Bayesian model averaging (BMA)

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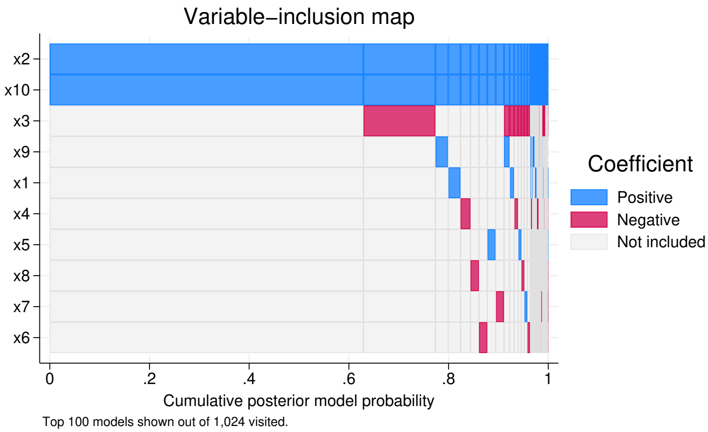
Outline

Teaser


Variable–inclusion map
x2
x10
x3
x9
x1
x4
x5
x8
x7
x6
0
.2
.4
.6
.8
1
Cumulative posterior model probability
Top 100 models shown out of 1,024 visited.
Coefficient
Positive
Negative
Not included

What is Bayesian model averaging (BMA)?

- The concept of *uncertainty* is fundamental to statistical analyses.
- We assess uncertainty about parameter estimates, predictions, hypothesis testing, etc.
- We often assume there is a true data-generating model (DGM), which we infer from the observed data.
- Traditionally, we select a model that fits the data well and proceed with our analysis. This typically does not incorporate uncertainty about the selected model.
- Model averaging accounts for *model* uncertainty in data analyses.
- BMA (Leamer 1978, Hoeting et al. 1999) uses the Bayesian principles, specifically the Bayes theorem, to account for model uncertainty.

Why BMA?

- Sometimes we may have a strong evidence for selecting a certain model for our data analysis.
- More often, however, there may be several plausible models that support our theory.
- In that case, choosing only one model may lead to overly optimistic or even wrong conclusions (if the selected model is drastically different from the true DGM).
- Model averaging considers a set of candidate models and accounts for model uncertainty by averaging the estimates across the models and weighting them according to how likely each model is.
- BMA uses posterior model probabilities (PMPs) as weights, which provide an intuitive and unified across analyses way to interpret models' importance.

- BMA also provides a way to assess a variable's importance by using posterior inclusion probabilities (PIPs) and interrelations between variables across the model space.
- BMA can be used for sensitivity analyses of the importance of different models and predictors.
- BMA can be used for model choice, prediction, and inference.
- See **[BMA] Intro** for details.
- Also see, for instance, Steel (2020) and Moral-Benito (2015) for a systematic review of BMA.

Brief review of Bayesian analysis

- Observed data sample y is fixed and model parameters $\boldsymbol{\theta}$ are random. (y is viewed as a result of a one-time experiment.)
- A parameter is summarized by an entire distribution of values instead of one fixed value as in classical frequentist analysis.
- There is some prior (before seeing the data!) knowledge about $\boldsymbol{\theta}$ formulated as a **prior distribution** $p(\boldsymbol{\theta}) = \pi(\boldsymbol{\theta})$.
- After data y are observed, the information about $\boldsymbol{\theta}$ is updated based on the **likelihood** $f(y|\boldsymbol{\theta})$.
- Information is updated by using the Bayes rule to form a **posterior distribution** $p(\boldsymbol{\theta}|y)$:

$$p(\boldsymbol{\theta}|y) = \frac{p(y,\boldsymbol{\theta})}{p(y)} = \frac{p(y|\boldsymbol{\theta})p(\boldsymbol{\theta})}{p(y)} = \frac{f(y|\boldsymbol{\theta})\pi(\boldsymbol{\theta})}{m(y)}$$

where $m(y)$ is the **marginal distribution** of the data y.

