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Figure 2. Procedure of Metropolis-Hastings (M-H) algorithm with multiple Markov chains.

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### 3.5 Evaluation Metrics for Model Performance

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Both *RMSE* (Equation (8)) and four types of uncertainty coefficients (*UC1 - UC4*, see Equations

308

(9) - (12)) (Huang and Merwade, 2023) defined based on the reliability of BMA prediction

309

distribution and the accuracy of BMA mean predictions are employed to evaluate the overall

310

model performance under EM and MCMC algorithms. In general, lower values of these metrics

311

indicate less uncertain model predictions, a “perfect” model will have can uncertainty coefficient

312

of zero. It is also important to note that these four types of uncertainty coefficients are

313

independent from each other, thus the model performance and the associated uncertainty can be

314

evaluated and quantified comprehensively from different perspectives.

$$315 \quad RMSE = \sqrt{\frac{\sum_{i=1}^n (y_{obs,i} - y_{BMA,i})^2}{n}} \quad (8)$$

$$316 \quad UCI = \frac{N_{obs-90\%}}{n} \cdot 100\% \quad (9)$$

$$317 \quad UC2 = 1 - NSE = \frac{RMSE^2}{\sigma_{obs}^2} \cdot 100\% \quad (10)$$

$$318 \quad UC3 = 1 - KGE = \sqrt{(r - 1)^2 + \left(\frac{\sigma_{BMA}}{\sigma_{obs}} - 1\right)^2 + \left(\frac{\bar{y}_{BMA}}{\bar{y}_{obs}} - 1\right)^2} \cdot 100\% \quad (11)$$

$$319 \quad UC4 = (1 - R^2 + |1 - Slope|) \cdot 100\% \quad (12)$$

320 where  $n$  is the total number of data points,  $\bar{y}_{obs}$  is the mean value of the observations  $y_{obs,i}$  at each  
 321 step  $i$ ,  $y_{BMA,i}$  is the  $i^{\text{th}}$  BMA mean prediction value,  $N_{obs-90\%}$  is the number of observed data  
 322 points located outside the 90% prediction interval,  $\sigma_{obs}$  is the standard deviation of the observed  
 323 data,  $r$  is the correlation coefficient between BMA mean predictions and observations,  $\sigma_{BMA}$  is  
 324 the standard deviation of BMA mean predictions,  $\bar{y}_{BMA}$  is the mean of the BMA mean  
 325 predictions,  $R^2$  is the coefficient of determination of a linear regression equation in the form of  
 326 “Observation =  $Slope$ \*BMA mean prediction”, and  $Slope$  is the slope of the linear regression  
 327 equation.

## 328 4 Results and Discussion

### 329 4.1 Effect of Sample Sizes in M-H MCMC Algorithm

330 The MCMC method aims to find a finite number of local moves that produce samples  
331 asymptotically from the “correct” distribution of the variables of interest, which are the BMA  
332 weights and variances in this study. However, an appropriate sample size for generating a  
333 MCMC chain that mixes rapidly is still based on modelers’ experience and this size varies  
334 significantly for different cases (Gelman et al., 1995; Robert et al., 1999). Moreover, a strong  
335 autocorrelation among the samples within a chain can reduce the effective sample size, thus  
336 reducing the efficiency of sampling (Luengo et al., 2020). For the high-dimensional problem in  
337 this study (i.e., BMA likelihood function), Figure 3 shows that the conventional MCMC method  
338 with one single chain gets trapped in a set of local optimal solutions, and all the trace plots of  
339 BMA weights and standard deviations tend to be stagnant. Even after the sample size reaches  
340 100,000, which is much larger than the values used in previous literature, the mixing of any  
341 MCMC chain does not improve. In other words, the proposed samples are always rejected due to  
342 the low acceptance rate  $\alpha$  (see Figure 2) and it is hard for a chain to jump outside the local mode  
343 of the posterior distribution of BMA parameters.

344

345 Given the poor mixing of the MCMC sampling with one single chain, multiple independent  
346 MCMC chains are considered in this study by using the last point of each chain to form a new  
347 chain (see Figure 2), which presents the target posterior distribution. The trace plots (see Figure  
348 3) of multiple MCMC chains with different sample sizes show that a chain is very unlikely to  
349 accept a new sample after about 2000 iterations. Thus, 2000 samples are generated in each chain  
350 and the number of chains is set to be 100. The trace plots and autocorrelation functions (ACF) of

351 the BMA weights and variances of Model 1 (a model member with the lowest variance of model  
352 errors) and Model 9 (a model with the largest variance of model errors) in the numerical  
353 experiments (see Figures 4 and 5) indicate that the samples drawn from multiple independent  
354 MCMC chains are mixing very well and the autocorrelation is quickly dropping within the 5%  
355 significant interval (shown in the light blue region in the ACF in Figures 4 and 5), which means  
356 the entire space of the BMA parameters has been fully explored, and individual samples in the  
357 MCMC chain follow stationary and independent identical distributions. The histograms in  
358 Figures 4 and 5 represent the posterior distributions of the BMA weights and standard deviations,  
359 and more importantly, these statistical distributions demonstrate the uncertainty of the mean  
360 estimates. The histograms of the BMA parameters of Model 1 are close to a normal distribution,  
361 while the histograms of the BMA weights and standard deviations of Model 9 seem to follow a  
362 positively skewed distribution and a uniform distribution, respectively. It should be noted that  
363 similar analyses can also be performed on the posterior distributions of BMA parameters of other  
364 model members.

365

366 As shown in the mixing trace plots and the ACFs in Figures 4 and 5, the posterior distribution of  
367 BMA parameters is stationary, and then the results from the 2000<sup>th</sup> sample in 100 independent  
368 chains are taken as a benchmark compared to the results obtained from multiple sizes of each  
369 chain. The comparison of mean BMA weights and standard deviations obtained from 100  
370 MCMC chains with different sample sizes is shown in Figures 6 and 7. The estimates from  
371 multiple sizes (3000, 4000, 5000, and 10000) are linearly regressed with those from 2000  
372 samples of each chain. The intercept of the regression equation is set to be zero, so only *Slope* is  
373 involved in the equation. The results show that the estimates of BMA parameters do not change

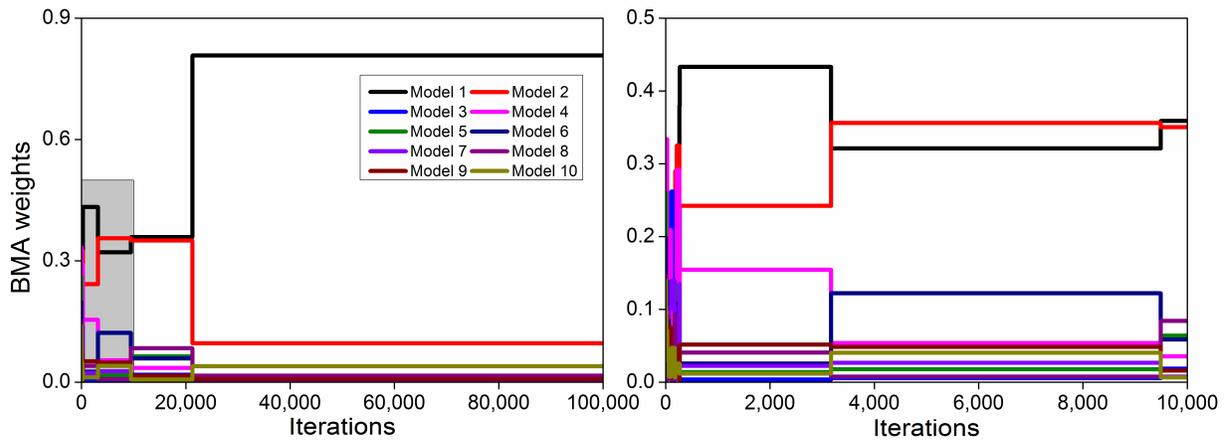
374 significantly (all the data points in Figure 6 are lying near the 45-degree line, and  $R^2$  is within  
375 0.95-1 and *Slope* is within 0.95-1.05 as shown in Figure 7) as the sample size increases, while  
376 the elapsed time of the sampling process carried out in a local personal computer becomes longer  
377 and longer (see Figure 7). Therefore, from the parsimony point of view, 2000 samples for each  
378 MCMC chain are adequate to guarantee the convergence of the target distribution of BMA  
379 parameters of the flood model ensemble with 10 or fewer members.

