BMA & Distributions

Hoff Chapter 9, Liang et al 2008, Hoeting et al (1999), Clyde & George (2004)

October 31, 2022

Bartlett's Paradox

The Bayes factor for comparing γ to the null model:

$$BF(\gamma : \gamma 0) = (1+g)^{(n-1-p_\gamma)/2}(1+g(1-R^2_\gamma))^{-(n-1)/2}$$

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- why is this a paradox?

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- BF converges to a fixed constant $(1+g)^{n-1-p_\gamma/2}$ (does not go to infinity

"Information Inconsistency" see Liang et al JASA 2008

Mixtures of g priors & Information consistency

- Need $BF \to \infty$ if $R^2_\gamma \to 1$
- Put a prior on g

$$BF(\gamma : \gamma_0) = \frac{C \int (1+g)^{(n-1-p_\gamma)/2}(1+g(1-R^2_\gamma))^{-(n-1)/2}\pi(g)dg}{C}$$

- interchange limit and integration as $R^2 \to 1$ want

$$E_g[(1+g)^{(n-1-p_\gamma)/2}]$$

  to diverge
- hyper-g prior (Liang et al JASA 2008)

$$p(g) = \frac{a-2}{2}(1+g)^{-a/2}$$

  or $g/(1+g) \sim Beta(1,(a-2)/2)$
- prior expectation converges if $a > n + 1 - p_\gamma$
- Consider minimal model $p_\gamma = 1$ and $n = 3$ (can estimate intercept, one coefficient, and σ^2, then $a > 3$ integral exists
- For $2 < a \leq 3$ integral diverges and resolves the information paradox!

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- robust prior (Bayarri et al Annals of Statistics 2012
- Intrinsic prior (Womack et al JASA 2015)

All have prior tails for β that behave like a Cauchy distribution and (the latter 4) marginal likelihoods that can be computed using special hypergeometric functions (${}_2F_1$, Appell F_1)

Computation

If $p > 35$ enumeration is difficult

- Gibbs sampler or Random-Walk algorithm on γ

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- slow convergence/poor mixing with high correlations
- Metropolis Hastings algorithms more flexibility (swap pairs of variables)

Diabetes Example from Hoff $p = 64$

```
> set.seed(8675309)
> source("yX.diabetes.train.txt")
> diabetes.train = as.data.frame(diabetes.train)
> source("yX.diabetes.test.txt")
> diabetes.test = as.data.frame(diabetes.test)
> colnames(diabetes.test)[1] = "y"
> str(diabetes.train)
'data.frame':        342 obs. of  65 variables:
 $ y       : num  -0.0147 -1.0005 -0.1444 0.6987 -0.2222 ...
 $ age     : num  0.7996 -0.0395 1.7913 -1.8703 0.113 ...
 $ sex     : num  1.064 -0.937 1.064 -0.937 -0.937 ...
 $ bmi     : num  1.296 -1.081 0.933 -0.243 -0.764 ...
 $ map     : num  0.459 -0.553 -0.119 -0.77 0.459 ...
 $ tc      : num  -0.9287 -0.1774 -0.9576 0.256 0.0826 ...
 $ ldl     : num  -0.731 -0.402 -0.718 0.525 0.328 ...
 $ hdl     : num  -0.911 1.563 -0.679 -0.757 0.171 ...
 $ tch     : num  -0.0544 -0.8294 -0.0544 0.7205 -0.0544 ...
 $ ltg     : num  0.4181 -1.4349 0.0601 0.4765 -0.6718 ...
```