- Estimating a posterior distribution $p(\boldsymbol{\theta}|y)$ is at the heart of Bayesian analysis.
- Various summaries of this distribution are used for inference.
- Point estimates: posterior means, modes, medians, percentiles.
- Interval estimates: **credible intervals** (CrIs)—(fixed) ranges to which a parameter is known to belong with a pre-specified probability.
- Monte-Carlo standard error (MCSE)—represents precision about posterior mean estimates.
- Predictions and model checking are based on a **posterior predictive distribution**:

$$p(y^{new}|y) = \int f(y^{new}|\boldsymbol{\theta})p(\boldsymbol{\theta}|y)d\boldsymbol{\theta}$$

BMA for linear regression

- I'll focus on BMA in the context of a (*simpler*) linear regression:

$$y_i = \alpha + \beta_1 x_{1i} + \beta_2 x_{2i} + \epsilon_i,\ \epsilon_i \sim N(0,\sigma^2),\ i = 1, 2, \ldots, n$$

- Model uncertainty in the context of a linear regression with p predictors amounts to selecting predictors in a model.
- For instance, with $p = 2$ predictors, there are $2^p = 4$ possible models (ignoring potential interaction and nonlinear terms; see **Regression modeling and model space** in *Introduction to BMA linear regression* of **[BMA] bmaregress**):

$$\begin{aligned}
M_1\text{: } y_i &= \alpha + \epsilon_i^{(1)} \\
M_2\text{: } y_i &= \alpha + \beta_1^{(2)} x_{1i} + \epsilon_i^{(2)} \\
M_3\text{: } y_i &= \alpha + \beta_2^{(3)} x_{2i} + \epsilon_i^{(3)} \\
M_4\text{: } y_i &= \alpha + \beta_1^{(4)} x_{1i} + \beta_2^{(4)} x_{2i} + \epsilon_i^{(4)}
\end{aligned}$$

- By construction, $\beta_1^{(1)} = \beta_2^{(1)} = \beta_2^{(2)} = \beta_1^{(3)} = 0$.

- In matrix notation,

$$\mathbf{y} = \alpha \mathbf{1}_n + \mathbf{X}_j \boldsymbol{\beta}_j + \boldsymbol{\epsilon}_j$$

where $\mathbf{X}_j$ and $\boldsymbol{\beta}_j$ are predictors and regression coefficients specific to model M_j.

- Priors for parameters:

$$\begin{aligned} \boldsymbol{\beta}_j | \alpha, \sigma, M_j &\sim N(\mathbf{0}, g\sigma^2(\mathbf{X}_j'\mathbf{X}_j)^{-1}) \\ \alpha | \sigma, M_j &\sim 1 \\ \sigma | M_j &\sim \sigma^{-1} \end{aligned}$$

- Priors for models: BMA treats model M_j as random with a discrete prior $\mathrm{P}(M_j)$ for $j = 1, 2, \ldots, p$.
- Priors for g: fixed value or random hyperprior $p(g)$.

BMA fundamentals

- Posterior distribution of $\boldsymbol{\beta}$ over the model space:

$$g(\boldsymbol{\beta}|\mathbf{y}) = \sum_{j=1}^{2^p} \mathrm{P}(M_j|\mathbf{y}) g(\boldsymbol{\beta}|\mathbf{y}, M_j)$$

- From the Bayes theorem applied to the model space, PMP is defined as

$$\mathrm{P}(M_j|\mathbf{y}) = \frac{f(\mathbf{y}|M_j)\mathrm{P}(M_j)}{p(\mathbf{y})}$$

where $f(\mathbf{y}|M_j)$ is the likelihood of $\mathbf{y}$ under model M_j and $p(\mathbf{y})$ is the marginal probability/likelihood over the model space.

- BMA linear regression coefficient estimates:

$$\widehat{\beta}_1^{\mathrm{BMA}} = \sum_{j=1}^{4} \widehat{\mathrm{P}}(M_j|y)\widehat{\beta}_1^{(j)}$$
$$\widehat{\beta}_2^{\mathrm{BMA}} = \sum_{j=1}^{4} \widehat{\mathrm{P}}(M_j|y)\widehat{\beta}_2^{(j)}$$

- $\widehat{\mathrm{P}}(M_j|y)$ is the estimate of the posterior probability of model M_j (probability of M_j given the observed data y).
- $\widehat{\beta}_1^{(j)}$ and $\widehat{\beta}_2^{(j)}$ are the posterior mean estimates of regression coefficients from model M_j.
- The above BMA estimates correspond to the estimates of posterior means of regression coefficients over the model space, $E(\boldsymbol{\beta}|\mathbf{y})$, based on $g(\boldsymbol{\beta}|\mathbf{y})$.