380

381 Table 4 and Table 5 present the BMA parameters estimated through EM and MCMC algorithms,  
382 respectively. Because the model errors of Model 1 and Model 2 have the smallest variance, the  
383 results from different algorithms show good agreement that these two models are assigned the  
384 highest BMA weight among the 10 model members. The EM algorithm can quickly identify the  
385 model member with lower-variance errors (i.e., Model 1 and Model 2) and a small weight that is  
386 close to zero is assigned to the other model members with poorer prediction performances (i.e.,  
387 Model 3 - Model 10). Since the prior distribution of BMA weights spans from 0 to 1, it is  
388 unlikely for the weight to be zero in the MCMC sampling process. However, it is important to  
389 highlight that the magnitudes of BMA weights obtained via these two algorithms are similar and  
390 the 90% confidence intervals from the MCMC algorithm do contain the deterministic value from  
391 the EM algorithm. The histograms in Figures 4 and 5 also show that the EM estimates are  
392 located around the mode of the statistical distribution. On the other hand, the BMA standard  
393 deviations of Model 3 - Model 10 estimated from the EM algorithm is quite close to zero, which  
394 is far away from the “true” standard deviation of the given model errors. This issue may be due  
395 to the original set up of the EM algorithm for the standard deviation (see Equations (5) and (7))  
396 and hence it makes the estimates difficult to interpret. On the contrary, corresponding estimates

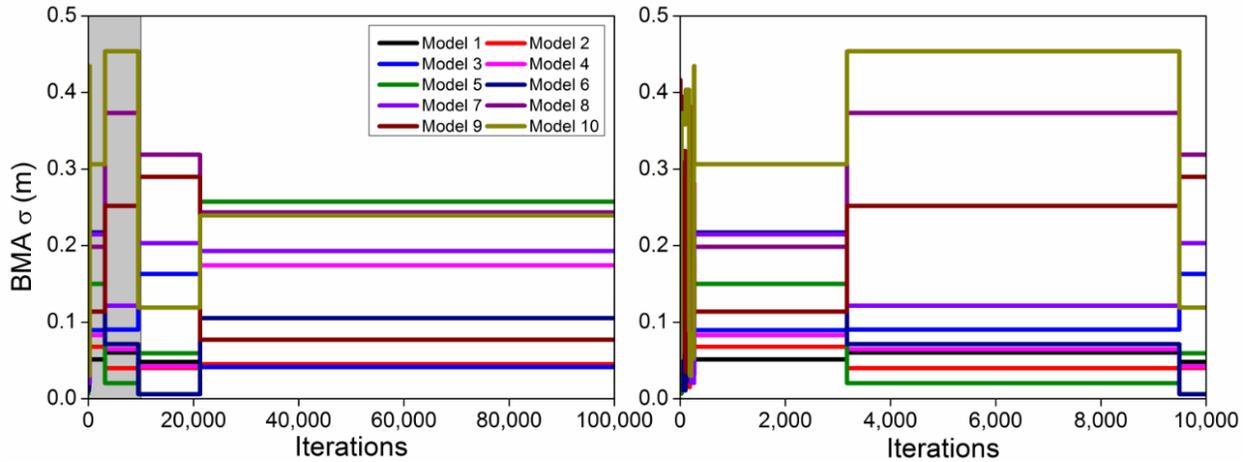
397 from the MCMC algorithm are quite close to the known standard deviation and it makes much  
 398 more sense that a model member with a larger BMA variance usually gets a lower BMA weight.  
 399 Additionally, it is important to note that even though the given errors have the same variance for  
 400 two model members (e.g., Model 1 and Model 2, Model 3 and Model 4, and so on) in the  
 401 numerical experiment, the BMA parameters of each pair are slightly different due to the  
 402 randomness of the model errors. This further implies that fixed values of BMA parameters would  
 403 introduce more uncertainty to these estimates. Thus, the posterior statistical distribution obtained  
 404 through the MCMC algorithm is a more reliable way to demonstrate and quantify the uncertainty  
 405 associated with BMA parameters.

406



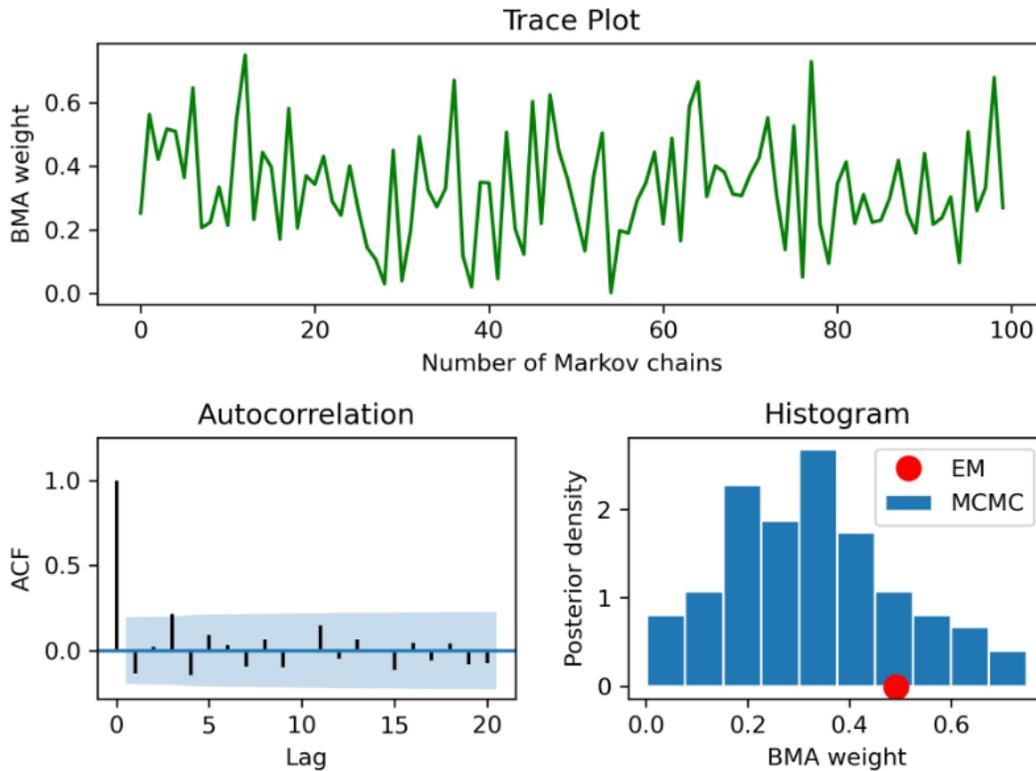
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408 (a) BMA weights obtained from a single MCMC chain (100k samples & top 10k samples in the  
 409 grey region).  
 410