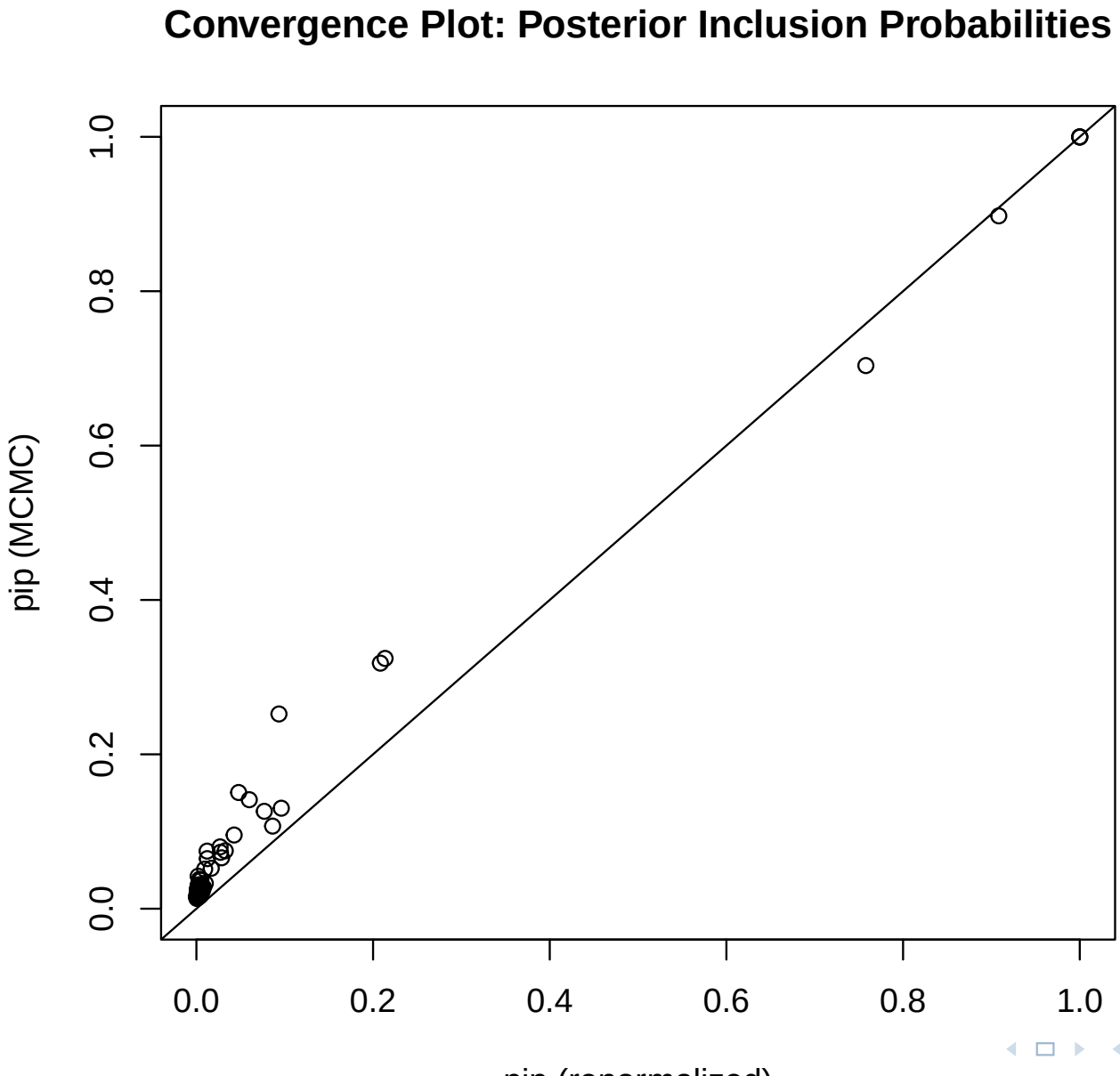
MCMC with BAS

```
> diabetes.bas = bas.lm(y ~ ., data=diabetes.train,
+                       prior = "JZS",
+                       method="MCMC",
+                       n.models = 10000,
+                       MCMC.iterations=150000,
+                       thin = 10,
+                       initprobs="eplogp",
+                       force.heredity=FALSE)
> system.time(bas.lm(y ~ ., data=diabetes.train,
+                      prior = "JZS",
+                      method="MCMC", n.models = 10000,
+                      MCMC.iterations=150000,
+                      thin = 10,  initprobs="eplogp",
+                      force.heredity=FALSE))
   user  system elapsed
  7.100   0.313   7.423
>
```