Toy example

- See **[BMA]** for various real-world BMA examples.
- Simulated data: $n = 200$; $p = 10$; x1 through x10 are independent standard normal.
- DGM:

$$\mathrm{y} = 0.5 + 1.2 \times \mathrm{x2} + 5 \times \mathrm{x10} + N(0,1)$$

```
. webuse bmaintro
(Simulated data for BMA example)

. summarize
```

Variable	Obs	Mean	Std. dev.	Min	Max
y	200	.9944997	4.925052	-13.332	13.06587
x1	200	-.0187403	.9908957	-3.217909	2.606215
x2	200	-.0159491	1.098724	-2.999594	2.566395
x3	200	.080607	1.007036	-3.016552	3.020441
x4	200	.0324701	1.004683	-2.410378	2.391406
x5	200	-.0821737	.9866885	-2.543018	2.133524
x6	200	.0232265	1.006167	-2.567606	3.840835
x7	200	-.1121034	.9450883	-3.213471	1.885638
x8	200	-.0668903	.9713769	-2.871328	2.808912
x9	200	-.1629013	.9550258	-2.647837	2.472586
x10	200	.083902	.8905923	-2.660675	2.275681

```
. bmaregress y x1-x10
Enumerating models ...
Computing model probabilities ...

Bayesian model averaging                       No. of obs         =    200
Linear regression                              No. of predictors  =     10
Model enumeration                                          Groups =     10
                                                           Always =      0
Priors:                                        No. of models      =  1,024
  Models: Beta-binomial(1, 1)                      For CPMP >= .9 =      9
   Cons.: Noninformative                       Mean model size    =  2.479
   Coef.: Zellner´s g
       g: Benchmark, g = 200                   Shrinkage, g/(1+g) = 0.9950
  sigma2: Noninformative                       Mean sigma2        =  1.272

------------------------------------------------------------------------------
           y |      Mean   Std. dev.                          Group        PIP
-------------+----------------------------------------------------------------
          x2 |  1.198105   .0733478                               2          1
         x10 |   5.08343   .0900953                              10          1
          x3 | -.0352493   .0773309                               3     .21123
          x9 |   .004321   .0265725                               9    .051516
          x1 |  .0033937   .0232163                               1    .046909
          x4 | -.0020407   .0188504                               4    .039267
          x5 |  .0005972   .0152443                               5    .033015
          x8 | -.0005639   .0153214                               8    .032742
          x7 | -8.23e-06    .015497                               7    .032386
          x6 | -.0003648   .0143983                               6    .032361
-------------+----------------------------------------------------------------
Always       |
       _cons |  .5907923   .0804774                               0          1
------------------------------------------------------------------------------
Note: Coefficient posterior means and std. dev. estimated from 1,024 models.
Note: Default priors are used for models and parameter g.
```

- Estimation: Model enumeration (few predictors, fixed g); $2^{10} = 1{,}024$ considered models.
- Default priors: Beta-binomial(1,1) for models and fixed $g = 200$.
- Little shrinkage: $g/(1+g) = 0.995$ close to 1.
- Mean model size is 2.48.
- Important predictors: Estimated PIPs of `x2` and `x10` are 1; others are small.
- BMA coefficient estimates for `x2` and `x10` (1.2 and 5.1) are close to the true values.
- BMA estimates of other coefficients are close to zero.
- BMA estimates are based on 1,024 models; see *Interpretation of BMA regression coefficients* in **[BMA] bmaregress**.

- Store BMA estimation results for later use:

```
. bmaregress, saving(bmareg)
note: file bmareg.dta saved.
. estimates store bmareg
```

- As with other Bayesian commands, we save the BMA MCMC simulation file first by using `bmaregress`'s `saving()` option (available on replay).
- We then use `estimates store` to save the BMA estimation results.