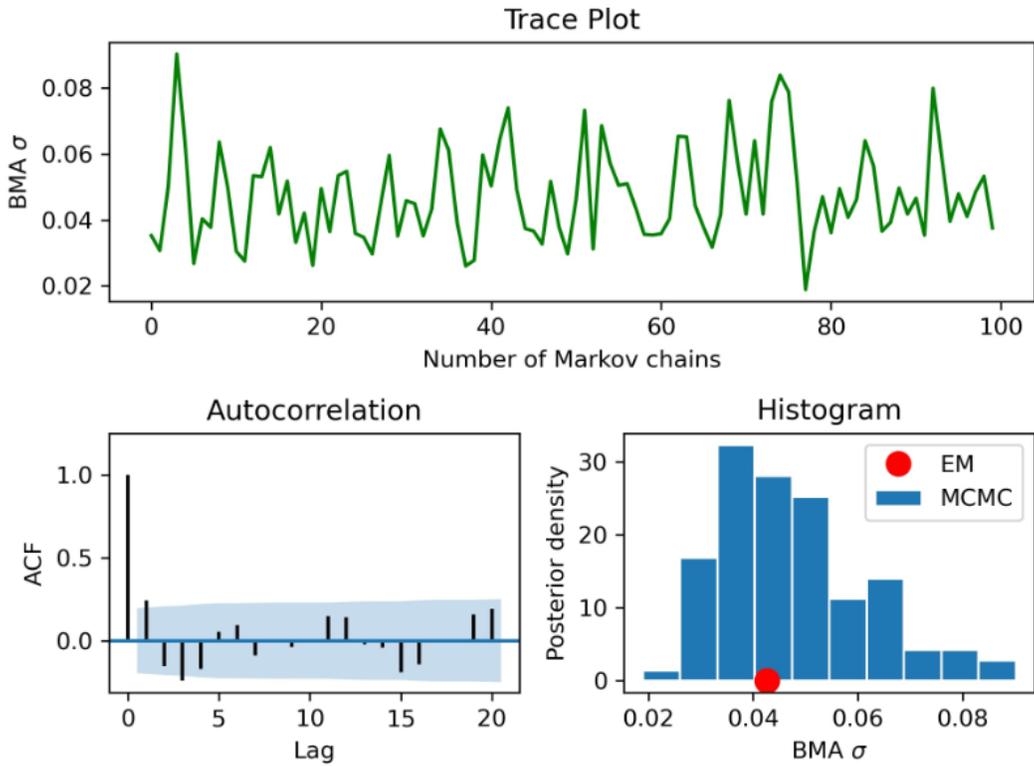


411  
412 (b) BMA standard deviations obtained from a single MCMC chain (100k samples and top 10k  
413 samples in the grey region).

414 Figure 3. Trace plots of BMA parameters from M-H algorithm with a single MCMC chain with  
415 100k samples.  
416



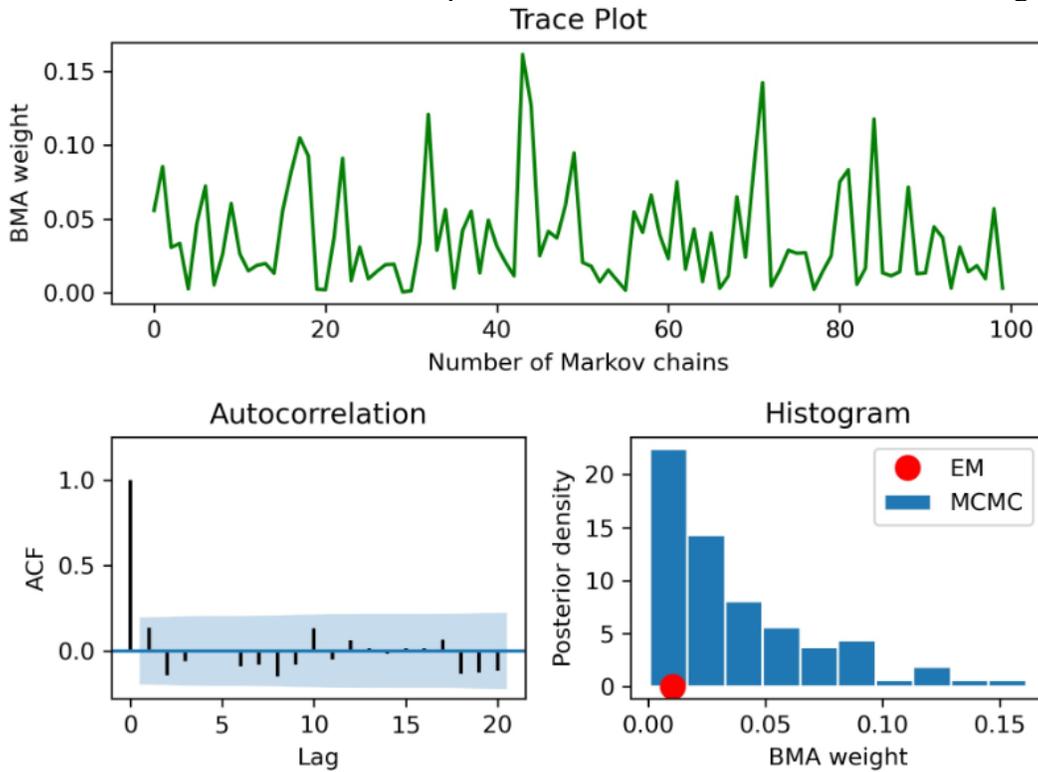
417  
418 (a) BMA weight.  
419



420  
421  
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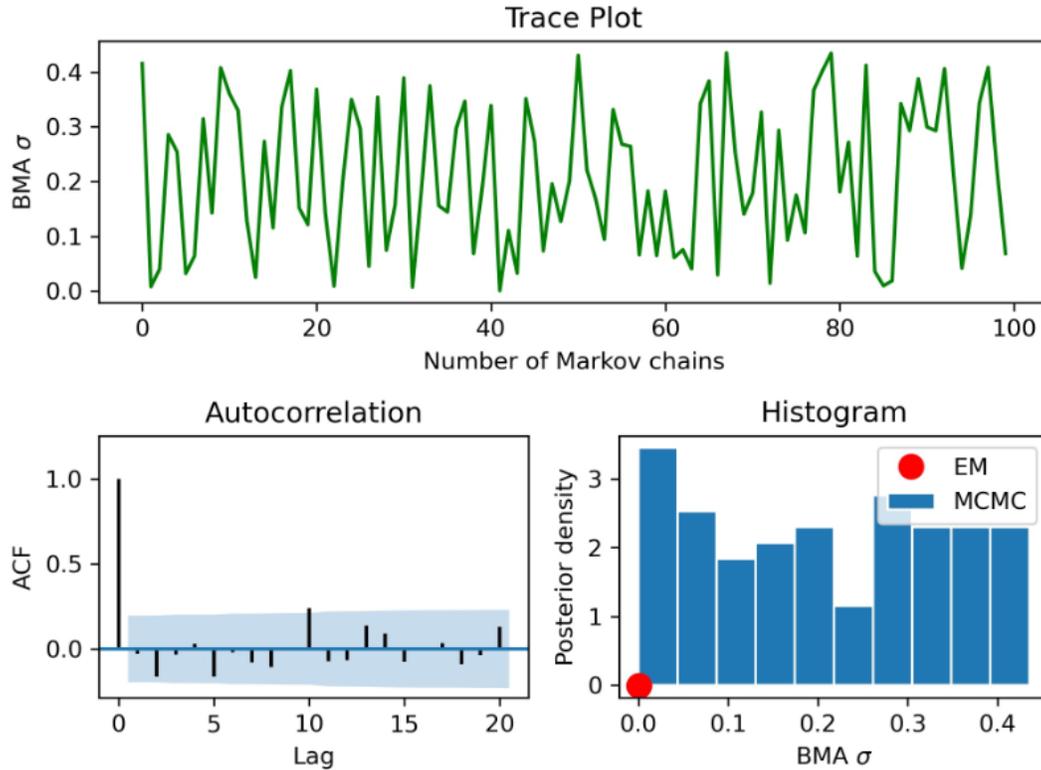
(b) BMA standard deviation (m).

Figure 4. Posterior distribution of BMA parameters of Model 1 from M-H MCMC algorithm.



423  
424

(a) BMA weight.