Time is in seconds

Diagnostics

```
> diagnostics(diabetes.bas, type="pip")
```

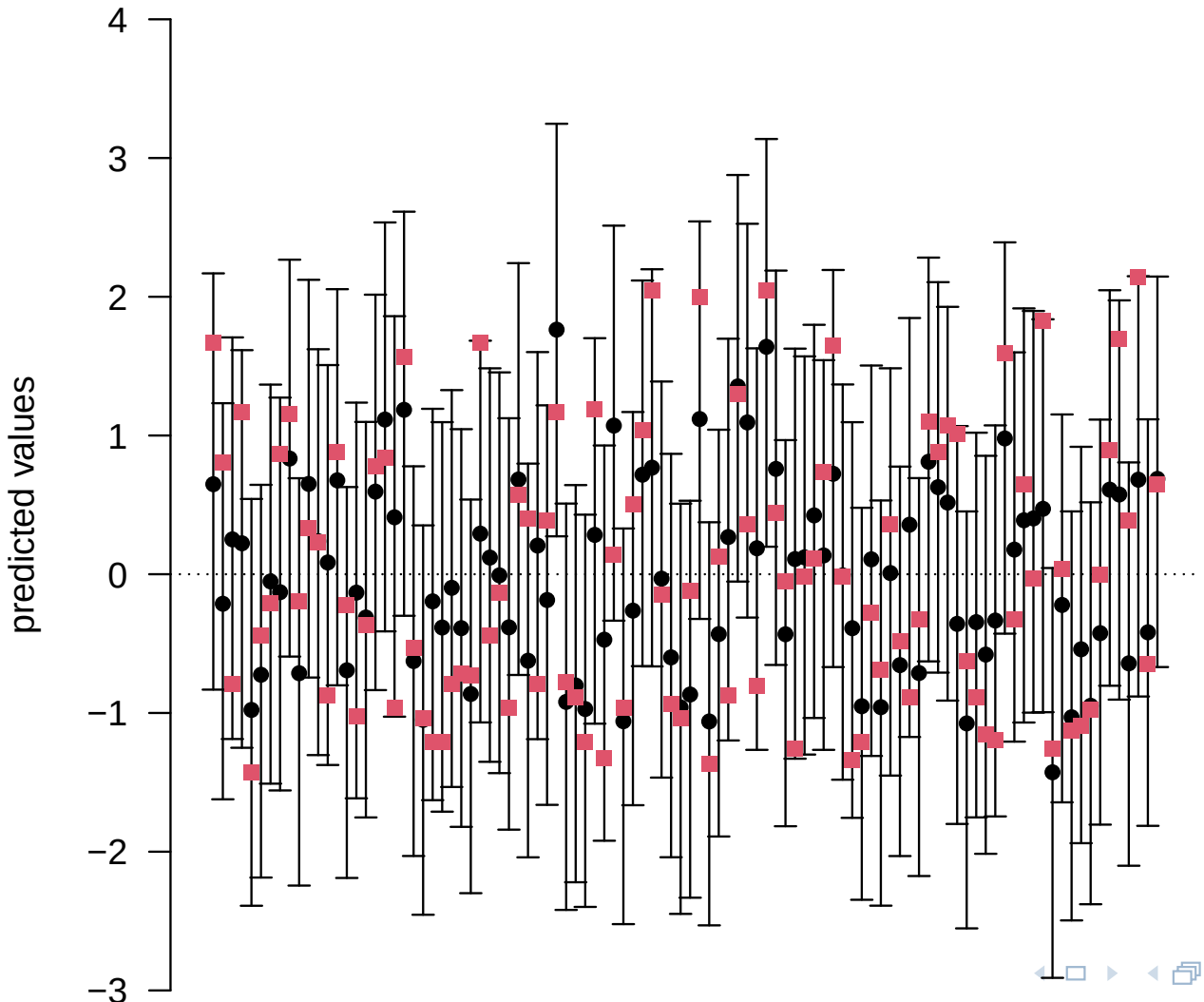


Prediction

```
> pred.bas = predict(diabetes.bas,
+                    newdata=diabetes.test,
+                    estimator="BMA",
+                    se=TRUE)
> mean((pred.bas$fit- diabetes.test$y)^2)
[1] 0.4552798
```

95% prediction intervals

```
> ci.bas = confint(pred.bas); plot(ci.bas)
NULL
> points(diabetes.test$y, col=2, pch=15)
```



Selection and Prediction

- BMA - optimal for squared error loss Bayes
- HPM: Highest Posterior Probability model (not optimal for prediction) but for selection
- MPM: Median Probabilty model (select model where PIP $>$ 0.5) (optimal under certain conditions; nested models)
- BPM: Best Probability Model - Model closest to BMA under loss (usually includes more predictors than HPM or MPM)

Selection

```
> pred.bas = predict(diabetes.bas,
+                    newdata=diabetes.test,
+                    estimator="BPM",
+                    se=TRUE)
> #MSE
> mean((pred.bas$fit- diabetes.test$y)^2)
[1] 0.4740667
> #Coverage
> ci.bas = confint(pred.bas)
> mean(diabetes.test$y > ci.bas[,1] &
+      diabetes.test$y < ci.bas[,2])
[1] 0.98
```

Alternatives to MCMC

- "Stochastic Search" (no guarantee samples represent posterior)

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- If $p > n$, can use a generalized inverse, but requires care for prior on γ!

Model averaging versus Model Selection – what are objectives?

Effect Estimation

- Coefficients in each model are adjusted for other variables in the model
- OLS: leave out a predictor with a non-zero coefficient then estimates are biased!
- Model Selection in the presence of high correlation, may leave out "redundant" variables;
- improved MSE for prediction (Bias-variance tradeoff)
- in BMA all variables are included, but coefficients are shrunk to 0
- Care needed for "causal" questions and confounder adjustment! With confounding, should not use plain BMA. Need to change prior to include potential confounders (advanced topic)