Classical linear regression

```
. regress y x1-x10
```

Source	SS	df	MS
Model	4607.24837	10	460.724837
Residual	219.723235	189	1.1625568
Total	4826.9716	199	24.2561387

Number of obs	=	200
F(10, 189)	=	396.30
Prob > F	=	0.0000
R-squared	=	0.9545
Adj R-squared	=	0.9521
Root MSE	=	1.0782

y	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
x1	.0753537	.0781737	0.96	0.336	-.0788513	.2295587
x2	1.18854	.0716658	16.58	0.000	1.047172	1.329907
x3	-.1871012	.0789484	-2.37	0.019	-.3428344	-.0313679
x4	-.0459335	.0785503	-0.58	0.559	-.2008813	.1090144
x5	.0343498	.0793095	0.43	0.665	-.1220956	.1907953
x6	-.0149194	.0767357	-0.19	0.846	-.1662879	.136449
x7	.007174	.0831239	0.09	0.931	-.1567958	.1711437
x8	-.0384917	.0810626	-0.47	0.635	-.1983953	.1214119
x9	.0968948	.0817218	1.19	0.237	-.0643093	.2580989
x10	5.13251	.0877447	58.49	0.000	4.959426	5.305595
_cons	.617996	.0791152	7.81	0.000	.4619337	.7740582

- Compare the estimates:

	regress	bmaregress
y		
x1	0.075	0.003
	(0.078)	(0.023)
x2	1.189	1.198
	(0.072)	(0.073)
x3	-0.187	-0.035
	(0.079)	(0.077)
x4	-0.046	-0.002
	(0.079)	(0.019)
x5	0.034	0.001
	(0.079)	(0.015)
x6	-0.015	-0.000
	(0.077)	(0.014)
x7	0.007	-0.000
	(0.083)	(0.015)
x8	-0.038	-0.001
	(0.081)	(0.015)
x9	0.097	0.004
	(0.082)	(0.027)
x10	5.133	5.083
	(0.088)	(0.090)
_cons	0.618	0.591
	(0.079)	(0.080)
Number of observations	200	200

- BMA coefficients for "unimportant" predictors are shrunk toward zero.
- Let's continue with our BMA analysis:

```
. estimates restore bmareg
(results bmareg are active now)
```

Credible intervals (CrIs)

- For computational reasons, `bmaregress` does not compute CrIs by default.
- For fixed g, analytical closed-form formulas are available for BMA posterior means and standard deviations.
- The formulas for CrIs are not as straightforward; `bmaregress` computes them from the posterior sample of parameters.
- Obtaining the posterior sample of parameters requires a potentially time-consuming simulation and may not always be needed, depending on a BMA analysis objective.
- But this sample can be generated by using `bmacoefsample` following `bmaregress`.
- Many standard Bayesian postestimation commands such as `bayesstats summary` can then be used.

```
. bmacoefsample, rseed(18) mcmcsize(1000)
Simulation (1000): . done
. bayesstats summary
Posterior summary statistics                      MCMC sample size =     1,000
```

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
y						
x1	.0017904	.0176576	.000549	0	0	.0230942
x2	1.201273	.0695129	.00224	1.201107	1.06427	1.337961
x3	-.0361735	.0755013	.002435	0	-.2537224	0
x4	-.0010145	.0156635	.000495	0	0	0
x5	.0003393	.0114519	.000383	0	0	0
x6	-.0003742	.0145684	.000478	0	0	0
x7	.0002788	.0156012	.000423	0	0	0
x8	-.0003383	.0152805	.000483	0	0	0
x9	.0048314	.0291115	.000906	0	0	.0924737
x10	5.08115	.0841466	.002581	5.079152	4.913381	5.247999
_cons	.5879177	.0841129	.002632	.5879514	.4153159	.7560713
sigma2	1.273245	.1288853	.003956	1.266904	1.045943	1.55155
g	200	0	0	200	200	200