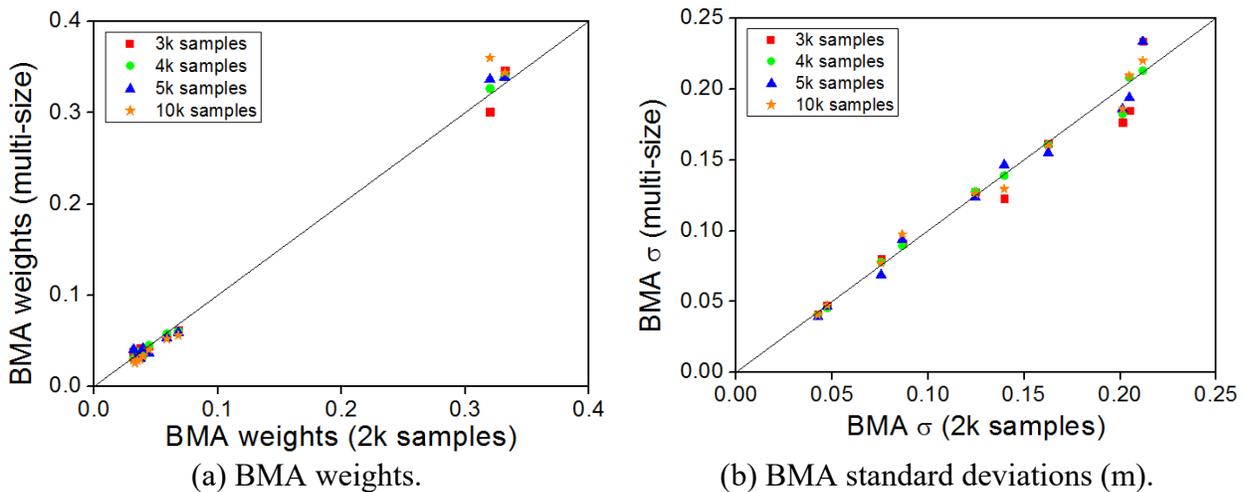


(b) BMA standard deviation (m).

Figure 5. Posterior distribution of BMA parameters of Model 9 from M-H MCMC algorithm.

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426  
427

428

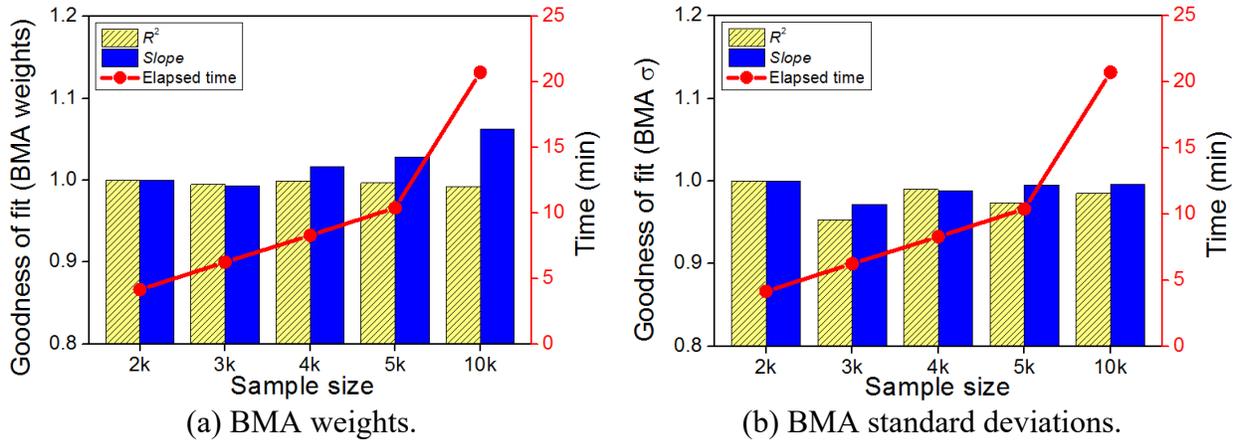


(a) BMA weights.

(b) BMA standard deviations (m).

Figure 6. Comparison of BMA weights from M-H algorithm with 100 MCMC chains with different sample sizes.

429  
430  
431



432 Figure 7. Comparison of elapsed time (Desktop processor specifications: Intel(R) Core(TM) i7-  
 433 9700 CPU @ 3.00GHz) and  $R^2$  & Slope of linear regression from M-H algorithm with 100  
 434 MCMC chains with different sample sizes.

435 Table 4. BMA parameters obtained from EM algorithm.

No.	Model	Weight	$\sigma$ (m)
1	$\varepsilon \sim N(0, 0.06^2)$	0.492	0.04
2	$\varepsilon \sim N(0, 0.06^2)$	0.497	0.04
3	$\varepsilon \sim N(0, 0.12^2)$	0.0002	0.02
4	$\varepsilon \sim N(0, 0.12^2)$	0	0.05
5	$\varepsilon \sim N(0, 0.18^2)$	0	0.08
6	$\varepsilon \sim N(0, 0.18^2)$	0	0.02
7	$\varepsilon \sim N(0, 0.24^2)$	0	0.11
8	$\varepsilon \sim N(0, 0.24^2)$	0	0.05
9	$\varepsilon \sim N(0, 0.3^2)$	0.01	0.001
10	$\varepsilon \sim N(0, 0.3^2)$	0	0.09

436

437 Table 5. BMA parameters obtained from MCMC algorithm.

No.	Model	Mean weight	90% interval of weight	Mean $\sigma$ (m)	90% interval of $\sigma$ (m)
1	$\varepsilon \sim N(0, 0.06^2)$	0.332	[0.05, 0.65]	0.05	[0.02, 0.08]
2	$\varepsilon \sim N(0, 0.06^2)$	0.32	[0.07, 0.60]	0.04	[0.01, 0.07]
3	$\varepsilon \sim N(0, 0.12^2)$	0.068	[0, 0.17]	0.08	[0.02, 0.14]
4	$\varepsilon \sim N(0, 0.12^2)$	0.059	[0, 0.16]	0.09	[0.01, 0.17]
5	$\varepsilon \sim N(0, 0.18^2)$	0.04	[0, 0.11]	0.14	[0.02, 0.27]
6	$\varepsilon \sim N(0, 0.18^2)$	0.044	[0, 0.12]	0.12	[0.02, 0.23]
7	$\varepsilon \sim N(0, 0.24^2)$	0.035	[0, 0.10]	0.16	[0.02, 0.30]
8	$\varepsilon \sim N(0, 0.24^2)$	0.032	[0, 0.09]	0.2	[0.04, 0.35]
9	$\varepsilon \sim N(0, 0.3^2)$	0.037	[0, 0.11]	0.2	[0.01, 0.41]
10	$\varepsilon \sim N(0, 0.3^2)$	0.033	[0, 0.09]	0.21	[0.02, 0.43]

438

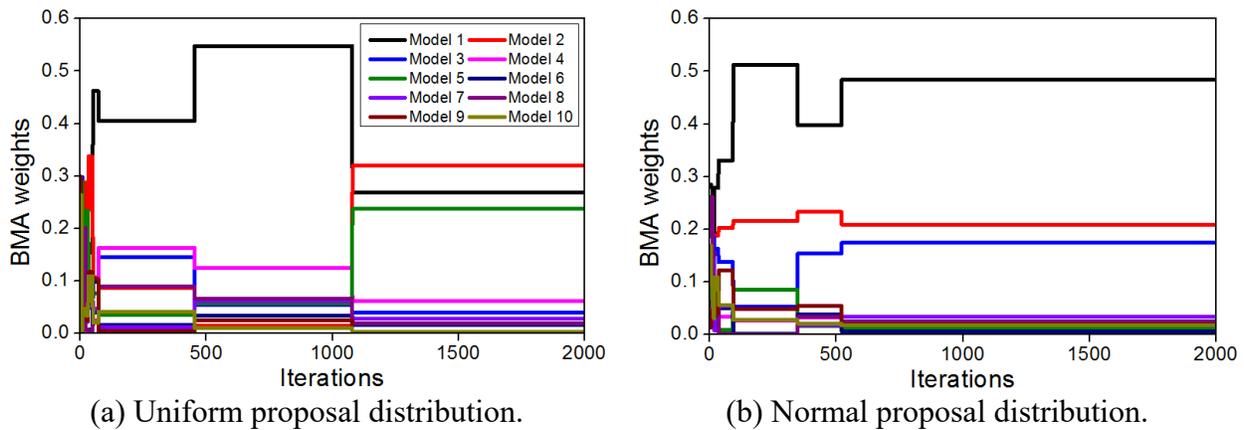
## 439 4.2 Impact of Proposal Distributions in M-H MCMC Algorithm