Influential models

- Compute PMPs to identify influential models:

```
. bmastats models
Computing model probabilities ...
Model summary          Number of models:
                                Visited = 1,024
                               Reported =     5

─────────────┬────────────────────────────────
             │   Analytical PMP     Model size
─────────────┼────────────────────────────────
Rank         │
           1 │            .6292              2
           2 │            .1444              3
           3 │            .0258              3
           4 │            .0246              3
           5 │           .01996              3
─────────────┴────────────────────────────────

Variable-inclusion summary
─────────────┬────────────────────────────────────────────────────────
             │    Rank       Rank       Rank       Rank       Rank
             │      1          2          3          4          5
─────────────┼────────────────────────────────────────────────────────
          x2 │      x          x          x          x          x
         x10 │      x          x          x          x          x
          x3 │                 x
          x9 │                            x
          x1 │                                       x
          x4 │                                                  x
─────────────┴────────────────────────────────────────────────────────
Legend:
  x - estimated
```

- Cumulative PMPs (CPMPs):

```
. bmastats models, cumulative
Computing model probabilities ...
Model summary          Number of models:
                                Visited = 1,024
                               Reported =     5
```

	Analytical CPMP	Model size
Rank		
1	.6292	2
2	.7736	3
3	.7994	3
4	.824	3
5	.844	3

Variable-inclusion summary

	Rank 1	Rank 2	Rank 3	Rank 4	Rank 5
x2	x	x	x	x	x
x10	x	x	x	x	x
x3		x			
x9			x		
x1				x	
x4					x

Legend:
  x - estimated

- Specify a CPMP cutoff:

```
. bmastats models, cumulative(0.75)
Computing model probabilities ...
Model summary              Number of models:
                                    Visited = 1,024
                                   Reported =     2
```

	Analytical CPMP	Model size
Rank		
1	.6292	2
2	.7736	3

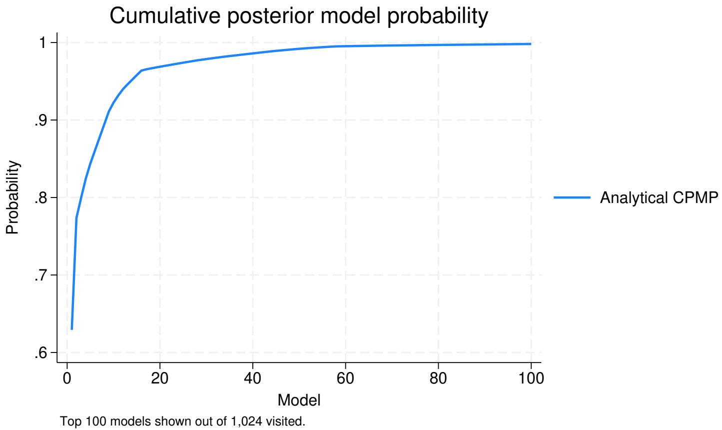
Variable-inclusion summary

	Rank 1	Rank 2
x2	x	x
x10	x	x
x3		x

```
Legend:
  x - estimated
```

- Plot CPMPs:

```
. bmagraph pmp, cumulative
note: frequency estimates not available with model enumeration; option
      nofreqline implied.
```



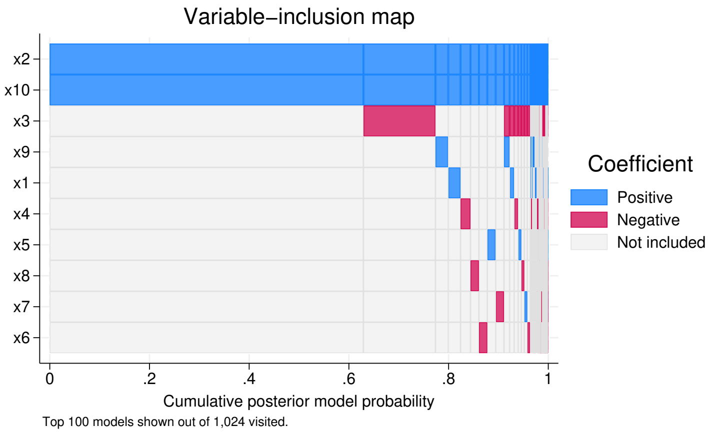
Important predictors

- Report PIPs:

```
. bmastats pip

Posterior inclusion probability (PIP)

No. of obs          =    200
No. of predictors   =     10
            Groups  =     10
            Always  =      0
          Reported  =     10
No. of models       =  1,024
Mean model size     =  2.479

-------------------------------------
             |        PIP       Group
-------------+-----------------------
          x2 |          1           2
         x10 |          1          10
          x3 |     .21123           3
          x9 |    .051516           9
          x1 |    .046909           1
          x4 |    .039267           4
          x5 |    .033015           5
          x8 |    .032742           8
          x7 |    .032386           7
          x6 |    .032361           6
-------------+-----------------------
Always       |
       _cons |          1           0
-------------------------------------
Note: Using analytical PMPs.
```