440 The proposal distribution in the MCMC method is a conditional distribution (see  $q(\theta^* | \theta_n)$  and  
441  $q(\theta_n | \theta^*)$  in Figure 2) that is used to generate a new sample  $\theta^*$  given the current sample  $\theta_n$ , and  
442 vice versa. However, the selection of the proposal distribution tends to be subjective in practice.  
443 To investigate the effect of proposal distributions on the estimates of BMA weights, a normal  
444 proposal distribution is proposed to compare with the uniform proposal distribution used in the  
445 previous section. The standard deviation of the normal prior distribution is taken as 0.1 through a  
446 trial and error procedure. If the standard deviation is too small, it is very likely that a new sample  
447 BMA weight to be rejected; if the standard deviation is assigned a large value, a new sample  
448 BMA weight might be negative, which would contradict the assumption of nonnegative BMA  
449 weights. Similarly, the number of samples in each chain is assigned to be 2000 since the larger  
450 sample size does not change the estimates significantly. Figure 8 shows that the trace plots of  
451 BMA weights generated based on both proposal distribution are already stagnant when the  
452 sample size reaches 2000. To be consistent with the sampling based on a uniform proposal  
453 distribution, the number of independent chains is also set to be 100. The estimates of BMA  
454 weights based on the normal proposal distributions in the M-H MCMC sampling are presented in  
455 Table 6. Comparing Tables 5 and 6, the mean estimates of BMA weights obtained from both  
456 uniform and normal proposal distributions are quite close to each other. However, the 90%  
457 confidence interval of the BMA weights based on the normal proposal distribution is narrower  
458 compared to that from the uniform proposal distribution, which means the former one gives a  
459 more precise and confident assessment on the performance of individual model members.

460

461 Based on the BMA parameters estimated from the EM algorithm and the MCMC method with  
 462 different proposal distributions, the prediction distributions of water stage produced through a  
 463 Monte Carlo sampling procedure are shown in Figure 9 and the model uncertainty quantified  
 464 based on multiple independent evaluation metrics are presented in Table 7. Figure 9 shows that  
 465 these three sets of BMA mean predictions match the observations very well and the difference in  
 466 model performance is similar visually. However, it is obvious that the 90% confidence interval  
 467 of the BMA prediction distribution obtained from the EM algorithm is narrower due to its  
 468 extreme low values of the BMA variances. The values of *RMSE* and *UC1 - UC4* indicate that the  
 469 overall model performance based on MCMC method is better than the EM algorithm, and the  
 470 normal proposal distribution in the M-H MCMC algorithm is slightly better than the uniform  
 471 proposal distribution. Therefore, the results of the numerical experiment demonstrate that the  
 472 MCMC method with multiple independent chains and a normal proposal distribution in the M-H  
 473 algorithm can be a better alternative to the default EM algorithm for estimating the reliable BMA  
 474 parameters (weights and variances) in the BMA analysis.

475



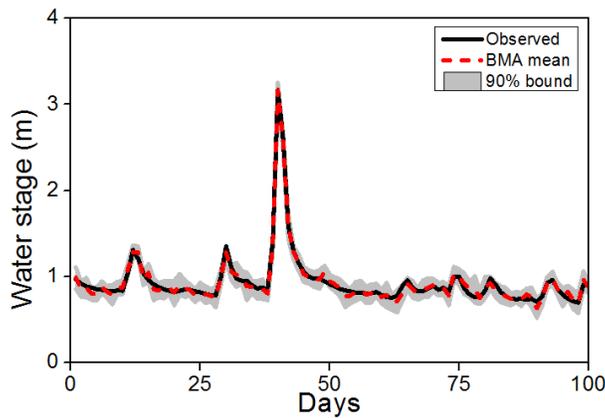
476 Figure 8. Trace plots of BMA weights from M-H algorithm with different proposal distributions.

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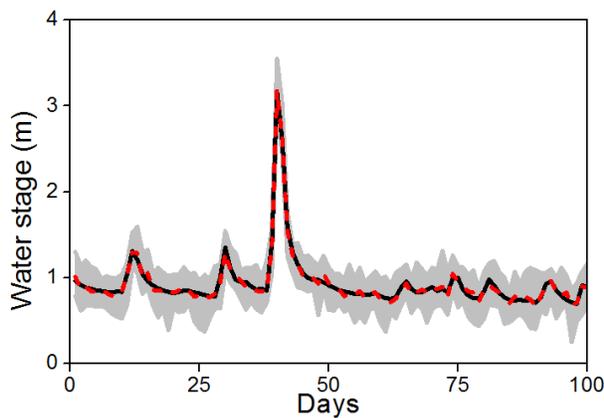
478 Table 6. BMA weights obtained from normal proposal distributions in M-H MCMC algorithm.

No.	Model	Mean weight	90% interval of weight
1	$\varepsilon \sim N(0, 0.06^2)$	0.354	[0.23, 0.50]
2	$\varepsilon \sim N(0, 0.06^2)$	0.35	[0.21, 0.49]
3	$\varepsilon \sim N(0, 0.12^2)$	0.062	[0, 0.14]
4	$\varepsilon \sim N(0, 0.12^2)$	0.053	[0, 0.14]
5	$\varepsilon \sim N(0, 0.18^2)$	0.034	[0, 0.09]
6	$\varepsilon \sim N(0, 0.18^2)$	0.033	[0, 0.09]
7	$\varepsilon \sim N(0, 0.24^2)$	0.029	[0, 0.09]
8	$\varepsilon \sim N(0, 0.24^2)$	0.028	[0, 0.08]
9	$\varepsilon \sim N(0, 0.3^2)$	0.028	[0, 0.07]
10	$\varepsilon \sim N(0, 0.3^2)$	0.028	[0, 0.07]

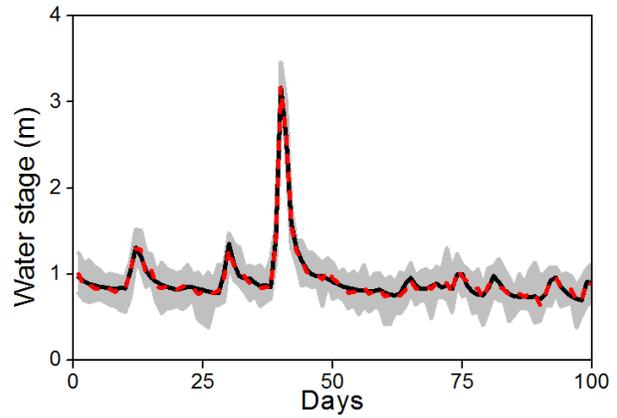
479



(a) EM algorithm.



(b) Uniform proposal distribution in M-H MCMC algorithm.



(c) Normal proposal distribution in M-H MCMC algorithm.

480 Figure 9. Water stage predictions obtained from EM and M-H MCMC algorithms with different  
481 proposal distributions.

482

Table 7. Comparison of model performance under different algorithms.

<b>Algorithm</b>	<b><i>RMSE</i> of mean predictions (m)</b>	<b>Average 90% prediction interval (m)</b>	<b><i>UC1</i> (%)</b>	<b><i>UC2</i> (%)</b>	<b><i>UC3</i> (%)</b>	<b><i>UC4</i> (%)</b>
EM	0.041	0.19	5.00	1.61	1.06	2.00
M-H MCMC (uniform)	0.037	0.47	0.00	1.33	1.04	1.66
M-H MCMC (normal)	0.037	0.41	0.00	1.33	0.96	1.64

483

### 484 **4.3 Influence of Conditional PDFs in BMA analysis**

485 One of the advantages of using the MCMC method, compared to the EM algorithm, in the BMA  
486 analysis is its flexibility in assuming a conditional PDF. The EM algorithm is strictly limited to  
487 the normal conditional PDF (see Equation (3)). Even though the normal conditional PDF is  
488 assumed initially in the BMA analysis (Raftery et al., 2005), it is probably true for some climate  
489 variable (e.g., temperature), but some nonnegative hydrologic variables (e.g., rainfall, streamflow,  
490 and water stage) may not be normally distributed. Because the probability of the negative  
491 hydrologic variable must be equal to zero, the corresponding PDF should be skewed to some  
492 extent. To explore the impact the conditional PDFs on the BMA parameters, the results from ten  
493 HEC-RAS model configurations of the two study reaches in Indiana and Texas under both  
494 normal and gamma conditional distributions are compared. Figures 10 and 11 exhibit the  
495 posterior distribution of the BMA parameters of individual model members under different  
496 conditional PDFs, and Tables 8 and 9 present their mean estimates. For the HEC-RAS models  
497 used in this study, the statistical distributions obtained from both normal and gamma conditional  
498 PDFs are slightly different, but the overall patterns are quite similar. For the White River in

499 Indiana, the BMA weight of Model 9 ranks first and its distribution tends to be normal. The  
500 BMA weights of Model 6 and Model 8 come second and third, respectively. The statistical  
501 distributions of the BMA weights of other model members are highly positively skewed and the  
502 mean values are less than 0.1. Figures 10(c) and 10(d) show that the statistical distributions of  
503 the BMA standard deviations of the model members with a good performance (i.e., a higher  
504 BMA weight) are usually narrowly dispersed and the corresponding mean values in Table 9 are  
505 also lower than those of the model members with a poor performance (i.e., a lower BMA weight).

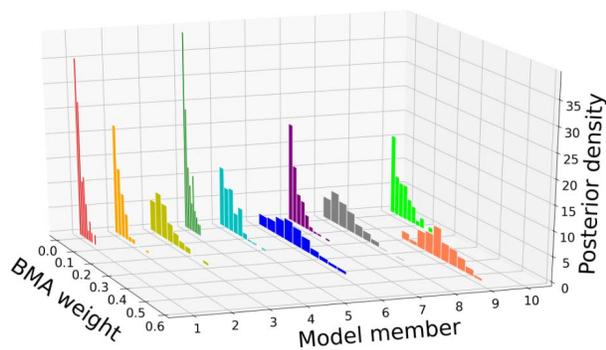
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507 For the East Fork San Jacinto River in Texas, the performance of most of the model members is  
508 very close, and hence produce similar posterior distributions and mean values for the BMA  
509 parameters are yielded (see Figure 11). Among the model ensemble, Model 9, Model 3, and  
510 model 10 are assigned a relatively higher BMA weight and a relatively lower BMA standard  
511 deviation. Overall, this conclusion based on the HEC-RAS models from the two study reaches is  
512 consistent with the findings obtained from the numerical experiment. More importantly, the  
513 MCMC method can provide a comprehensive view of the uncertainty associated with the BMA  
514 parameters, and hence more informed decisions on the flood risk control can be made based on  
515 the flood model members with robust and consistent prediction capacities.

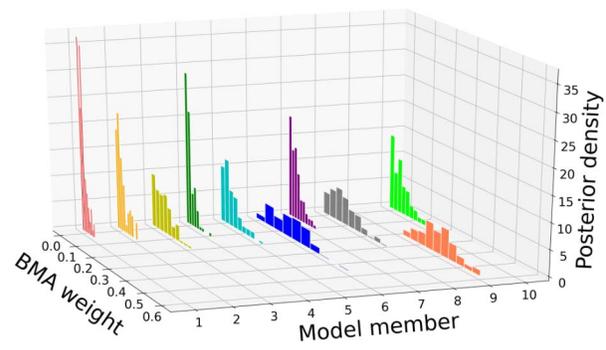
516

517 Based on the BMA parameters estimated from the MCMC method under different conditional  
518 PDFs, the prediction distributions of water stage are created through a Monte Carlo sampling  
519 procedure and are shown in Figure 12. The rank of water stage *RMSEs* from each model member  
520 is presented in Figure 13 and the values of different uncertainty coefficients (Equations 8-12) to

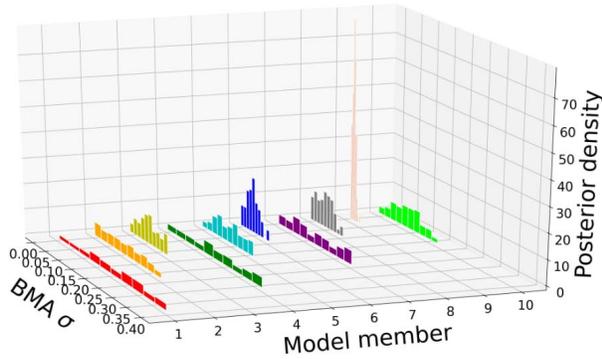
521 quantify the model performance are presented in Table 10. Both visual and the quantitative  
522 comparison of the water stage predictions demonstrate that the model performance under the  
523 normal and gamma conditional PDFs are comparable, because all the model members of these  
524 two study reaches presents relatively good prediction skills (e.g.,  $RMSEs < 0.5m$  and  $UCs < 15\%$ )  
525 and the model residuals do not demonstrate a dominated pattern (e.g., either normal or gamma  
526 PDF in this study). It is, however, important to note that that the gamma conditional PDF yields a  
527 slightly better performance, which means the pattern of model residuals fit a gamma distribution  
528 better than a normal one. Additionally, it is interesting to note in Figure 13 that the  $RMSEs$  of  
529 Model 6 for the White River and Model 3 for the East Fork San Jacinto River rank first  
530 compared to other model members and two sets of BMA mean predictions. It implies that some  
531 other types of conditional PDF that fits the water stage residuals of the model members better  
532 than the normal or gamma PDF used in this study might exist, which, however, has to be found  
533 through a trial-and-error procedure.



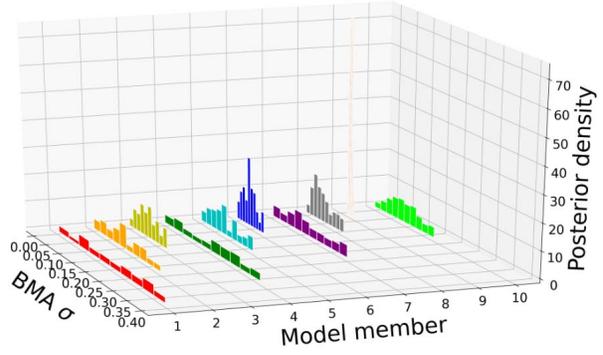
(a) BMA weights (normal conditional PDF).



(b) BMA weights (gamma conditional PDF).



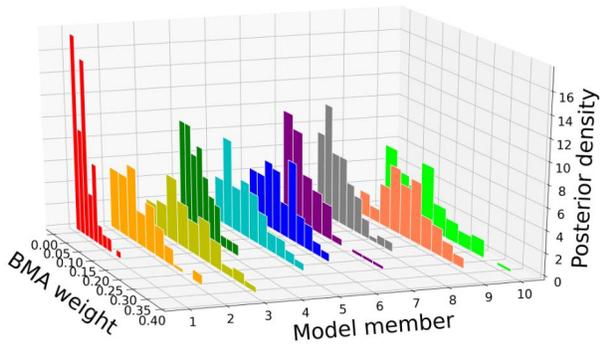
(c) BMA standard deviations in meters (normal conditional PDF).



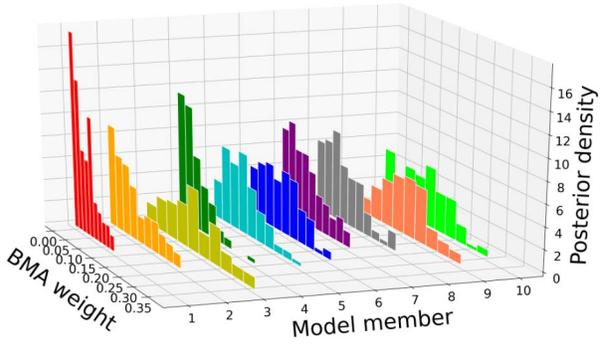
(d) BMA standard deviations in meters (gamma conditional PDF).