- Variable-inclusion map:

```
. bmagraph varmap
Computing model probabilities ...
```



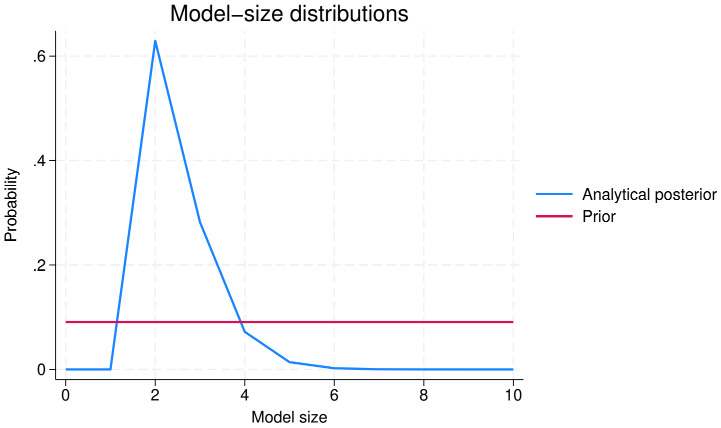
Model-size distribution

```
. bmastats msize

Model-size summary

Number of models = 1,024
Model size:
  Minimum =  0
  Maximum = 10
```

	Mean	Median
Prior		
Analytical	5.0000	5
Posterior		
Analytical	2.4794	2

```
Note: Frequency summaries not available.
```

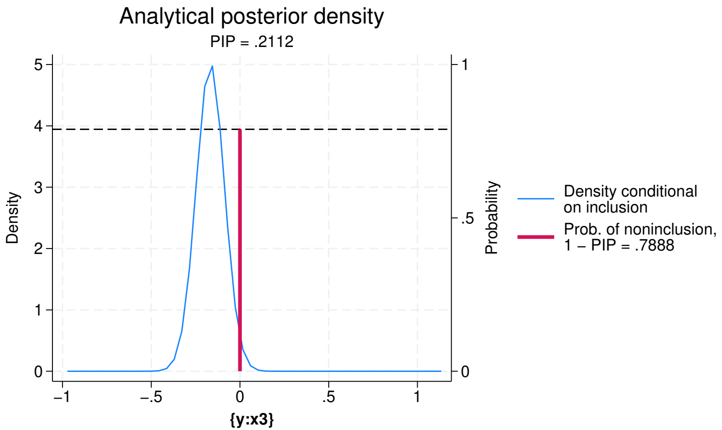
```
. bmagraph msize
note: frequency posterior model-size distribution not available.
```



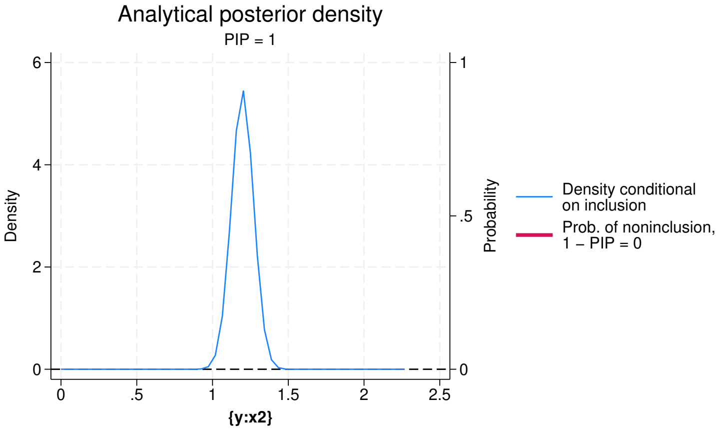
Posterior distribution of coefficients

- Mixture of a point mass at zero with $1 - PIP$ and a continuous density conditional on inclusion:

```
. bmagraph coefdensity {x3}
```



```
. bmagraph coefdensity {x2}
```