534 Figure 10. Comparison of the BMA parameters obtained from different BMA conditional PDFs  
 535 for White River.  
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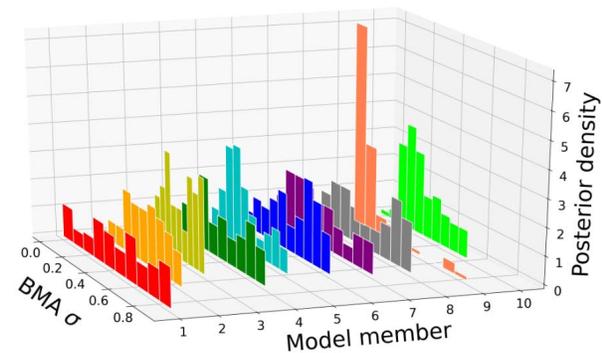
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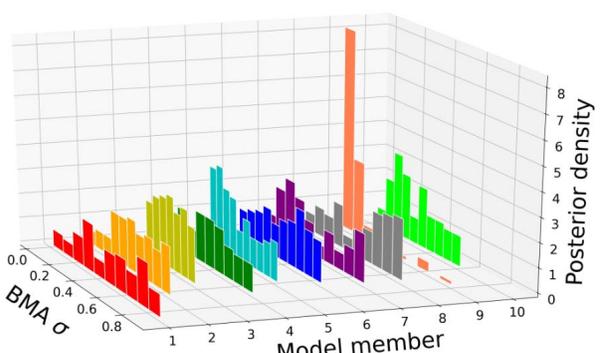
(a) BMA weights (normal conditional PDF).



(b) BMA weights (gamma conditional PDF).



(c) BMA standard deviations in meters (normal conditional PDF).



(d) BMA standard deviations in meters (gamma conditional PDF).

538 Figure 11. Comparison of the BMA parameters obtained from different BMA conditional PDFs  
 539 for East Fork San Jacinto River.

540 Table 8. Comparison of mean BMA weights under different conditional PDFs.

<b>River</b> <b>Model No.</b>	<b>White</b>		<b>East Fork San Jacinto</b>	
	<b>Normal</b>	<b>Gamma</b>	<b>Normal</b>	<b>Gamma</b>
1	0.022	0.02	0.041	0.045
2	0.032	0.035	0.1	0.083
3	0.083	0.066	0.15	0.17
4	0.023	0.025	0.064	0.054
5	0.057	0.055	0.104	0.097
6	0.193	0.184	0.105	0.108
7	0.039	0.037	0.069	0.076
8	0.11	0.112	0.071	0.085
9	0.387	0.411	0.178	0.162
10	0.054	0.054	0.119	0.121

541  
542

543

544 Table 9. Comparison of mean BMA standard deviations (m) under different conditional PDFs.

<b>River</b> <b>Model No.</b>	<b>White</b>		<b>East Fork San Jacinto</b>	
	<b>Normal</b>	<b>Gamma</b>	<b>Normal</b>	<b>Gamma</b>
1	0.22	0.21	0.49	0.5
2	0.12	0.11	0.4	0.4
3	0.07	0.07	0.37	0.38
4	0.18	0.17	0.4	0.38
5	0.1	0.09	0.3	0.33
6	0.05	0.05	0.41	0.41
7	0.14	0.12	0.32	0.35
8	0.05	0.06	0.4	0.45
9	0.03	0.03	0.19	0.16
10	0.09	0.09	0.31	0.32

545

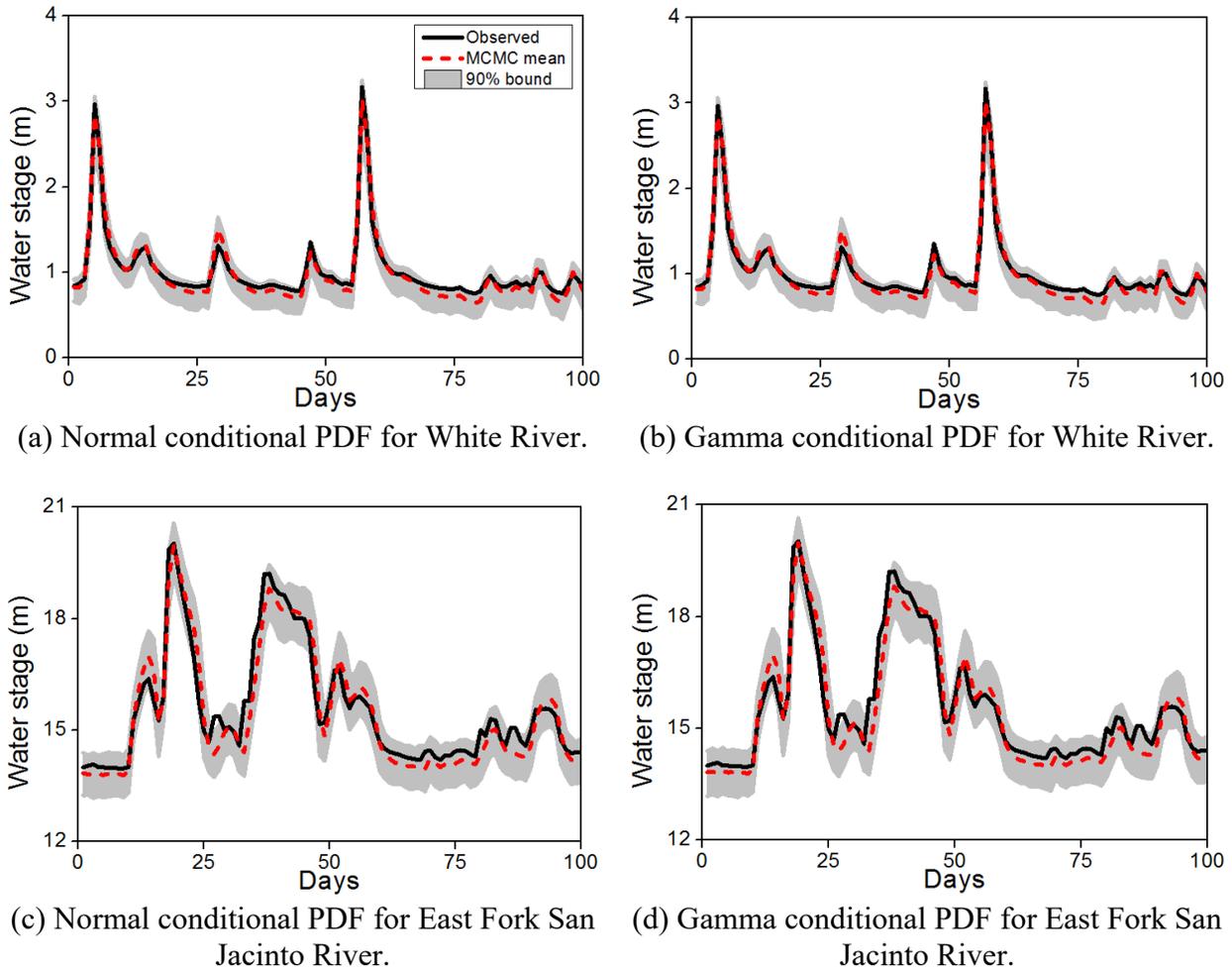


Figure 12. Water stage predictions from different BMA conditional PDFs for study area.

546  
547

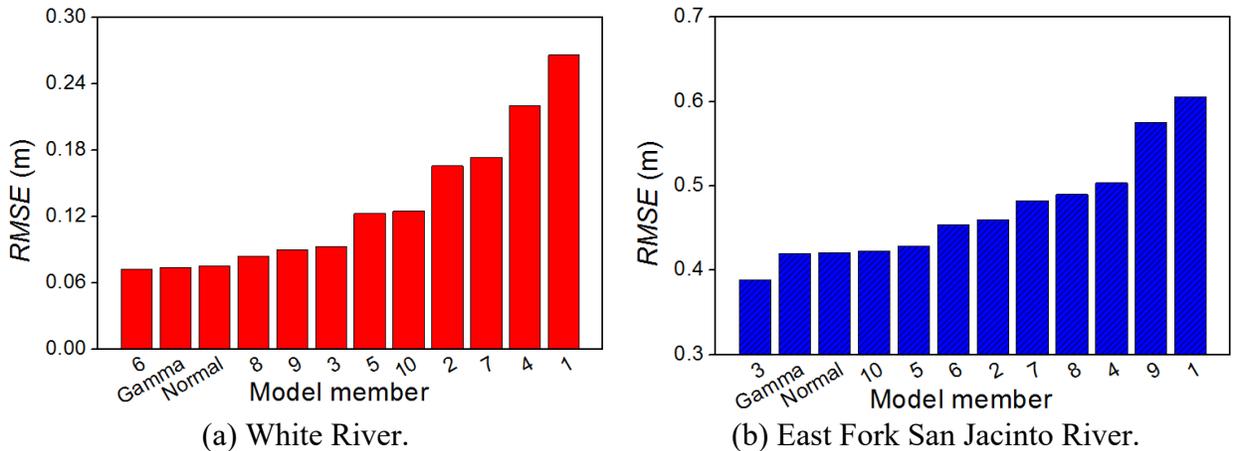


Figure 13. Rank of RMSEs of daily water stage from model ensembles for study area.

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Table 10. Comparison of prediction performances under different BMA conditional PDFs.

549

Study	Conditional	RMSE of	Average 90%	UC1	UC2	UC3	UC4
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<b>stream</b>	<b>PDF</b>	<b>mean predictions (m)</b>	<b>prediction interval (m)</b>	<b>(%)</b>	<b>(%)</b>	<b>(%)</b>	<b>(%)</b>
White	Normal	0.075	0.32	5.00	3.43	5.94	4.87
	Gamma	0.074	0.32	5.00	3.34	5.97	4.62
East Fork San Jacinto	Normal	0.421	1.32	13.00	7.54	5.69	7.76
	Gamma	0.419	1.34	11.00	7.48	5.67	7.71

550

551 **5 Conclusions**

552 Reliable, robust, and accurate flood predictions are critical for understanding flood risk and  
553 taking actions. A computational model based on certain assumptions and simplifications of the  
554 complicated hydrologic system is subject to uncertainty that must not be ignored. Thus, it is wise  
555 to make decisions based on predictions from multiple competing candidate models rather than  
556 relying on one single model even if it has been well calibrated. Among all kinds of multi-model  
557 methods, quite a few studies have shown successful applications of the BMA method in the  
558 fields of hydrologic and hydraulic engineering. Accurate estimates of BMA parameters (weights  
559 and variances) determine the performance of BMA predictions. However, the uncertainty  
560 associated with BMA parameters estimated through the default EM algorithm has not been  
561 investigated systematically. Given the research gap in the previous literature, the M-H MCMC  
562 method with multiple independent chains is proposed in this study to address the limitations of  
563 the EM algorithm that provide deterministic estimates for the BMA parameters. The applicability  
564 of the MCMC method is examined based on both numerical experiment with known patterns of  
565 model errors and the case studies of two 1D HEC-RAS models in the states of Indiana and Texas  
566 of the United States. Following major conclusions are drawn from this study:

567 (1) Results of the numerical experiment show that the estimates of BMA parameters obtained  
568 from the MCMC method do not change significantly beyond a sample size of 2000, but  
569 the computational cost of the sampling process increases as the sample size increases.  
570 Considering both the accuracy of estimates and the sampling efficiency, 2000 samples  
571 per individual MCMC chains are adequate to generate a stationary distribution of BMA  
572 parameters for the model ensemble of 10 or fewer members. As the posterior distribution  
573 estimated from the M-H algorithm is found to be stationary, the chain number that is  
574 greater than 30 should be sufficient to draw inferences for the population properties of  
575 BMA parameters, but 100 independent chains are employed in this study to be more  
576 conservative.

577 (2) The numerical experiment demonstrates that the prediction performance of the M-H  
578 MCMC algorithm in the BMA analysis is less uncertain than the default EM algorithm in  
579 terms of multiple independent evaluation metrics (*RMSE* and *UCI - UCA*). The  
580 magnitudes of BMA weights estimated from both algorithms are similar, but the standard  
581 deviations estimated from the MCMC method are closer to the “true” values of model  
582 errors in Table 2. Furthermore, the normal proposal distribution with a standard deviation  
583 of 0.1 for the BMA weight can slightly improve the performance of the MCMC method.  
584 Overall, the BMA parameters obtained from the MCMC method are more interpretable in  
585 terms of the model performance comparison than the EM algorithm, since the model  
586 members with a better prediction performance are assigned a higher BMA weight and a  
587 lower BMA variance, and vice versa.

588 (3) Results of the case studies based on two HEC-RAS models show that the estimates of  
589 BMA parameters based on both the normal and gamma conditional PDFs are close to

590 each other. As a result, BMA predictions under these two assumptions of the posterior  
591 distribution of the predictor variable yield a similar performance. However, it should be  
592 noted that the gamma conditional PDF is slightly better in terms of multiple evaluation  
593 metrics, which implies that the posterior distribution of the water stage data fits the  
594 gamma PDF better than the normal PDF for these two study areas.

595 (4) This study indicates that the M-H MCMC method with multiple independent chains is  
596 valid in estimating the BMA parameters and it is superior to the default EM algorithm in  
597 the BMA analysis. The application of MCMC method makes it easy and flexible to  
598 release and modify the strict assumption of the model residuals which are assumed to  
599 follow a normal distribution in the EM algorithm. A better fit of the conditional PDF of  
600 the variable of interest will produce more accurate and reliable BMA predictions. Most  
601 importantly, the MCMC sampling approach can provide a complete perspective and a full  
602 picture of the uncertainty in the BMA parameters through the corresponding posterior  
603 distributions.

604

605 As per authors' knowledge, this is the first study to apply the M-H MCMC method with multiple  
606 independent chains to estimating the BMA parameters of ensemble flood modeling. The basic  
607 M-H algorithm is used in this study since it is relatively easy to set up, the computational cost is  
608 feasible, and it requires few subjective selections of algorithm parameters. Some more  
609 appropriate prior and proposal distributions besides uniform and normal distributions can be  
610 attempted in the M-H algorithm to investigate any further improvement in the results. The slight  
611 improvement in the performance of the gamma conditional PDF in the case studies also imply

612 the potential room for better BMA predictions due to a better fit of specific hydrologic variables.  
613 In the case that the sufficient knowledge of the shape of conditional PDFs is not available, some  
614 transformation procedures (Box and Cox, 1964) might be required for pre-processing the raw  
615 data, but whether the desired assumption of the conditional PDF is satisfied after the  
616 transformation needs to be carefully validated. Moreover, some advanced and more complicated  
617 MCMC algorithms, such as the Hamiltonian Monte Carlo (Gebraad et al., 2020; Ulzega and  
618 Albert, 2022), particle filtering (Fan et al., 2022; Shen et al., 2022), reversible-jump MCMC  
619 (Jiménez et al., 2016; Ouarda and El-Adlouni, 2011), etc., can also be attempted in this specific  
620 issue of BMA parameter estimation, but the benefits of more efficient sampling and better  
621 hydrologic predictions may not be guaranteed. Furthermore, more hydrologic and hydraulic  
622 models of regions with different geomorphic features should be employed to extend and  
623 reinforce the findings obtained in this study.

#### 624 **Data Availability**

625 All the data used in this study, including the daily streamflow and water stage data, are publicly  
626 available from the United States Geological Survey (USGS) website. FEMA's HEC-RAS  
627 models used in this study are available from the Indiana Department of Natural Resources'  
628 Hydrology and Hydraulics Model Library at  
629 <https://dnrmaps.dnr.in.gov/appsphp/model/index.php> and FEMA's Estimated Base Flood  
630 Elevation Viewer at <https://webapps.usgs.gov/infrm/estbfe/>.

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