Jointness

- Tendency of the predictors to appear together, separately, or independently in the models:

```
. bmastats jointness x2 x10
Variables: x2 x10

──────────────────────────────────────
                      │   Jointness
──────────────────────┼───────────────
      Doppelhofer-Weeks │      75.947
       Ley-Steel type 1 │           1
       Ley-Steel type 2 │    3.59e+35
               Yule´s Q │           1
──────────────────────────────────────
Notes: Using analytical PMPs. See
       thresholds.
```

- x2 and x10 are strong *complements*—they tend to be included in the models together.
- Strong or decisive jointness; see **[BMA] bmastats jointness** for the thresholds or click on blue "thresholds" in the Stata output.

BMA predictions

- Posterior predictive means:

```
. bmapredict pmean, mean
note: computing analytical posterior predictive means.
```

- Predictive CrIs:

```
. bmacoefsample, saving(bmacoef)
note: saving existing MCMC simulation results without resampling; specify
      option simulate to force resampling in this case.
note: file bmacoef.dta saved.

. bmapredict cri_l cri_u, cri rseed(18)
note: computing credible intervals using simulation.

Computing predictions ...
```

- Summary:

```
. summarize y pmean cri*
```

Variable	Obs	Mean	Std. dev.	Min	Max
y	200	.9944997	4.925052	-13.332	13.06587
pmean	200	.9944997	4.783067	-13.37242	12.31697
cri_l	200	-1.24788	4.787499	-15.66658	10.03054
cri_u	200	3.227426	4.779761	-11.06823	14.58301

Sensitivity analysis: Random g-prior

- Random prior (hyperprior) for g instead of treating it as fixed.
- Hyperpriors are often suggested for robustness.
- Specify a hyper-g prior with hyperparameter 4 for g:

```
. bmaregress y x1-x10, gprior(hyperg 4) rseed(18)
Burn-in ...
Simulation ...
Computing model probabilities ...

Bayesian model averaging                          No. of obs        =    200
Linear regression                                 No. of predictors =     10
MC3 and adaptive MH sampling                                 Groups =     10
                                                             Always =      0
                                                  No. of models     =     27
                                                     For CPMP >= .9 =      2
Priors:                                           Mean model size   =  2.175
  Models: Beta-binomial(1, 1)                     Burn-in           =  2,500
   Cons.: Noninformative                          MCMC sample size  = 10,000
   Coef.: Zellner's g                             Acceptance rate   = 0.3838
       g: Hyper-g(4)
  sigma2: Noninformative                          Mean sigma2       =  1.184

Sampling correlation = 0.9985
```

y	Mean	Std. dev.	Group	PIP
x2	1.205111	.0706146	2	1
x10	5.101085	.0869608	10	1
x3	-.0153289	.0534981	3	.0921
x4	-.00075	.0112903	4	.0151
x9	.0010838	.0132084	9	.0137
x1	.0008948	.0118064	1	.0124
x5	.0002045	.008905	5	.0121
x6	-.0001291	.00818	6	.0111
Always				
_cons	.5871921	.0774449	0	1

Note: Coefficient posterior means and std. dev. estimated from 27 models.
Note: Default prior is used for models.
Note: 2 predictors with PIP less than .01 not shown.

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred.	interval]
g	1991.648	9547.263	186.39	1129.102	330.1158	7337.703
Shrinkage	.9989299	.0007563	.000016	.9991151	.9969799	.9998637

- Estimation: MC3 and adaptive MH sampling.
- Only 27 models explored compared with the total of 1,024.
- Mean model size is 2.18.
- The header now reports some standard MCMC summaries.
- The sampling correlation is also reported. (More about this later.)
- Analytical formulas are not available.
- BMA results are similar, but PIPs for all but the `x2` and `x10` coefficients are smaller.
- Parameter g (and shrinkage) are now random, and thus the posterior summaries are reported for them.
- Let's store these BMA results for later comparison:

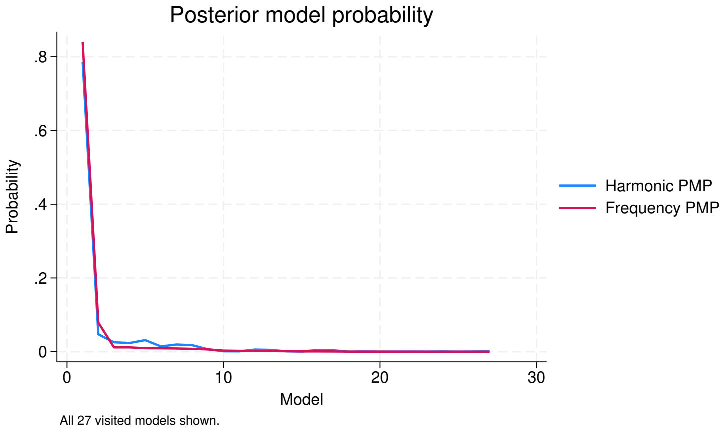
```
. bmaregress, saving(bmareg_hyperg)
note: file bmareg_hyperg.dta saved.
. estimates store bmareg_hyperg
```

Model convergence

- Sampling correlation is used to evaluate the MCMC convergence of the BMA model.
- This is the correlation between the analytical (whenever available) and frequency PMPs.
- The estimated sampling correlation of 0.9985 does not indicate any convergence issues.
- See *Convergence of BMA* in **[BMA] bmaregress** for details.

- We can also explore the BMA convergence visually:

```
. bmagraph pmp
```



Sensitivity analysis: Informative prior

- We can consider a more informative prior for the model space:

```
. bmaregress y x1-x10, mprior(binomial x2 x10 0.5 x1 x3-x9 0.05) saving(bmareg_
> inf)
Enumerating models ...
Computing model probabilities ...
Bayesian model averaging                          No. of obs          =    200
Linear regression                                 No. of predictors   =     10
Model enumeration                                             Groups  =     10
                                                              Always  =      0
Priors:                                           No. of models       =  1,024
  Models: Binomial, IP varies                         For CPMP >= .9  =      1
   Cons.: Noninformative                          Mean model size     =  2.062
   Coef.: Zellner´s g
       g: Benchmark, g = 200                      Shrinkage, g/(1+g)  = 0.9950
  sigma2: Noninformative                          Mean sigma2         =  1.277
```

y	Mean	Std. dev.	Group	PIP
x2	1.201574	.0729557	2	1
x10	5.080061	.0899387	10	1
x3	-.0051795	.0320662	3	.031299
Always				
_cons	.5879401	.0803296	0	1

```
Note: Coefficient posterior means and std. dev. estimated from 1,024 models.
Note: Default prior is used for parameter g.
Note: 7 predictors with PIP less than .01 not shown.
file bmareg_inf.dta saved.
. estimates store bmareg_inf
```

Log predictive-score (LPS)

- LPS is the negative of the log of the posterior predictive density evaluated at an observation.
- The smaller the LPS value, the better the model fit.
- We can use LPS to compare the model fit of different BMA models:

```
. bmastats lps bmareg bmareg_hyperg bmareg_inf, compact
Log predictive-score (LPS)
Number of observations = 200
```

LPS	Mean	Minimum	Maximum
bmareg	1.485701	1.040332	6.110174
bmareg_hyp~g	1.484734	1.004092	6.480865
bmareg_inf	1.489453	1.041369	6.272715

```
Notes: Results using analytical and frequency PMPs.
       Result bmareg_hyperg has the smallest mean LPS.
```

- The `hyperg` model is reported to have the smallest LPS value, but all considered models have similar LPS values.
- We can use LPS to compare in-sample and out-of-sample predictive performance of models; see **[BMA] bmastats lps**.
- We can also use prediction mean squared error and empirical coverage of CrIs to compare predictive performance of BMA models; see **[BMA]**.

Summary

- BMA may not be your final solution to every regression analysis, but, at the very least, it is definitely a beneficial exploratory tool!
- You can use BMA for prediction and for inference to account for model uncertainty.
- If you need to choose a model, you can use BMA's PMPs to guide your decision in a principled and unified way.
- You can use BMA to learn about interrelations between predictors across the model space.
- You can use BMA to explore the sensitivity of your results to various assumptions about the importance of different models and predictors.

References

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